Association between weight history and PRL params

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Purpose: to determine whether the PRL hDDMrl parameters can be associated to the behavioral characteristics of participants, after accounting for the individual differences explained by the questionnaires data.

```
## here() starts at /Users/corrado/Documents/papers/ED_patients
```

```
## CmdStan path set to: /Users/corrado/cmdstan
```

```
## Warning in find_bad_controls(THRESHOLD): NA introdotti per coercizione
```

```
## `summarise()` has grouped output by 'is_patient'. You can override using the `.groups` argument.
```

```
## [1] 176
```

```
## [1] 38
```

```
##     subj_idx      subj_code           a_neither          v_food
##  Min.   :  0.0   Length:131         Min.   :0.7961   Min.   :-5.315
##  1st Qu.: 72.5   Class  :character  1st Qu.:1.1191   1st Qu.: 1.257
##  Median :141.0   Mode   :character  Median :1.3104   Median : 1.928
##  Mean   :147.7                      Mean   :1.3008   Mean   : 2.007
##  3rd Qu.:221.0                      3rd Qu.:1.4680   3rd Qu.: 2.695
##  Max.   :302.0                      Max.   :1.7508   Max.   : 5.786
##                                                      NA's   :7
##     v_social          t_food           t_social          z_food
##  Min.   :0.8035   Min.   :0.06597   Min.   :0.0757   Min.   :0.4666
##  1st Qu.:1.7820   1st Qu.:0.14400   1st Qu.:0.1546   1st Qu.:0.4887
##  Median :2.2819   Median :0.18360   Median :0.1965   Median :0.4944
##  Mean   :2.4186   Mean   :0.18983   Mean   :0.1973   Mean   :0.4943
##  3rd Qu.:3.1090   3rd Qu.:0.22966   3rd Qu.:0.2281   3rd Qu.:0.5007
##  Max.   :7.5216   Max.   :0.60062   Max.   :0.5384   Max.   :0.5172
##  NA's   :10       NA's   :7         NA's   :10       NA's   :7
##     z_social      alpha_neg_food   alpha_neg_social alpha_pos_food
##  Min.   :0.4702   Min.   :-6.167   Min.   :-2.766   Min.   :-7.2959
##  1st Qu.:0.4918   1st Qu.: 1.254   1st Qu.: 1.615   1st Qu.:-0.7276
##  Median :0.4974   Median : 4.222   Median : 4.688   Median : 1.2491
##  Mean   :0.4970   Mean   : 3.442   Mean   : 3.686   Mean   : 0.8231
##  3rd Qu.:0.5030   3rd Qu.: 5.833   3rd Qu.: 5.878   3rd Qu.: 2.5662
##  Max.   :0.5220   Max.   : 6.877   Max.   : 7.106   Max.   : 4.1822
##  NA's   :10       NA's   :7        NA's   :10       NA's   :7
##  alpha_pos_social    bsq14_tot        ros_tot      dass21_stress
##  Min.   :-3.1442   Min.   :14.00   Min.   :11.00   Min.   : 0.000
##  1st Qu.: 0.0122   1st Qu.:29.00   1st Qu.:17.00   1st Qu.: 7.000
##  Median : 2.1575   Median :46.00   Median :23.00   Median : 9.000
##  Mean   : 1.7165   Mean   :45.23   Mean   :22.68   Mean   : 9.867
##  3rd Qu.: 3.2640   3rd Qu.:58.00   3rd Qu.:27.00   3rd Qu.:13.000
##  Max.   : 4.3755   Max.   :79.00   Max.   :39.00   Max.   :19.000
##  NA's   :10        NA's   :18      NA's   :18      NA's   :18
##  dass21_anxiety     dass21_dep          sias           mps_ps
##  Min.   : 0.000   Min.   : 0.000   Min.   : 5.00   Min.   :11.00
##  1st Qu.: 3.000   1st Qu.: 4.000   1st Qu.:19.00   1st Qu.:19.00
##  Median : 5.000   Median : 7.000   Median :31.00   Median :22.00
##  Mean   : 5.699   Mean   : 8.018   Mean   :30.62   Mean   :22.42
##  3rd Qu.: 8.000   3rd Qu.:12.000   3rd Qu.:41.00   3rd Qu.:26.00
##  Max.   :16.000   Max.   :19.000   Max.   :64.00   Max.   :34.00
##  NA's   :18       NA's   :18       NA's   :18      NA's   :18
##      mps_o          mps_cmd         mps_pepc        orto_tot
##  Min.   :10.00   Min.   :19.00   Min.   : 8.00   Min.   : 7.00
##  1st Qu.:20.00   1st Qu.:36.00   1st Qu.:14.00   1st Qu.:15.00
##  Median :22.00   Median :43.00   Median :18.00   Median :19.00
##  Mean   :22.24   Mean   :43.99   Mean   :18.49   Mean   :18.14
##  3rd Qu.:26.00   3rd Qu.:51.00   3rd Qu.:22.00   3rd Qu.:22.00
##  Max.   :30.00   Max.   :67.00   Max.   :37.00   Max.   :26.00
##  NA's   :18      NA's   :18      NA's   :18      NA's   :18
##     dieting          bulimia        oral_control    eat26_at_risk
##  Min.   : 0.000   Min.   : 3.000   Min.   : 0.000   Min.   :0.0000
##  1st Qu.: 2.000   1st Qu.: 3.000   1st Qu.: 0.000   1st Qu.:0.0000
##  Median : 4.000   Median : 3.000   Median : 1.000   Median :0.0000
##  Mean   : 8.324   Mean   : 5.481   Mean   : 3.093   Mean   :0.2685
##  3rd Qu.:11.000   3rd Qu.: 8.000   3rd Qu.: 3.000   3rd Qu.:1.0000
##  Max.   :33.000   Max.   :13.000   Max.   :19.000   Max.   :1.0000
##  NA's   :23       NA's   :23       NA's   :23       NA's   :23
##    is_patient        group               eat26
##  Min.   :0.0000   Length:131          Min.   : 3.0
##  1st Qu.:0.0000   Class :character   1st Qu.: 6.0
##  Median :0.0000   Mode  :character   Median :10.0
##  Mean   :0.2901                      Mean   :16.9
##  3rd Qu.:1.0000                      3rd Qu.:23.0
##  Max.   :1.0000                      Max.   :59.0
##                                      NA's   :23
```

```
## 
##  0  1  2 
## 70 12 38
```

```
## 
##  0  1  2 
## 70 12 38
```

```
## [1] "ordered" "factor"
```

```
## 
##  0  1  2 
## 56 10 37
```

```
## 
##  0  2 
## 56 37
```

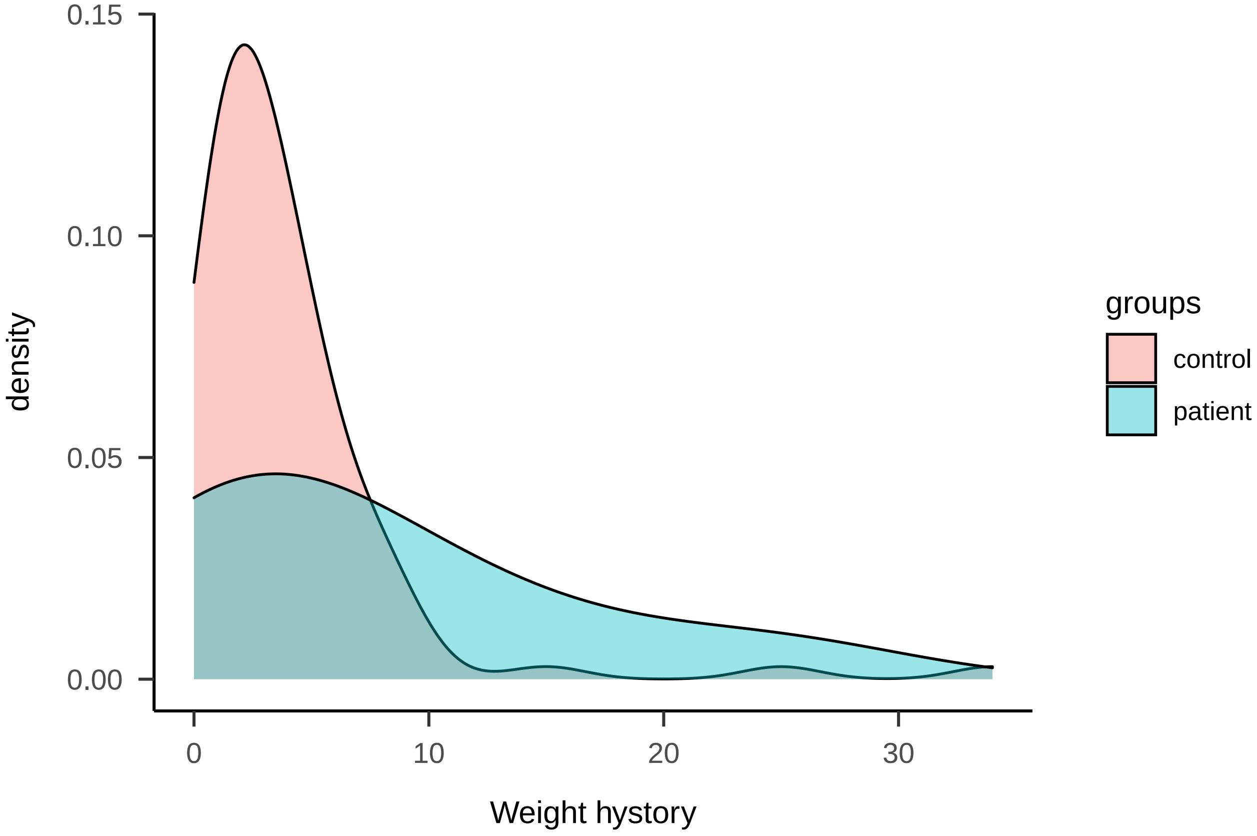
```
## Warning in if (class(df[, colName]) == "integer" | class(df[, colName]) == : la
## condizione ha lunghezza > 1 e solo il primo elemento sarà utilizzato
```

```
## 
##  0  1
## 56 37
```

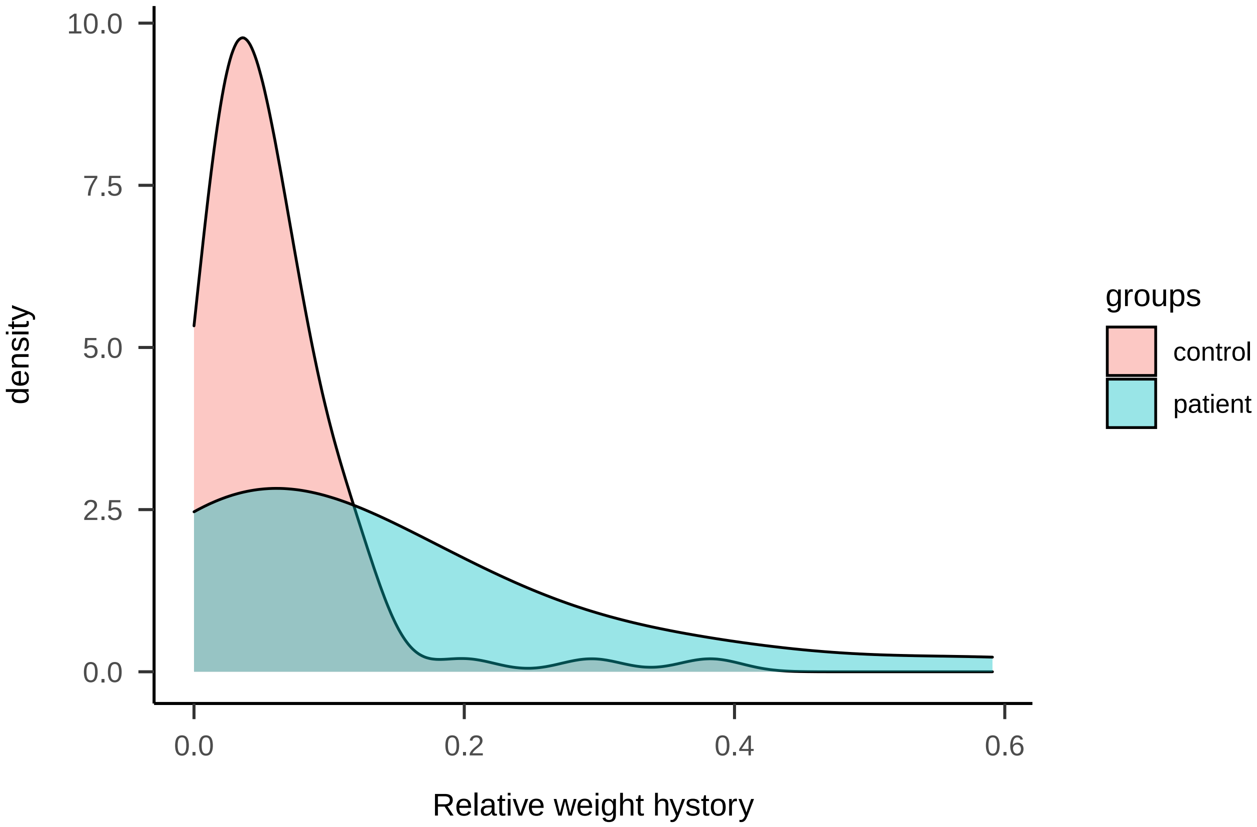
```
## Warning in if (class(df[, colName]) == "integer" | class(df[, colName]) == : la
## condizione ha lunghezza > 1 e solo il primo elemento sarà utilizzato
```

```
##
##  0  1
## 75 37
```

```
## Warning: Removed 21 rows containing non-finite values (stat_density).
```



```
## Warning: Removed 20 rows containing non-finite values (stat_density).
```



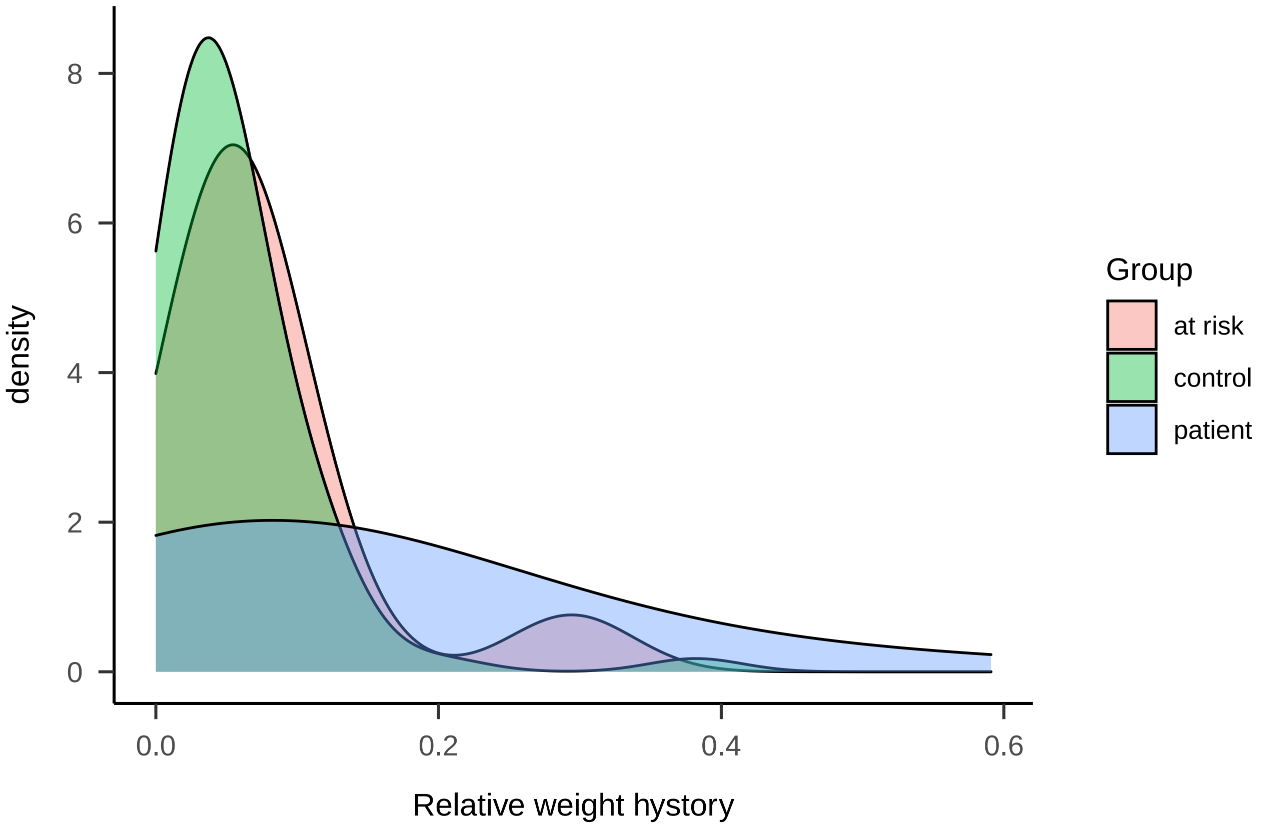
Split participants in patients, at-risk, and control

```
dd$Group <- factor(
  ifelse(dd$group == 0, "control", ifelse(dd$group == 1, "at risk", "patient")))

foo <- dd[!is.na(dd$Group), ]
table(foo$Group)
```

```
##
## at risk control patient
##      12      68      37
```

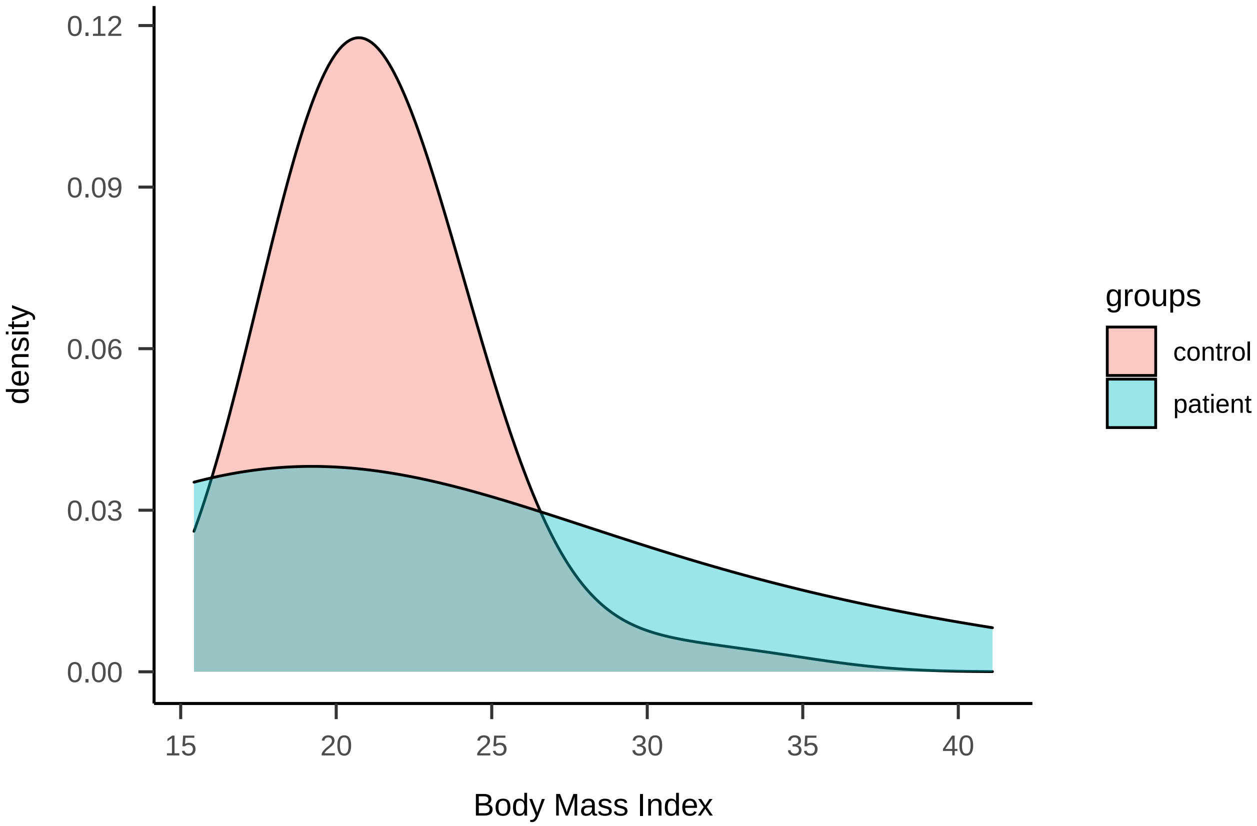
```
## Warning: Removed 16 rows containing non-finite values (stat_density).
```



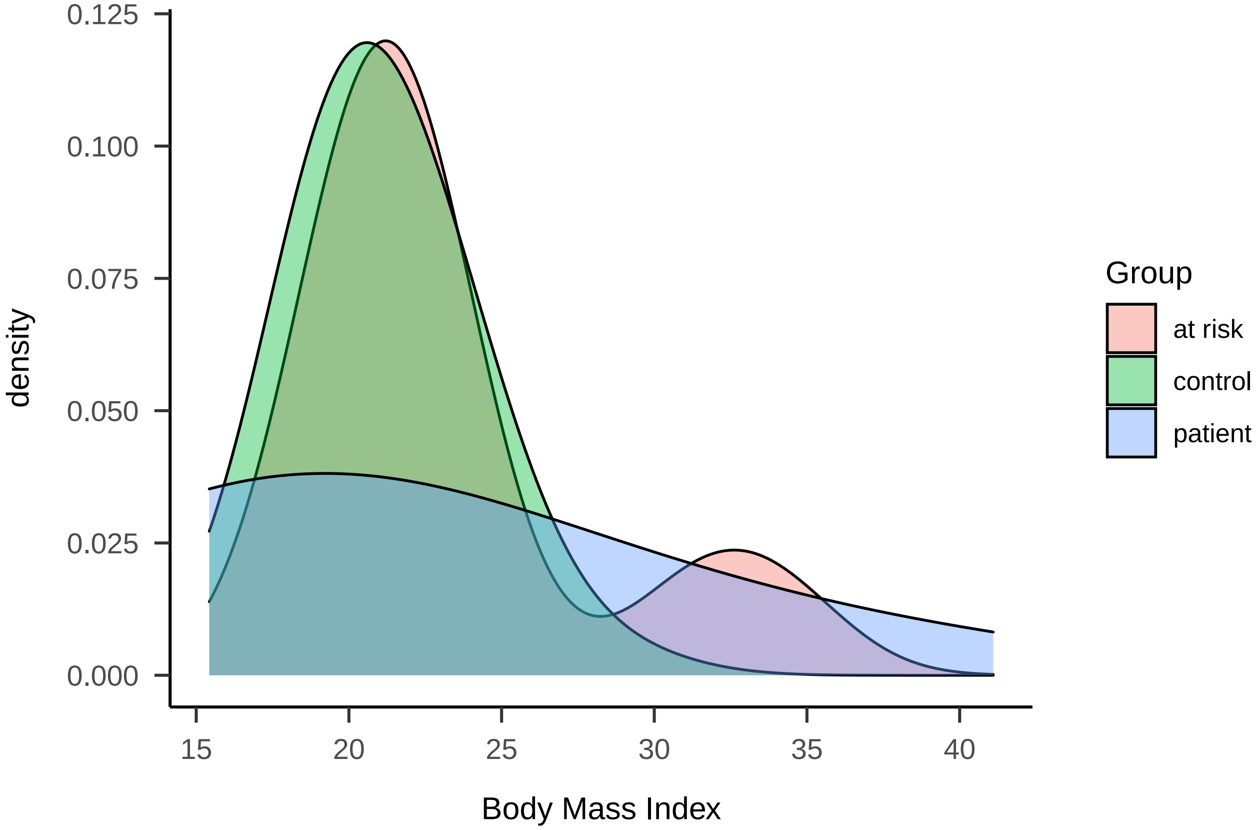
The at-risk group is very similar to the control group, and both differs from the patient group.

```
# Compute BMI
foo$BMI <- foo$present_weight / (foo$height/100)^2
foo$bmi <- as.numeric(scale(foo$BMI))
```

```
## Warning: Removed 16 rows containing non-finite values (stat_density).
```



```
## Warning: Removed 16 rows containing non-finite values (stat_density).
```



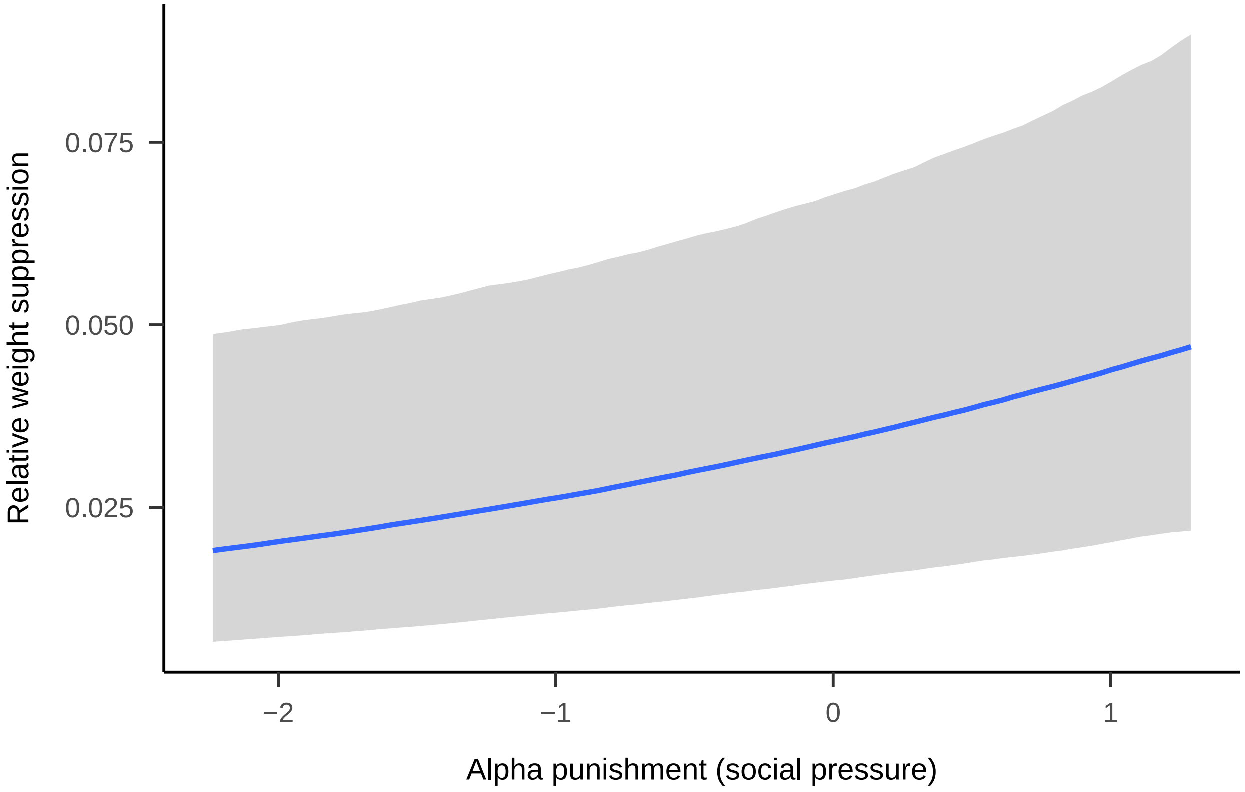
```
##          [,1] [,2]
## at risk    1    0
## control    0    1
## patient   -1   -1
```

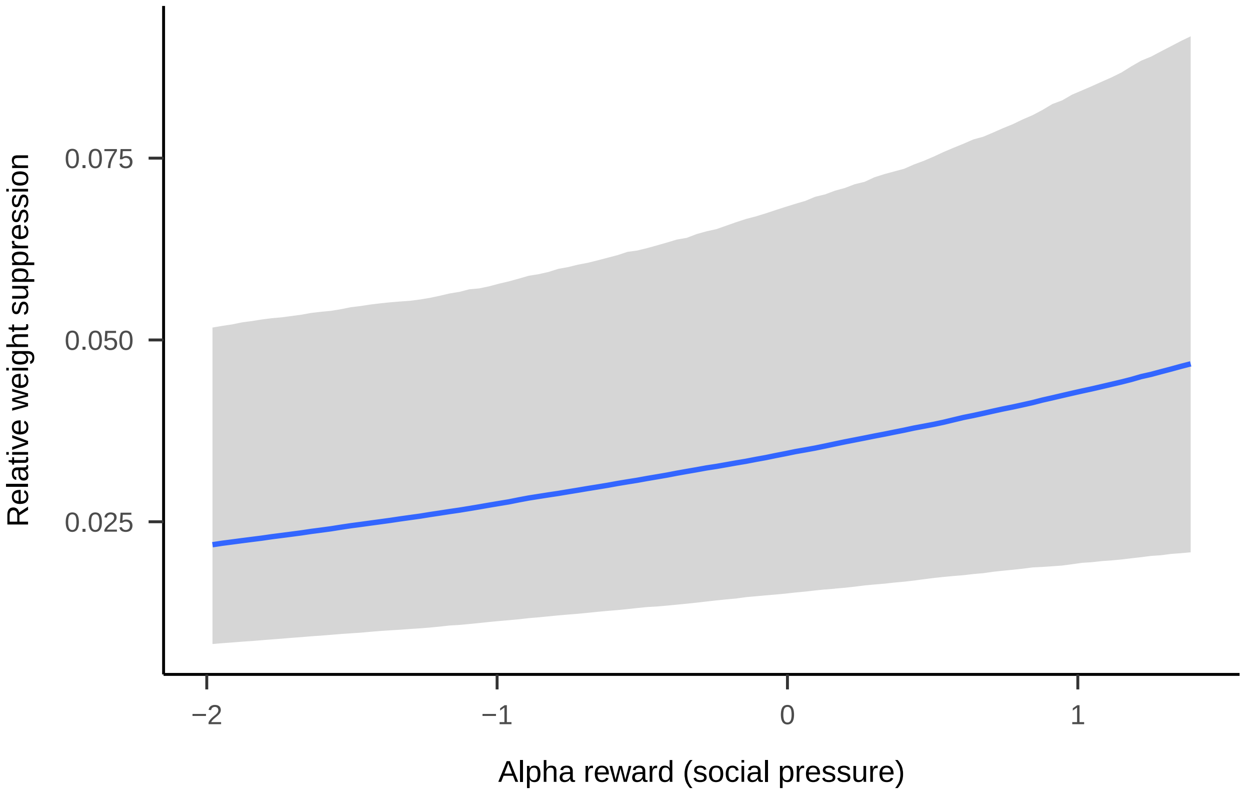
```
## Warning: Rows containing NAs were excluded from the model.
```

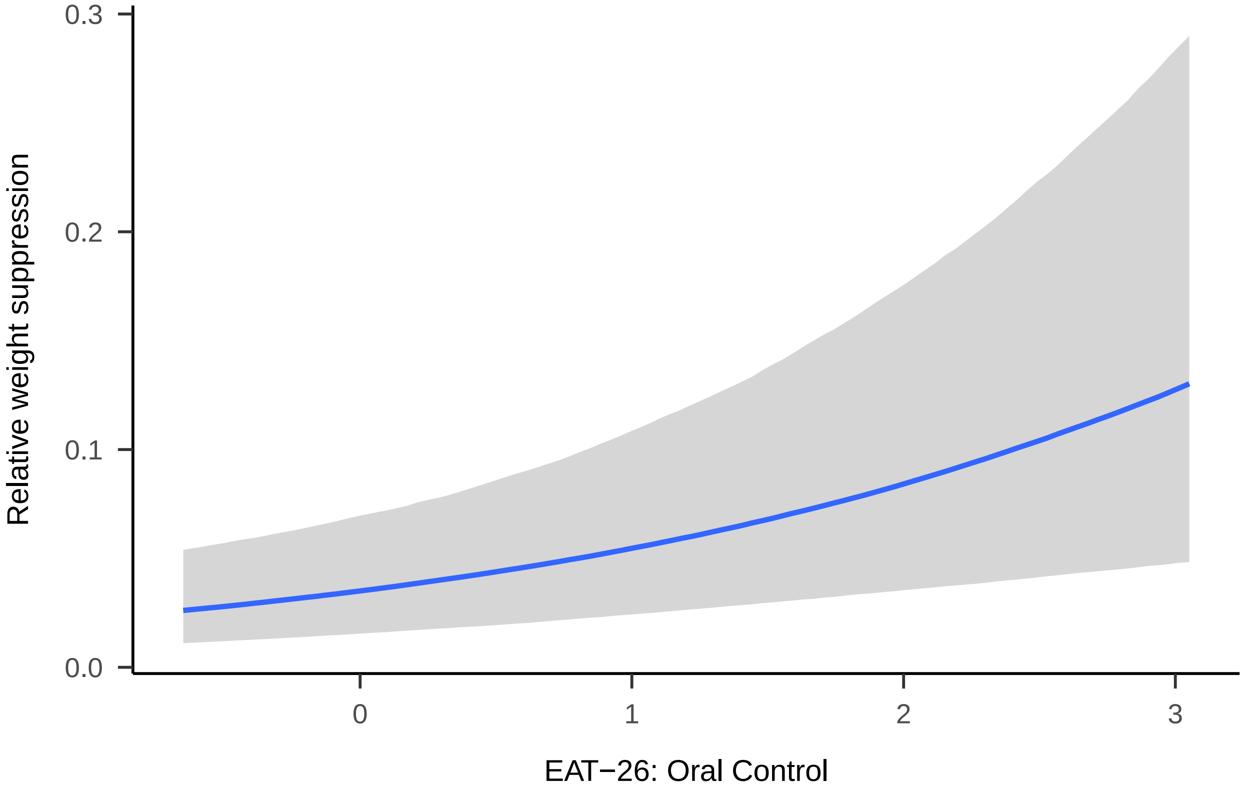
```
## Start sampling
```

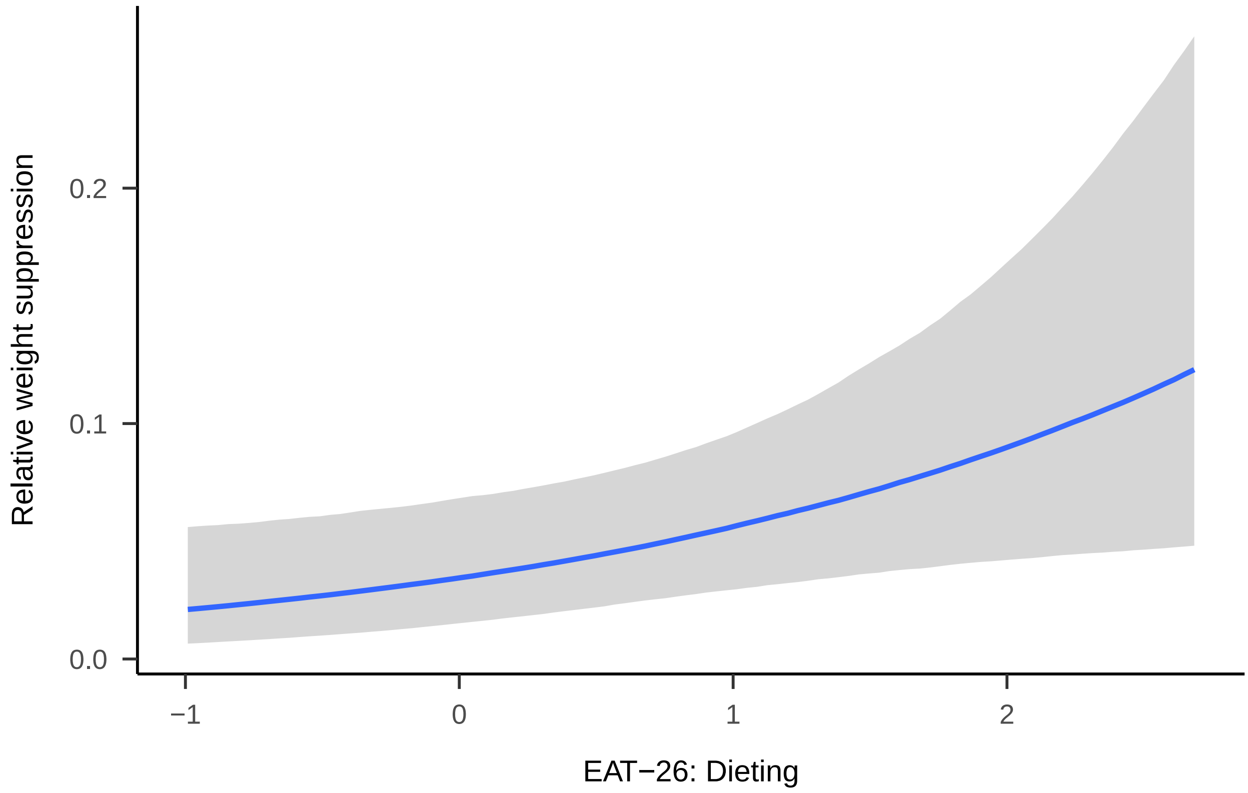
```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 2 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 3 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 4 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 2 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 3 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 4 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 1 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 4 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 4 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 1 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 2 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 3 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 4 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 1 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 3 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 2 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 4 Iteration:  500 / 4000 [ 12%]  (Warmup)
## Chain 1 Iteration:  500 / 4000 [ 12%]  (Warmup)
## Chain 3 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 4 Iteration:  600 / 4000 [ 15%]  (Warmup)
## Chain 1 Iteration:  600 / 4000 [ 15%]  (Warmup)
## Chain 2 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 4 Iteration:  700 / 4000 [ 17%]  (Warmup)
## Chain 1 Iteration:  700 / 4000 [ 17%]  (Warmup)
## Chain 2 Iteration:  500 / 4000 [ 12%]  (Warmup)
## Chain 3 Iteration:  500 / 4000 [ 12%]  (Warmup)
## Chain 4 Iteration:  800 / 4000 [ 20%]  (Warmup)
## Chain 2 Iteration:  600 / 4000 [ 15%]  (Warmup)
## Chain 3 Iteration:  600 / 4000 [ 15%]  (Warmup)
## Chain 1 Iteration:  800 / 4000 [ 20%]  (Warmup)
## Chain 1 Iteration:  900 / 4000 [ 22%]  (Warmup)
## Chain 2 Iteration:  700 / 4000 [ 17%]  (Warmup)
## Chain 4 Iteration:  900 / 4000 [ 22%]  (Warmup)
## Chain 3 Iteration:  700 / 4000 [ 17%]  (Warmup)
## Chain 4 Iteration: 1000 / 4000 [ 25%]  (Warmup)
## Chain 1 Iteration: 1000 / 4000 [ 25%]  (Warmup)
## Chain 2 Iteration:  800 / 4000 [ 20%]  (Warmup)
## Chain 3 Iteration:  800 / 4000 [ 20%]  (Warmup)
## Chain 4 Iteration: 1100 / 4000 [ 27%]  (Warmup)
## Chain 1 Iteration: 1100 / 4000 [ 27%]  (Warmup)
## Chain 2 Iteration:  900 / 4000 [ 22%]  (Warmup)
## Chain 1 Iteration: 1200 / 4000 [ 30%]  (Warmup)
## Chain 2 Iteration: 1000 / 4000 [ 25%]  (Warmup)
## Chain 3 Iteration:  900 / 4000 [ 22%]  (Warmup)
## Chain 4 Iteration: 1200 / 4000 [ 30%]  (Warmup)
## Chain 4 Iteration: 1300 / 4000 [ 32%]  (Warmup)
## Chain 1 Iteration: 1300 / 4000 [ 32%]  (Warmup)
## Chain 2 Iteration: 1100 / 4000 [ 27%]  (Warmup)
## Chain 3 Iteration: 1000 / 4000 [ 25%]  (Warmup)
## Chain 4 Iteration: 1400 / 4000 [ 35%]  (Warmup)
## Chain 1 Iteration: 1400 / 4000 [ 35%]  (Warmup)
## Chain 2 Iteration: 1200 / 4000 [ 30%]  (Warmup)
## Chain 3 Iteration: 1100 / 4000 [ 27%]  (Warmup)
## Chain 4 Iteration: 1500 / 4000 [ 37%]  (Warmup)
## Chain 1 Iteration: 1500 / 4000 [ 37%]  (Warmup)
## Chain 2 Iteration: 1300 / 4000 [ 32%]  (Warmup)
## Chain 3 Iteration: 1200 / 4000 [ 30%]  (Warmup)
## Chain 4 Iteration: 1600 / 4000 [ 40%]  (Warmup)
## Chain 1 Iteration: 1600 / 4000 [ 40%]  (Warmup)
## Chain 2 Iteration: 1400 / 4000 [ 35%]  (Warmup)
## Chain 3 Iteration: 1300 / 4000 [ 32%]  (Warmup)
## Chain 4 Iteration: 1700 / 4000 [ 42%]  (Warmup)
## Chain 1 Iteration: 1700 / 4000 [ 42%]  (Warmup)
## Chain 2 Iteration: 1500 / 4000 [ 37%]  (Warmup)
## Chain 3 Iteration: 1400 / 4000 [ 35%]  (Warmup)
## Chain 4 Iteration: 1800 / 4000 [ 45%]  (Warmup)
## Chain 1 Iteration: 1800 / 4000 [ 45%]  (Warmup)
## Chain 2 Iteration: 1600 / 4000 [ 40%]  (Warmup)
## Chain 3 Iteration: 1500 / 4000 [ 37%]  (Warmup)
## Chain 4 Iteration: 1900 / 4000 [ 47%]  (Warmup)
## Chain 1 Iteration: 1900 / 4000 [ 47%]  (Warmup)
## Chain 2 Iteration: 1700 / 4000 [ 42%]  (Warmup)
## Chain 2 Iteration: 1800 / 4000 [ 45%]  (Warmup)
## Chain 3 Iteration: 1600 / 4000 [ 40%]  (Warmup)
## Chain 4 Iteration: 2000 / 4000 [ 50%]  (Warmup)
## Chain 4 Iteration: 2001 / 4000 [ 50%]  (Sampling)
## Chain 1 Iteration: 2000 / 4000 [ 50%]  (Warmup)
## Chain 1 Iteration: 2001 / 4000 [ 50%]  (Sampling)
## Chain 4 Iteration: 2100 / 4000 [ 52%]  (Sampling)
## Chain 2 Iteration: 1900 / 4000 [ 47%]  (Warmup)
## Chain 3 Iteration: 1700 / 4000 [ 42%]  (Warmup)
## Chain 1 Iteration: 2100 / 4000 [ 52%]  (Sampling)
## Chain 3 Iteration: 1800 / 4000 [ 45%]  (Warmup)
## Chain 4 Iteration: 2200 / 4000 [ 55%]  (Sampling)
## Chain 1 Iteration: 2200 / 4000 [ 55%]  (Sampling)
## Chain 2 Iteration: 2000 / 4000 [ 50%]  (Warmup)
## Chain 2 Iteration: 2001 / 4000 [ 50%]  (Sampling)
## Chain 3 Iteration: 1900 / 4000 [ 47%]  (Warmup)
## Chain 4 Iteration: 2300 / 4000 [ 57%]  (Sampling)
## Chain 4 Iteration: 2400 / 4000 [ 60%]  (Sampling)
## Chain 2 Iteration: 2100 / 4000 [ 52%]  (Sampling)
## Chain 1 Iteration: 2300 / 4000 [ 57%]  (Sampling)
## Chain 4 Iteration: 2500 / 4000 [ 62%]  (Sampling)
## Chain 2 Iteration: 2200 / 4000 [ 55%]  (Sampling)
## Chain 3 Iteration: 2000 / 4000 [ 50%]  (Warmup)
## Chain 3 Iteration: 2001 / 4000 [ 50%]  (Sampling)
## Chain 1 Iteration: 2400 / 4000 [ 60%]  (Sampling)
## Chain 4 Iteration: 2600 / 4000 [ 65%]  (Sampling)
## Chain 2 Iteration: 2300 / 4000 [ 57%]  (Sampling)
## Chain 3 Iteration: 2100 / 4000 [ 52%]  (Sampling)
## Chain 4 Iteration: 2700 / 4000 [ 67%]  (Sampling)
## Chain 1 Iteration: 2500 / 4000 [ 62%]  (Sampling)
## Chain 2 Iteration: 2400 / 4000 [ 60%]  (Sampling)
## Chain 3 Iteration: 2200 / 4000 [ 55%]  (Sampling)
## Chain 4 Iteration: 2800 / 4000 [ 70%]  (Sampling)
## Chain 1 Iteration: 2600 / 4000 [ 65%]  (Sampling)
## Chain 2 Iteration: 2500 / 4000 [ 62%]  (Sampling)
## Chain 3 Iteration: 2300 / 4000 [ 57%]  (Sampling)
## Chain 4 Iteration: 2900 / 4000 [ 72%]  (Sampling)
## Chain 1 Iteration: 2700 / 4000 [ 67%]  (Sampling)
## Chain 4 Iteration: 3000 / 4000 [ 75%]  (Sampling)
## Chain 2 Iteration: 2600 / 4000 [ 65%]  (Sampling)
## Chain 3 Iteration: 2400 / 4000 [ 60%]  (Sampling)
## Chain 1 Iteration: 2800 / 4000 [ 70%]  (Sampling)
## Chain 4 Iteration: 3100 / 4000 [ 77%]  (Sampling)
## Chain 2 Iteration: 2700 / 4000 [ 67%]  (Sampling)
## Chain 3 Iteration: 2500 / 4000 [ 62%]  (Sampling)
## Chain 1 Iteration: 2900 / 4000 [ 72%]  (Sampling)
## Chain 4 Iteration: 3200 / 4000 [ 80%]  (Sampling)
## Chain 2 Iteration: 2800 / 4000 [ 70%]  (Sampling)
## Chain 3 Iteration: 2600 / 4000 [ 65%]  (Sampling)
## Chain 4 Iteration: 3300 / 4000 [ 82%]  (Sampling)
## Chain 1 Iteration: 3000 / 4000 [ 75%]  (Sampling)
## Chain 4 Iteration: 3400 / 4000 [ 85%]  (Sampling)
## Chain 1 Iteration: 3100 / 4000 [ 77%]  (Sampling)
## Chain 2 Iteration: 2900 / 4000 [ 72%]  (Sampling)
## Chain 3 Iteration: 2700 / 4000 [ 67%]  (Sampling)
## Chain 4 Iteration: 3500 / 4000 [ 87%]  (Sampling)
## Chain 1 Iteration: 3200 / 4000 [ 80%]  (Sampling)
## Chain 2 Iteration: 3000 / 4000 [ 75%]  (Sampling)
## Chain 3 Iteration: 2800 / 4000 [ 70%]  (Sampling)
## Chain 4 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 2 Iteration: 3100 / 4000 [ 77%]  (Sampling)
## Chain 1 Iteration: 3300 / 4000 [ 82%]  (Sampling)
## Chain 3 Iteration: 2900 / 4000 [ 72%]  (Sampling)
## Chain 4 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 2 Iteration: 3200 / 4000 [ 80%]  (Sampling)
## Chain 4 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 1 Iteration: 3400 / 4000 [ 85%]  (Sampling)
## Chain 3 Iteration: 3000 / 4000 [ 75%]  (Sampling)
## Chain 4 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 1 Iteration: 3500 / 4000 [ 87%]  (Sampling)
## Chain 2 Iteration: 3300 / 4000 [ 82%]  (Sampling)
## Chain 4 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 4 finished in 6.9 seconds.
## Chain 3 Iteration: 3100 / 4000 [ 77%]  (Sampling)
## Chain 1 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 2 Iteration: 3400 / 4000 [ 85%]  (Sampling)
## Chain 3 Iteration: 3200 / 4000 [ 80%]  (Sampling)
## Chain 1 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 2 Iteration: 3500 / 4000 [ 87%]  (Sampling)
## Chain 3 Iteration: 3300 / 4000 [ 82%]  (Sampling)
## Chain 1 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 2 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 3 Iteration: 3400 / 4000 [ 85%]  (Sampling)
## Chain 1 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 3 Iteration: 3500 / 4000 [ 87%]  (Sampling)
## Chain 1 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 2 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 1 finished in 7.9 seconds.
## Chain 2 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 2 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 2 finished in 8.3 seconds.
## Chain 3 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 3 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 finished in 9.0 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 8.1 seconds.
## Total execution time: 9.3 seconds.
```

```
##  Family: zero_inflated_beta
##   Links: mu = logit; phi = identity; zi = identity
## Formula: rws ~ Group + bmi + (a_neither + v_food + v_social + t_food + t_social + z_food + z_social +
##    Data: foo (Number of observations: 95)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           -2.78      0.17    -3.14    -2.46 1.00     3791     4311
## Group1              -0.44      0.25    -0.95     0.04 1.00     3511     4235
## Group2               0.29      0.25    -0.18     0.81 1.00     4076     4776
## bmi                  0.17      0.13    -0.10     0.42 1.00     4484     5378
## a_neither           -0.10      0.10    -0.29     0.10 1.00     5768     5974
## v_food               0.15      0.21    -0.27     0.56 1.00     4009     5284
## v_social            -0.13      0.12    -0.37     0.11 1.00     5296     5742
## t_food              -0.30      0.16    -0.62     0.01 1.00     3660     4766
## t_social             0.27      0.15    -0.03     0.56 1.00     4246     5353
## z_food              -0.04      0.11    -0.26     0.18 1.00     5738     5902
## z_social             0.03      0.08    -0.13     0.21 1.00     6917     5742
## alpha_neg_food      -0.06      0.12    -0.29     0.18 1.00     5433     5930
## alpha_neg_social     0.26      0.11     0.05     0.47 1.00     6993     6123
## alpha_pos_food       0.04      0.12    -0.20     0.28 1.00     4816     5925
## alpha_pos_social     0.23      0.11     0.02     0.44 1.00     6281     6322
## oral_control         0.47      0.14     0.20     0.75 1.00     7231     5934
## dieting              0.51      0.23     0.08     0.98 1.00     3903     4539
## bulimia              0.03      0.20    -0.35     0.42 1.00     5246     5992
## bsq14_tot            0.03      0.21    -0.38     0.44 1.00     4497     5186
## ros_tot              0.01      0.19    -0.35     0.38 1.00     5521     6101
## sias                -0.28      0.15     -0.56     0.01 1.00     4840     5692
## mps_ps               0.06      0.11     -0.16     0.28 1.00     5865     5406
## mps_o               -0.06      0.10     -0.24     0.13 1.00     6972     5597
## mps_cmd             -0.05      0.20     -0.44     0.35 1.00     4537     5137
## mps_pepc             0.02      0.13     -0.25     0.27 1.00     4883     5889
## orto_tot             0.19      0.15     -0.10     0.49 1.00     5677     6195
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi    26.41      4.60    18.31    36.38 1.00     6353     5777
## zi      0.07      0.03     0.03     0.13 1.00    11762     5047
##
## Samples were drawn using sample(hmc). 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).
```




Relative weight suppression
0.075
0.050
0.025
−2
−1
0
1
Alpha reward (social pressure)

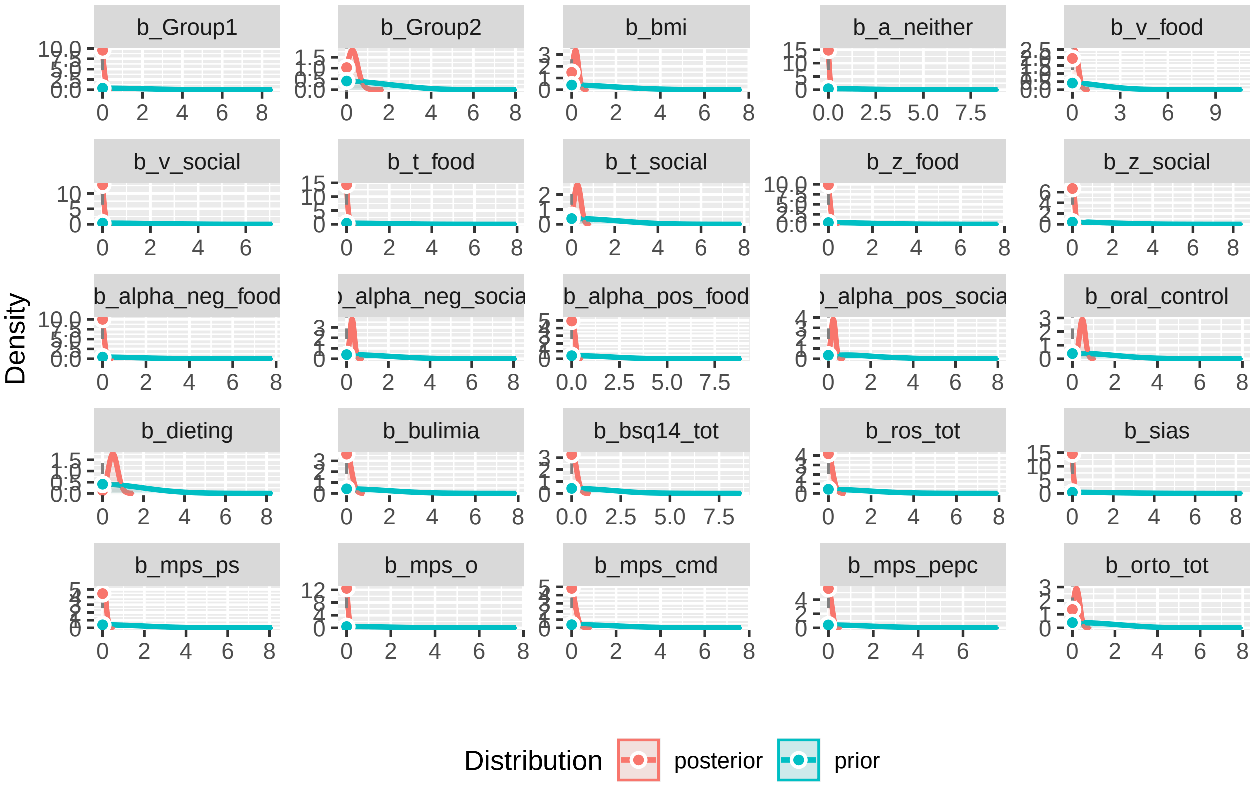

Relative weight suppression
0.3
0.2
0.1
0.0
0
1
2
3
EAT−26: Oral Control



```
## Sampling priors, please wait...

## Caricamento dei namespace richiesti: logspline

## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter          |       BF
## ---------------------------
## (Intercept)        | 0.00e+00
## Group1             |    0.040
## Group2             |    0.395
## bmi                |    0.271
## a_neither          |    0.026
## v_food             |    0.213
## v_social           |    0.030
## t_food             |    0.028
## t_social           |    0.649
## z_food             |    0.042
## z_social           |    0.061
## alpha_neg_food     |    0.044
## alpha_neg_social   |     2.12
## alpha_pos_food     |    0.082
## alpha_pos_social   |     1.01
## oral_control       |    24.61
## dieting            |     3.23
## bulimia            |    0.115
## bsq14_tot          |    0.127
## ros_tot            |    0.103
## sias               |    0.026
## mps_ps             |    0.089
## mps_o              |     0.033
## mps_cmd            |     0.080
## mps_pepc           |     0.075
## orto_tot           |     0.287
##
## * Evidence Against The Null: 0
## *                Direction: Right-Sided test
```



Marginal effects

Alpha punishment is not a robust effect. Alpha reward

```
m10 <- brm(
  rws ~ alpha_pos_social,
  data = foo,
  prior = prior_ma,
  family = zero_inflated_beta(),
  control = list(adapt_delta = 0.98),
  iter = 4000,
  cores = 6,
  backend = "cmdstan"
)
```

```
## Warning: Rows containing NAs were excluded from the model.
```

```
## Start sampling
```

```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 1 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 1 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 1 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 2 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 2 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 2 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 3 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 3 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 3 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 4 Iteration:    1 / 4000 [  0%]  (Warmup)
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## Chain 1 Iteration: 3500 / 4000 [ 87%]  (Sampling)
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## Chain 2 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 2 Iteration: 3700 / 4000 [ 92%]  (Sampling)
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## Chain 3 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 3 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 4 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 4 Iteration: 3700 / 4000 [ 92%]  (Sampling)
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## Chain 2 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 2 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 3 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 4 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 4 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 1 finished in 1.4 seconds.
## Chain 2 finished in 1.4 seconds.
## Chain 3 finished in 1.4 seconds.
## Chain 4 finished in 1.4 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 1.4 seconds.
## Total execution time: 1.5 seconds.
```
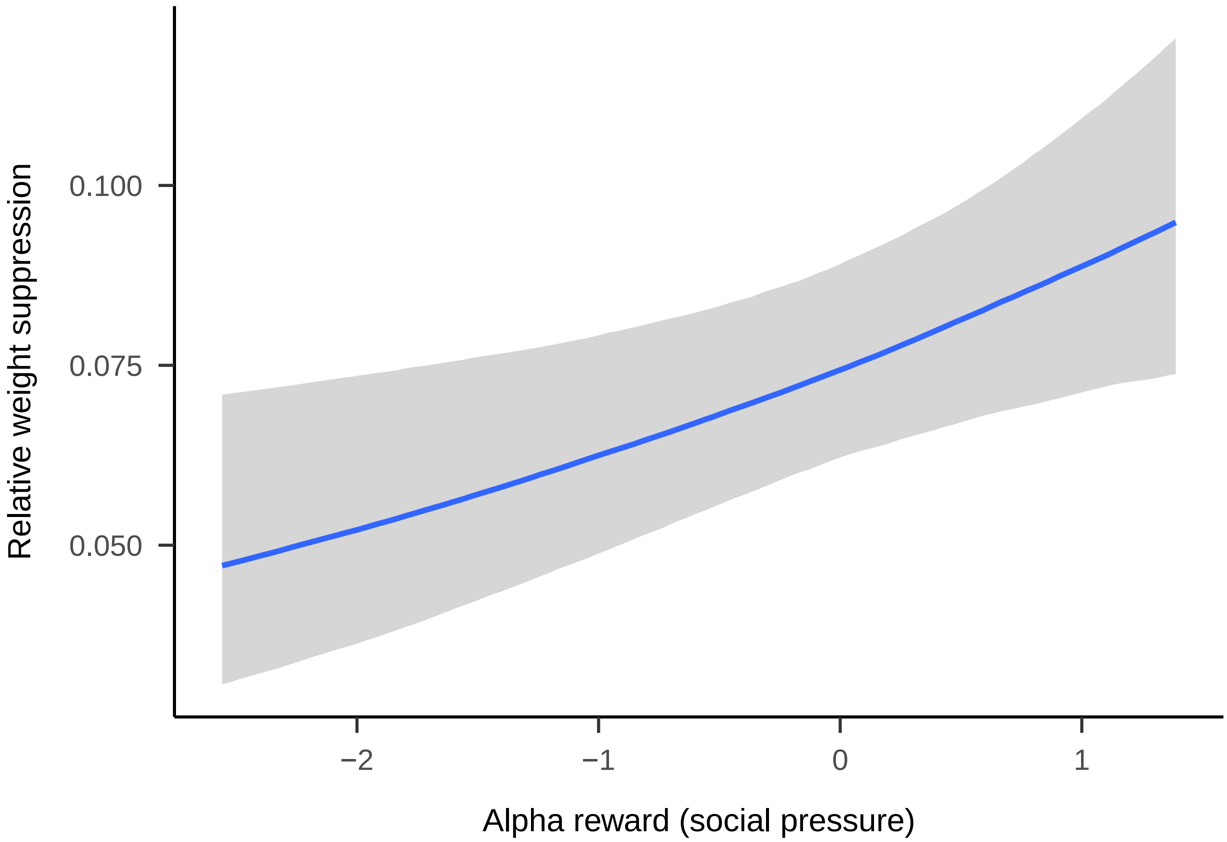

```
summary(m10)
```

```
##  Family: zero_inflated_beta
##   Links: mu = logit; phi = identity; zi = identity
## Formula: rws ~ alpha_pos_social
##    Data: foo (Number of observations: 98)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##                   Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           -2.43      0.10    -2.62    -2.24 1.00     5096     5323
## alpha_pos_social     0.19      0.08     0.04     0.34 1.00     6064     5075
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi    14.98      2.33    10.89    19.85 1.00     5635     5624
## zi      0.08      0.03     0.04     0.14 1.00     5863     4929
##
## Samples were drawn using sample(hmc). 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).
```

```
c_eff <- conditional_effects(m10, "alpha_pos_social")
my_plot <- plot(c_eff, plot = FALSE)[[1]] +
  labs(
    x = "Alpha reward (social pressure)",
    y = "Relative weight suppression"
  ) +
  papaja::theme_apa()
my_plot
```



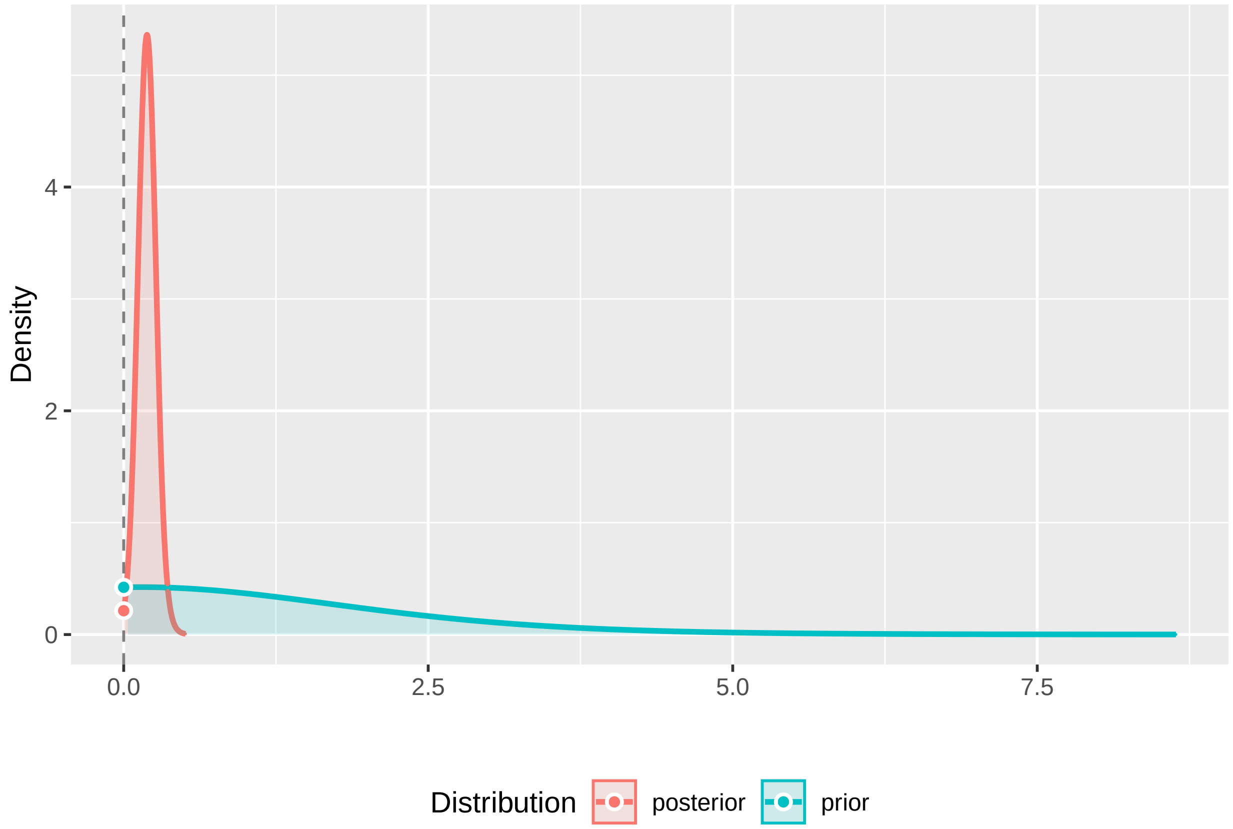
```
test_right <- bayestestR::bayesfactor_parameters(m10, direction = ">")
```

```
## Sampling priors, please wait...
```

```
test_right
```

```
## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter        |       BF
## ---------------------------
## (Intercept)      | 0.00e+00
## alpha_pos_social |     1.98
##
## * Evidence Against The Null: 0
## *                 Direction: Right-Sided test
```

```
plot(test_right)
```



Oral control

```
m11 <- brm(
  rws ~ oral_control,
  data = foo,
  prior = prior_ma,
  family = zero_inflated_beta(),
  control = list(adapt_delta = 0.98),
  iter = 4000,
  cores = 6,
  backend = "cmdstan"
)
```

```
## Warning: Rows containing NAs were excluded from the model.
```

```
## Start sampling
```

```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 1 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 1 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 1 Iteration:  400 / 4000 [ 10%]  (Warmup)
## Chain 2 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 2 Iteration:  100 / 4000 [  2%]  (Warmup)
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## Chain 3 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 4 Iteration: 3300 / 4000 [ 82%]  (Sampling)
## Chain 4 Iteration: 3400 / 4000 [ 85%]  (Sampling)
## Chain 1 finished in 1.2 seconds.
## Chain 2 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 3 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 4 Iteration: 3500 / 4000 [ 87%]  (Sampling)
## Chain 4 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 4 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 2 finished in 1.4 seconds.
## Chain 3 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 4 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 4 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 finished in 1.4 seconds.
## Chain 4 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 4 finished in 1.5 seconds.
```
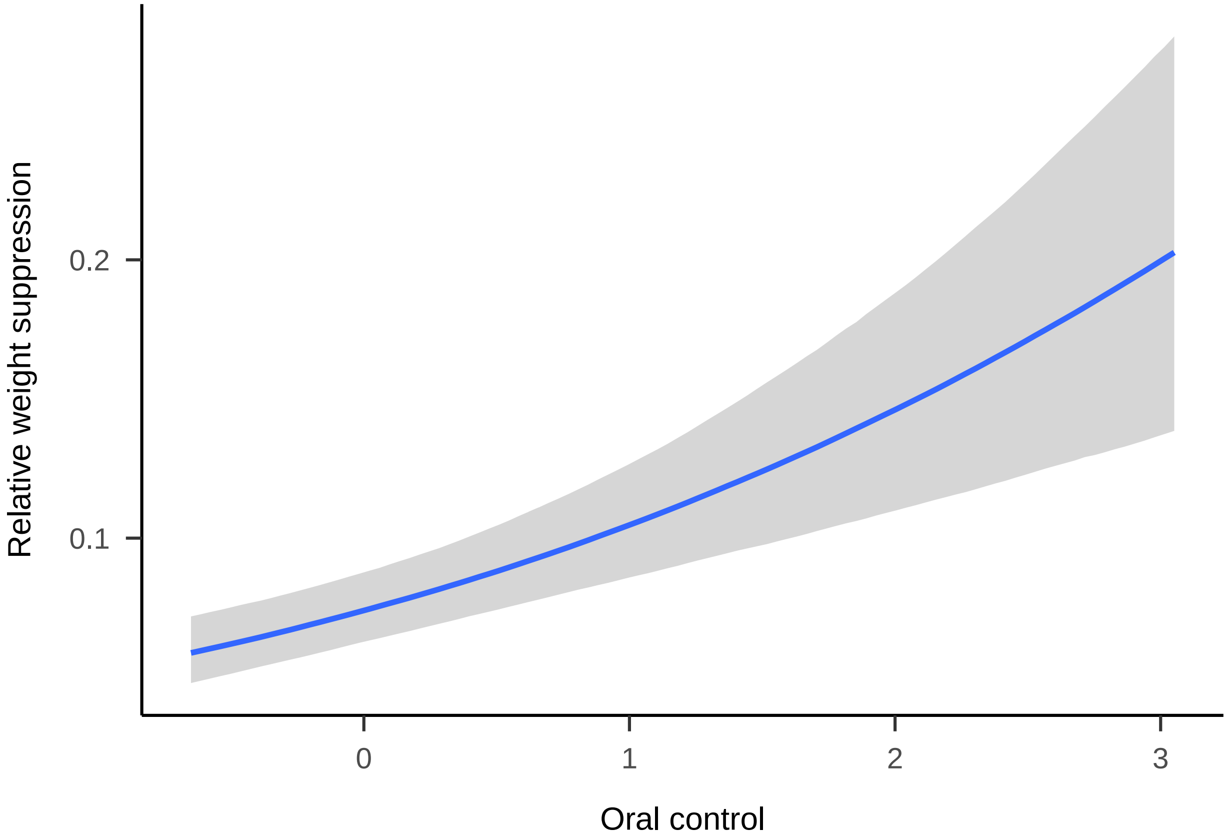

```
##
## All 4 chains finished successfully.
## Mean chain execution time: 1.4 seconds.
## Total execution time: 1.7 seconds.
```

```
summary(m11)
```

```
##  Family: zero_inflated_beta
##   Links: mu = logit; phi = identity; zi = identity
## Formula: rws ~ oral_control
##    Data: foo (Number of observations: 101)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept       -2.44      0.09    -2.61    -2.26 1.00     5205     4789
## oral_control     0.38      0.07     0.23     0.52 1.00     5325     4264
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi    18.15      2.75    13.14    24.03 1.00     5120     5313
## zi      0.08      0.03     0.04     0.14 1.00     6002     4688
##
## Samples were drawn using sample(hmc). 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).
```

```
c_eff <- conditional_effects(m11, "oral_control")
my_plot <- plot(c_eff, plot = FALSE)[[1]] +
  labs(
    x = "Oral control",
    y = "Relative weight suppression"
  ) +
  papaja::theme_apa()
my_plot
```



```
test_right <- bayestestR::bayesfactor_parameters(m11, direction = ">")
```

```
## Sampling priors, please wait...
```

```
test_right
```

```
## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter    |       BF
## ------------------------
## (Intercept)  | 0.00e+00
## oral_control |   420.59
##
## * Evidence Against The Null: 0
## *                 Direction: Right-Sided test
```

Dieting

```
m12 <- brm(
  rws ~ dieting,
  data = foo,
  prior = prior_ma,
  family = zero_inflated_beta(),
  control = list(adapt_delta = 0.98),
  iter = 4000,
  cores = 6,
  backend = "cmdstan"
)
```

```
## Warning: Rows containing NAs were excluded from the model.
```

```
## Start sampling
```

```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
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## Chain 3 Iteration:  100 / 4000 [  2%]  (Warmup)
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## Chain 3 Iteration: 3600 / 4000 [ 90%]  (Sampling)
## Chain 3 Iteration: 3700 / 4000 [ 92%]  (Sampling)
## Chain 4 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 4 finished in 1.2 seconds.
## Chain 1 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 1 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 2 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 2 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 3 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 3 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 1 finished in 1.4 seconds.
## Chain 2 finished in 1.4 seconds.
## Chain 3 finished in 1.4 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 1.3 seconds.
## Total execution time: 1.5 seconds.
```
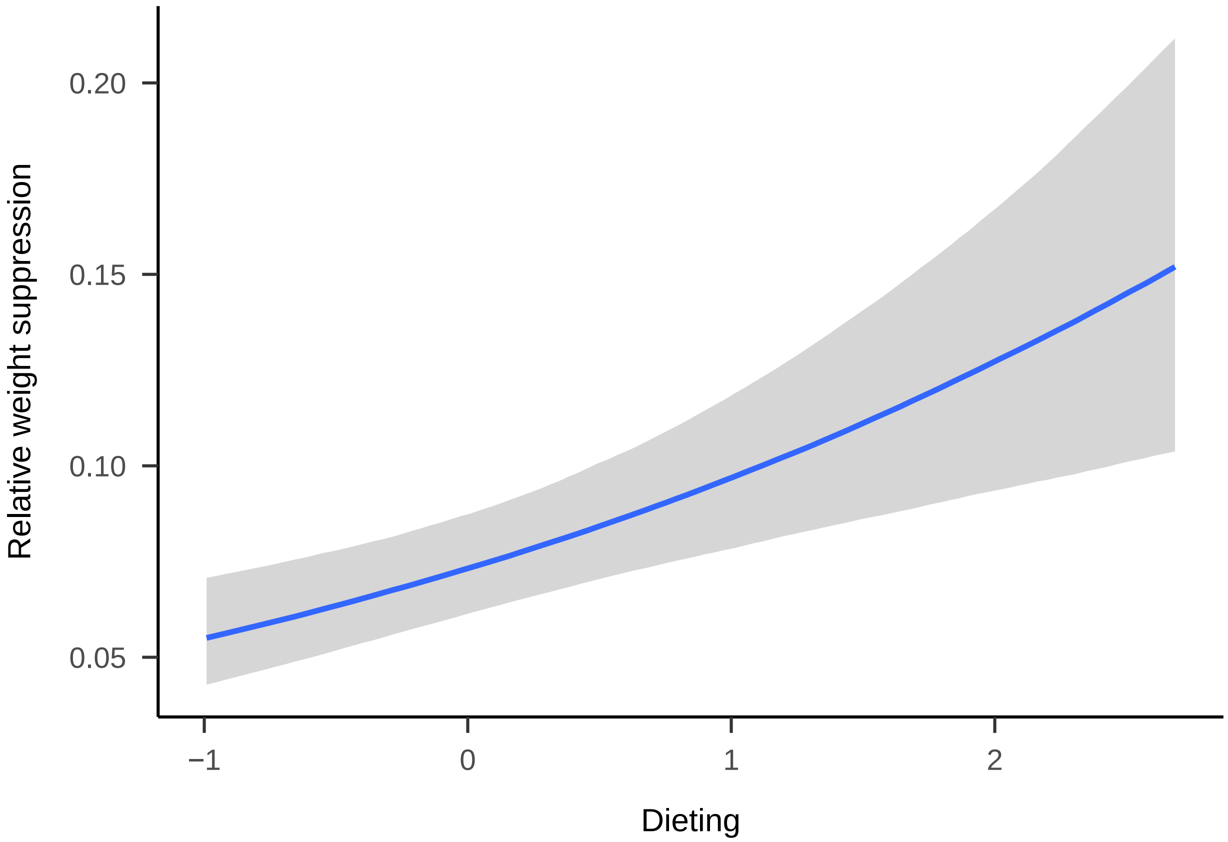

```
summary(m12)
```

```
##  Family: zero_inflated_beta
##   Links: mu = logit; phi = identity; zi = identity
## Formula: rws ~ dieting
##    Data: foo (Number of observations: 101)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -2.45      0.09    -2.63    -2.26 1.00     4427     4234
## dieting       0.31      0.08     0.15     0.46 1.00     6188     5180
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi    16.63      2.60    11.83    22.06 1.00     4534     4566
## zi      0.08      0.03     0.03     0.14 1.00     5188     4471
##
## Samples were drawn using sample(hmc). 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).
```

```
c_eff <- conditional_effects(m12, "dieting")
my_plot <- plot(c_eff, plot = FALSE)[[1]] +
  labs(
    x = "Dieting",
    y = "Relative weight suppression"
  ) +
  papaja::theme_apa()
my_plot
```



```r
test_right <- bayestestR::bayesfactor_parameters(m12, direction = ">")
```

```
## Sampling priors, please wait...
```

```r
test_right
```

```
## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter   |       BF
## ----------------------
## (Intercept) | 0.00e+00
## dieting     |    32.30
##
## * Evidence Against The Null: 0
## *                 Direction: Right-Sided test
```

Bulimia

```r
m13 <- brm(
  rws ~ bulimia,
  data = foo,
  prior = prior_ma,
  family = zero_inflated_beta(),
  control = list(adapt_delta = 0.98),
  iter = 4000,
  cores = 6,
  backend = "cmdstan"
)
```

```
## Warning: Rows containing NAs were excluded from the model.
```

```
## Start sampling
```

```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 1 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 2 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 2 Iteration:  100 / 4000 [  2%]  (Warmup)
## Chain 2 Iteration:  200 / 4000 [  5%]  (Warmup)
## Chain 2 Iteration:  300 / 4000 [  7%]  (Warmup)
## Chain 3 Iteration:    1 / 4000 [  0%]  (Warmup)
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## Chain 4 finished in 1.3 seconds.
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## Chain 1 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 1 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 2 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 3 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 2 finished in 1.4 seconds.
## Chain 3 finished in 1.3 seconds.
## Chain 1 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 1 finished in 1.5 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 1.4 seconds.
## Total execution time: 1.6 seconds.
```
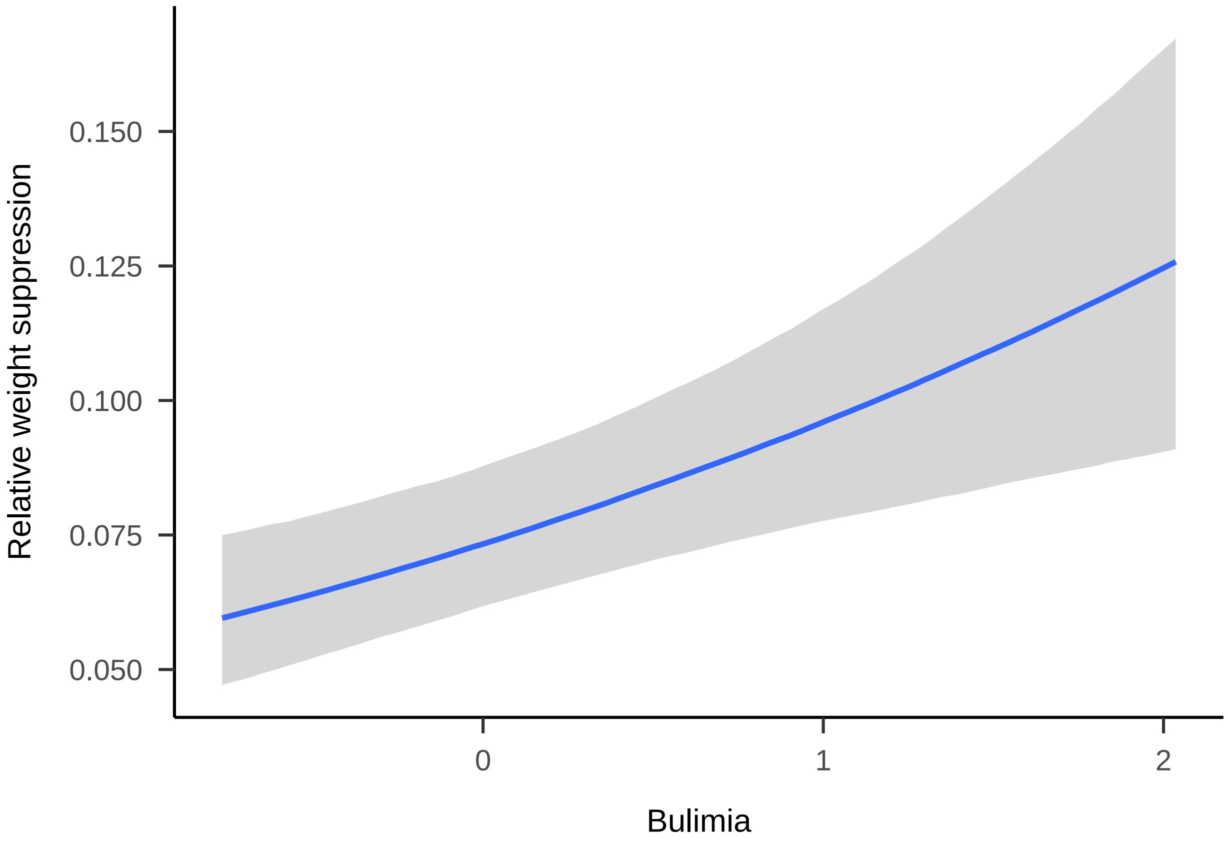

```
summary(m13)
```

```
##  Family: zero_inflated_beta
##   Links: mu = logit; phi = identity; zi = identity
## Formula: rws ~ bulimia
##    Data: foo (Number of observations: 101)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -2.45      0.09    -2.63    -2.26 1.00     4979     5397
## bulimia       0.29      0.08     0.13     0.45 1.00     5300     5129
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi    16.33      2.52    11.63    21.62 1.00     4542     5058
## zi      0.08      0.03     0.03     0.14 1.00     5655     4430
##
## Samples were drawn using sample(hmc). 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).
```

```
c_eff <- conditional_effects(m13, "bulimia")
my_plot <- plot(c_eff, plot = FALSE)[[1]] +
  labs(
    x = "Bulimia",
    y = "Relative weight suppression"
  ) +
  papaja::theme_apa()
my_plot
```



```
test_right <- bayestestR::bayesfactor_parameters(m13, direction = ">")
```

```
## Sampling priors, please wait...
```

```
test_right
```

```
## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter   |       BF
## ----------------------
## (Intercept) | 0.00e+00
## bulimia     |    13.23
##
## * Evidence Against The Null: 0
## *                 Direction: Right-Sided test
```

Difference between the present weight and the predicted weight that the participant expect, if she/he does not try to control her/his eating behavior

```
foo$predicted_weight <- recode_predicted_weight(foo)

imp <- mice::mice(foo, method = "mean", m = 1) # Impute data
```

```
##
##  iter imp variable
##   1   1  v_food  v_social  t_food  t_social  z_food  z_social  alpha_neg_food  alpha_neg_social  alph
##   2   1  v_food  v_social  t_food  t_social  z_food  z_social  alpha_neg_food  alpha_neg_social  alph
##   3   1  v_food  v_social  t_food  t_social  z_food  z_social  alpha_neg_food  alpha_neg_social  alph
##   4   1  v_food  v_social  t_food  t_social  z_food  z_social  alpha_neg_food  alpha_neg_social  alph
##   5   1  v_food  v_social  t_food  t_social  z_food  z_social  alpha_neg_food  alpha_neg_social  alpl
```

```
## Warning: Number of logged events: 191
```

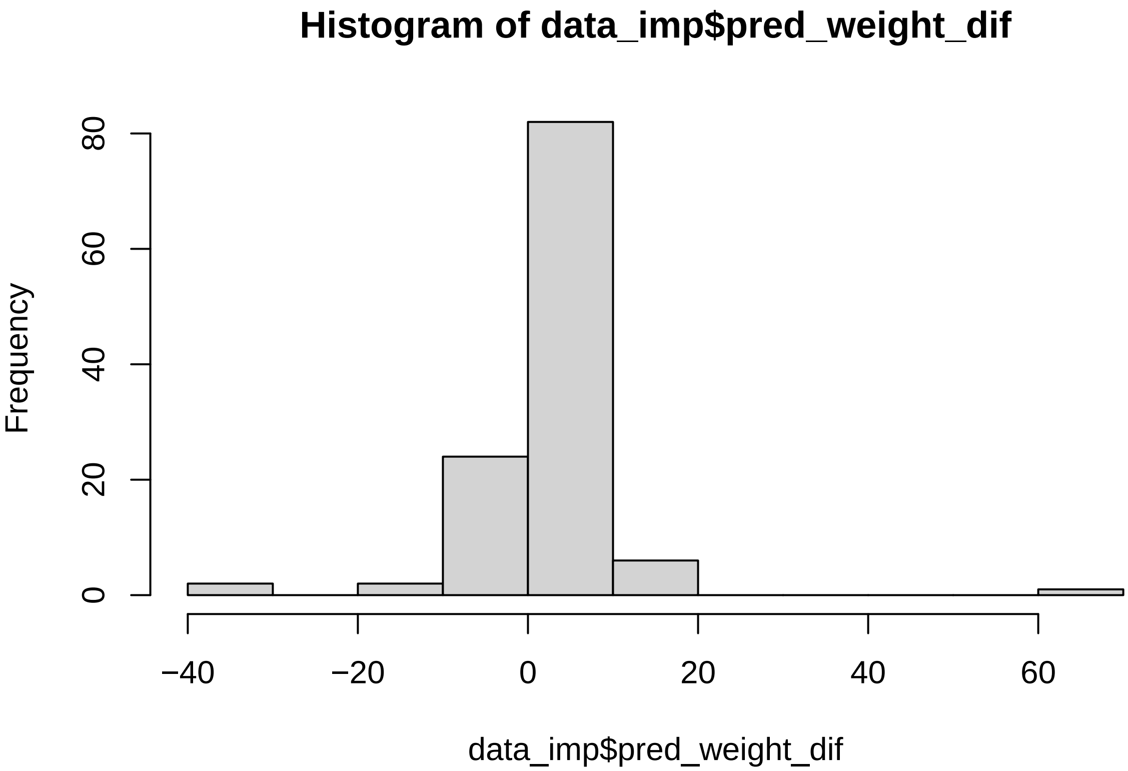
```
data_imp <- complete(imp) # Store data
```

Difference between predicted weight and actual weight

```
data_imp$pred_weight_dif <- data_imp$predicted_weight - data_imp$present_weight

data_imp %>%
  group_by(Group) %>%
  summarise(
    avg_dif = mean(pred_weight_dif, trim = 0.1)
  )
```

```
## # A tibble: 3 x 2
##   Group   avg_dif
##   <fct>     <dbl>
## 1 at risk    4.25
## 2 control    1.74
## 3 patient    3.43
```

```
hist(data_imp$pred_weight_dif)
```



```
# Control as baseline group
data_imp$Group <- relevel(data_imp$Group, ref = "control")
```

Predicted weight difference

```
m14 <- brm(
  pred_weight_dif ~ Group,
  data = data_imp,
  prior = prior_ma,
  family = student(),
  control = list(adapt_delta = 0.98),
  iter = 4000,
  cores = 6,
  backend = "cmdstan"
)
```

```
## Start sampling
```

```
## Running MCMC with 4 chains, at most 6 in parallel...
##
## Chain 1 Iteration:    1 / 4000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 4000 [  2%]  (Warmup)
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## Chain 2 finished in 0.4 seconds.
## Chain 3 finished in 0.4 seconds.
## Chain 4 finished in 0.4 seconds.
## Chain 1 Iteration: 3100 / 4000 [ 77%]  (Sampling)
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## Chain 1 Iteration: 3800 / 4000 [ 95%]  (Sampling)
## Chain 1 Iteration: 3900 / 4000 [ 97%]  (Sampling)
## Chain 1 Iteration: 4000 / 4000 [100%]  (Sampling)
## Chain 1 finished in 0.6 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 0.4 seconds.
## Total execution time: 0.9 seconds.
```
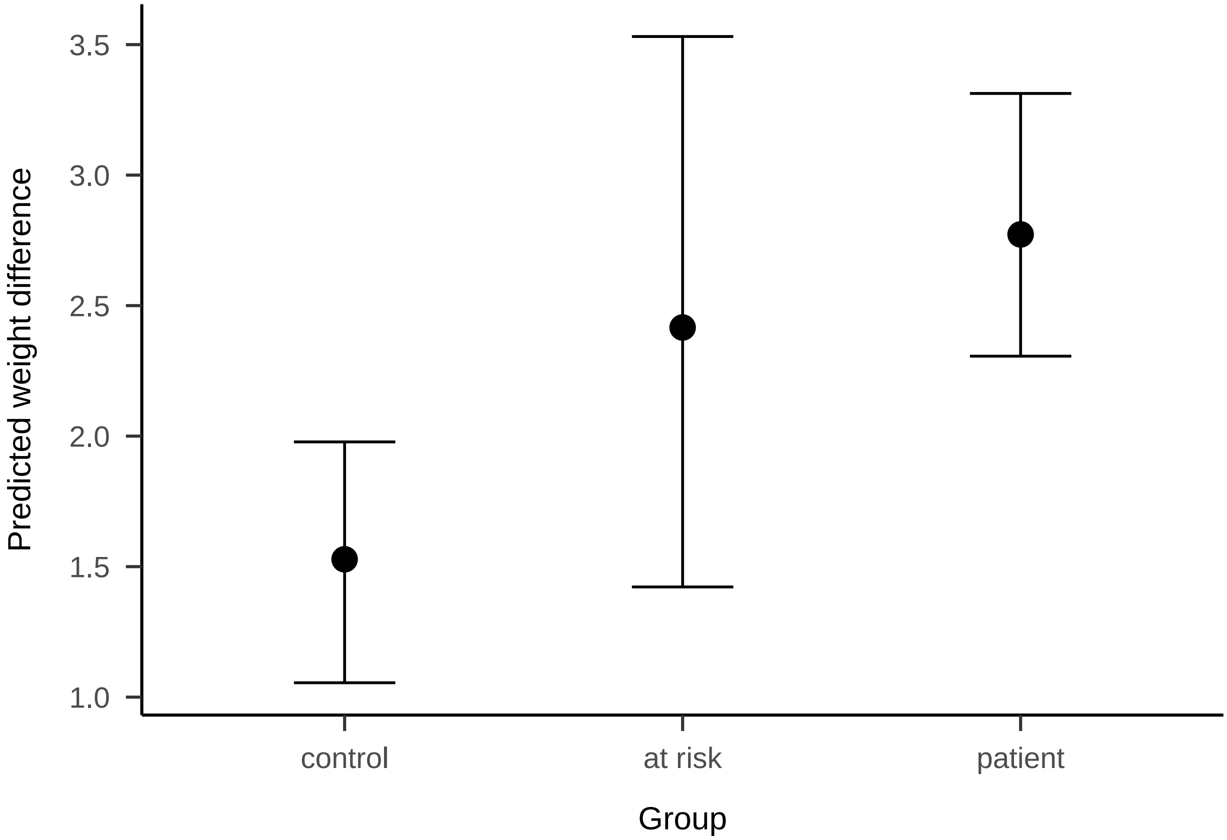

```r
summary(m14)
```

```
##  Family: student
##   Links: mu = identity; sigma = identity; nu = identity
## Formula: pred_weight_dif ~ Group
##    Data: data_imp (Number of observations: 117)
## Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup samples = 8000
##
## Population-Level Effects:
##              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept        1.53      0.23     1.06     1.98 1.00     5491     5076
## Groupatrisk      0.90      0.58    -0.20     2.09 1.00     6347     5206
## Grouppatient     1.25      0.34     0.62     1.94 1.00     5754     4579
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     1.34      0.20     0.99     1.78 1.00     5079     5114
## nu        1.19      0.15     1.01     1.58 1.00     3652     2429
##
## Samples were drawn using sample(hmc). 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).
```

```r
c_eff <- conditional_effects(m14, "Group")
my_plot <- plot(c_eff, plot = FALSE)[[1]] +
  labs(
    x = "Group",
    y = "Predicted weight difference"
  ) +
  papaja::theme_apa()
my_plot
```



```
test_right <- bayestestR::bayesfactor_parameters(m14, direction = ">")
```

```
## Sampling priors, please wait...
```

```
test_right
```

```
## Bayes Factor (Savage-Dickey density ratio)
##
## Parameter     |       BF
## ------------------------
## (Intercept)   | 1.05e+05
## Groupatrisk   |     1.94
## Grouppatient  |   363.08
##
## * Evidence Against The Null: 0
## *                 Direction: Right-Sided test
```

Patients expect to gain more weight than controls; there is no evidence of a difference between at-risk participants and controls. Summary statistics

```
foo %>%
  group_by(Group) %>%
  summarise(
    avg_rws = mean(rws, na.rm = TRUE),
    avg_ws = mean(ws, na.rm = TRUE),
    n = n()
  )
```

```
## # A tibble: 3 x 4
##   Group   avg_rws avg_ws     n
##   <fct>     <dbl>  <dbl> <int>
## 1 at risk  0.0767   5.75    12
## 2 control  0.0545   3.62    68
## 3 patient  0.130    7.48    37
```