Study 3

Contents

This file reproduces the preprocessing and analysis steps of Study 3. The data are automatically imported from Github and necessary packages will be downloaded and installed if they are not yet available.

Create directory to save plots:

```
if (!dir.exists('final_plots')) {dir.create('final_plots')}
```

```
set.seed(42)
```

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] gridExtra_2.3         emmeans_1.5.3         BayesFactor_0.9.12-4.2
##  [4] coda_0.19-4           brms_2.14.4           Rcpp_1.0.5
##  [7] afex_0.28-0           lme4_1.1-26           Matrix_1.2-18
## [10] forcats_0.5.0         stringr_1.4.0         dplyr_1.0.2
## [13] purrr_0.3.4           readr_1.4.0           tidyr_1.1.2
## [16] tibble_3.0.4          ggplot2_3.3.2         tidyverse_1.3.0
## [19] pacman_0.5.1
##
## loaded via a namespace (and not attached):
##   [1] readxl_1.3.1         backports_1.2.1      plyr_1.8.6
##   [4] igraph_1.2.6          splines_4.0.3         crosstalk_1.1.0.1
##   [7] TH.data_1.0-10        rstantools_2.1.1      inline_0.3.17
##  [10] digest_0.6.27         htmltools_0.5.0       rsconnect_0.8.16
##  [13] lmerTest_3.1-3        fansi_0.4.1           magrittr_2.0.1
##  [16] openxlsx_4.2.3        modelr_0.1.8          RcppParallel_5.0.2
##  [19] matrixStats_0.57.0    xts_0.12.1            sandwich_3.0-0
##  [22] prettyunits_1.1.1     colorspace_2.0-0      rvest_0.3.6
##  [25] haven_2.3.1           xfun_0.19             callr_3.5.1
##  [28] crayon_1.3.4          jsonlite_1.7.2        survival_3.2-7
##  [31] zoo_1.8-8             glue_1.4.2            gtable_0.3.0
##  [34] MatrixModels_0.4-1    V8_3.4.0              car_3.0-10
##  [37] pkgbuild_1.1.0        rstan_2.21.3          abind_1.4-5
##  [40] scales_1.1.1          mvtnorm_1.1-1         DBI_1.1.0
##  [43] miniUI_0.1.1.1        xtable_1.8-4          foreign_0.8-80
##  [46] StanHeaders_2.21.0-6 stats4_4.0.3          DT_0.16
##  [49] htmlwidgets_1.5.3     httr_1.4.2            threejs_0.3.3
##  [52] ellipsis_0.3.1        pkgconfig_2.0.3       loo_2.4.1
##  [55] dbplyr_2.0.0          tidyselect_1.1.0      rlang_0.4.9
##  [58] reshape2_1.4.4        later_1.1.0.1         munsell_0.5.0
##  [61] cellranger_1.1.0      tools_4.0.3           cli_2.2.0
##  [64] generics_0.1.0        broom_0.7.2           ggridges_0.5.2
##  [67] evaluate_0.14         fastmap_1.0.1         yaml_2.2.1
##  [70] processx_3.4.5        knitr_1.30            fs_1.5.0
##  [73] zip_2.1.1             pbapply_1.4-3         nlme_3.1-149
##  [76] mime_0.9              projpred_2.0.2        xml2_1.3.2
##  [79] compiler_4.0.3        bayesplot_1.7.2       shinythemes_1.1.2
##  [82] rstudioapi_0.13       curl_4.3              gamm4_0.2-6
##  [85] reprex_0.3.0          statmod_1.4.35        stringi_1.5.3
##  [88] ps_1.5.0              Brobdingnag_1.2-6     lattice_0.20-41
##  [91] nloptr_1.2.2.2        markdown_1.1          shinyjs_2.0.0
##  [94] vctrs_0.3.5           pillar_1.4.7          lifecycle_0.2.0
##  [97] bridgesampling_1.0-0 estimability_1.3      data.table_1.13.4
## [100] httpuv_1.5.4          R6_2.5.0              promises_1.1.1
## [103] rio_0.5.16            codetools_0.2-16      boot_1.3-25
## [106] colourpicker_1.1.0    MASS_7.3-53           gtools_3.8.2
## [109] assertthat_0.2.1      withr_2.3.0           shinystan_2.5.0
## [112] multcomp_1.4-15       mgcv_1.8-33           parallel_4.0.3
## [115] hms_0.5.3             grid_4.0.3            minqa_1.2.4
## [118] rmarkdown_2.6         carData_3.0-4         numDeriv_2016.8-1.1
## [121] shiny_1.5.0           lubridate_1.7.9.2     base64enc_0.1-3
## [124] dygraphs_1.1.1.6
```

Import data

```
github_link = 'https://raw.githubusercontent.com/mertensu/thinking-in-ratios/master/'
file_name = 'data_total_study3.csv'
df = read.csv(paste0(github_link, file_name))
```

Preprocessing

```
# replace zero ratings with 0.001
df[df$redness_rating == 0, 'redness_rating'] = 0.001


# compute correct binary choice
df = df %>% mutate(redness_correct = ifelse(saturation < 50, 0, 1))

df$correct_response = NA
df[df$condition == 'unidirectional', 'correct_response'] = df[df$condition == 'unidirectional', 'rednes

# remove wrong binary choice(s) in unidirectional condition
df = df %>% filter(!(correct_response == F &
                       condition == 'unidirectional'))

df[, "redness_rating_comparable"] = ifelse((df$condition == "unidirectional") &
                                              (df$redness_dichotom == 0),
                                            100 / df$redness_rating,
                                            df$redness_rating
)

df$saturation_factor = factor(df$saturation, levels = c(15, 25, 35, 45, 55, 65, 75, 85))

df$log_redness_rating = log(df$redness_rating_comparable)
# divide saturation by 100 to enable more efficient sampling
df$saturation = df$saturation/100
df$redness_rating_comparable = df$redness_rating_comparable/100
```

Demographics

```
psych::describe(df$age)
```

```
##    vars    n  mean   sd median trimmed  mad min max range skew kurtosis   se
## X1    1 1424 20.81 1.72     21   20.71 1.48  18  25     7  0.5    -0.12 0.05
```

```
df %>% distinct(File, .keep_all = T) %>% group_by(gender) %>% summarise(
  N = n(),
  Min =
    min(age),
  Max =
    max(age),
  Mean =
    mean(age),
  Sd =
    sd(age)
)
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
## # A tibble: 3 x 6
##   gender      N   Min   Max  Mean    Sd
##   <chr>  <int> <int> <int> <dbl> <dbl>
## 1 d          1    24    24  24    NA
## 2 m         15    19    25  21.3  1.49
## 3 w         20    18    24  20.3  1.72
```

```
df %>% distinct(File, .keep_all = T) %>% count(student)
```

```
##   student  n
## 1       0  1
## 2       1 35
```

```
df %>% distinct(File, .keep_all = T) %>% filter(student == 1) %>% count(psycho)
```

```
##   psycho  n
## 1      0 22
## 2      1 13
```

```
df %>% distinct(File, .keep_all = T) %>% count(condition)
```

```
##        condition  n
## 1       standard 18
## 2 unidirectional 18
```

Analysis

ANOVA I (mixed 2(method) x 8(saturation))

```
(
  fit = aov_ez(
    dv = "log_redness_rating",
    within = 'saturation_factor',
    between = "condition",
    id = "File",
    data = df
  )
)
```

frequentist fit

```
## Converting to factor: condition
```

```
## Warning: More than one observation per cell, aggregating the data using mean
## (i.e, fun_aggregate = mean)!
```

```
## Contrasts set to contr.sum for the following variables: condition
## Anova Table (Type 3 tests)
##
## Response: log_redness_rating
##                          Effect          df  MSE         F  ges p.value
## 1                     condition       1, 34 1.67 23.31 *** .123   <.001
## 2             saturation_factor 1.60, 54.51 4.03 56.05 *** .567   <.001
## 3 condition:saturation_factor 1.60, 54.51 4.03 12.20 *** .222   <.001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
##
## Sphericity correction method: GG
```

```
df$File = factor(df$File)
df$condition = factor(df$condition)
(
  bfs = anovaBF(
    log_redness_rating ~ saturation_factor * condition + File,
    whichRandom = 'File',
    whichModels = 'top',
    data = df
  )
)
```

bayesian fit

```
## Bayes factor top-down analysis
## --------------
## When effect is omitted from condition + saturation_factor + condition:saturation_factor + File , BF i
## [1] Omit condition:saturation_factor : 6.66287e-52  ±2.4%
## [2] Omit saturation_factor           : 1.59437e-198 ±1.74%
## [3] Omit condition                   : 0.003851911  ±1.39%
##
## Against denominator:
##   log_redness_rating ~ condition + saturation_factor + condition:saturation_factor + File
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
# BF saturation_factor
bf_1 = lmBF(log_redness_rating ~ condition + File,
            whichRandom = 'File',
            data = df)
bf_2 = lmBF(
  log_redness_rating ~ saturation_factor + condition + File,
  whichRandom = 'File',
  data = df
)
(bf_saturation_factor = bf_2 / bf_1)
```

```
## Bayes factor analysis
## --------------
## [1] saturation_factor + condition + File : 2.605844e+171 ±3.1%
##
## Against denominator:
##   log_redness_rating ~ condition + File
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
print(paste0('logBF ', bf_saturation_factor@bayesFactor$bf))
```

```
## [1] "logBF 394.699807445277"
```

```
# BF condition
bf_1 = lmBF(
  log_redness_rating ~ saturation_factor + File,
  whichRandom = 'File',
  data = df
)
bf_2 = lmBF(
  log_redness_rating ~ saturation_factor + condition + File,
  whichRandom = 'File',
  data = df
)
(bf_condition = bf_2 / bf_1)
```

```
## Bayes factor analysis
## --------------
## [1] saturation_factor + condition + File : 219.3636 ±3.76%
##
## Against denominator:
##   log_redness_rating ~ saturation_factor + File
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
print(paste0('logBF ', bf_condition@bayesFactor$bf))
```

```
## [1] "logBF 5.39073054965593"
```

```
# BF interaction
bf_1 = lmBF(
  log_redness_rating ~ saturation_factor + condition + File,
  whichRandom = 'File',
  data = df
)
bf_2 = lmBF(
  log_redness_rating ~ saturation_factor * condition + File,
  whichRandom = 'File',
  data = df
)
(bf_interaction = bf_2 / bf_1)
```

```
## Bayes factor analysis
## --------------
## [1] saturation_factor * condition + File : 1.545627e+51 ±2.33%
##
## Against denominator:
##   log_redness_rating ~ saturation_factor + condition + File
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
print(paste0('logBF ', bf_interaction@bayesFactor$bf))
```

```
## [1] "logBF 117.867269513412"
```

```
grid = data.frame(emmeans(fit,  ~ saturation_factor + condition))
grid$condition = factor(grid$condition,levels=c('unidirectional', 'standard'))

ggplot(grid, aes(
  x = saturation_factor,
  y = exp(emmean),
  group = condition
)) +
  geom_pointrange(aes(
    ymin = exp(lower.CL),
    ymax = exp(upper.CL),
    color = condition
  ), size =
    0.3) +
  scale_y_continuous(
    trans = 'log2',
    breaks = c(0.1, 1, 10, 100),
    limits = c(0.07, 100)
  ) +
  geom_line(linetype = 'dashed') +
  labs(y = 'Redness judgement', x = 'redness saturation (in %)') +
  scale_color_manual(
    values = c("darkgrey", "black"),
    name = "method",
  ) +
  scale_x_discrete(labels = substring(grid$saturation_factor, 2)) +
  theme_classic() +
  theme(
    legend.position = c(0.2, 0.85),
    legend.background = element_rect(color = "black")
  )
```

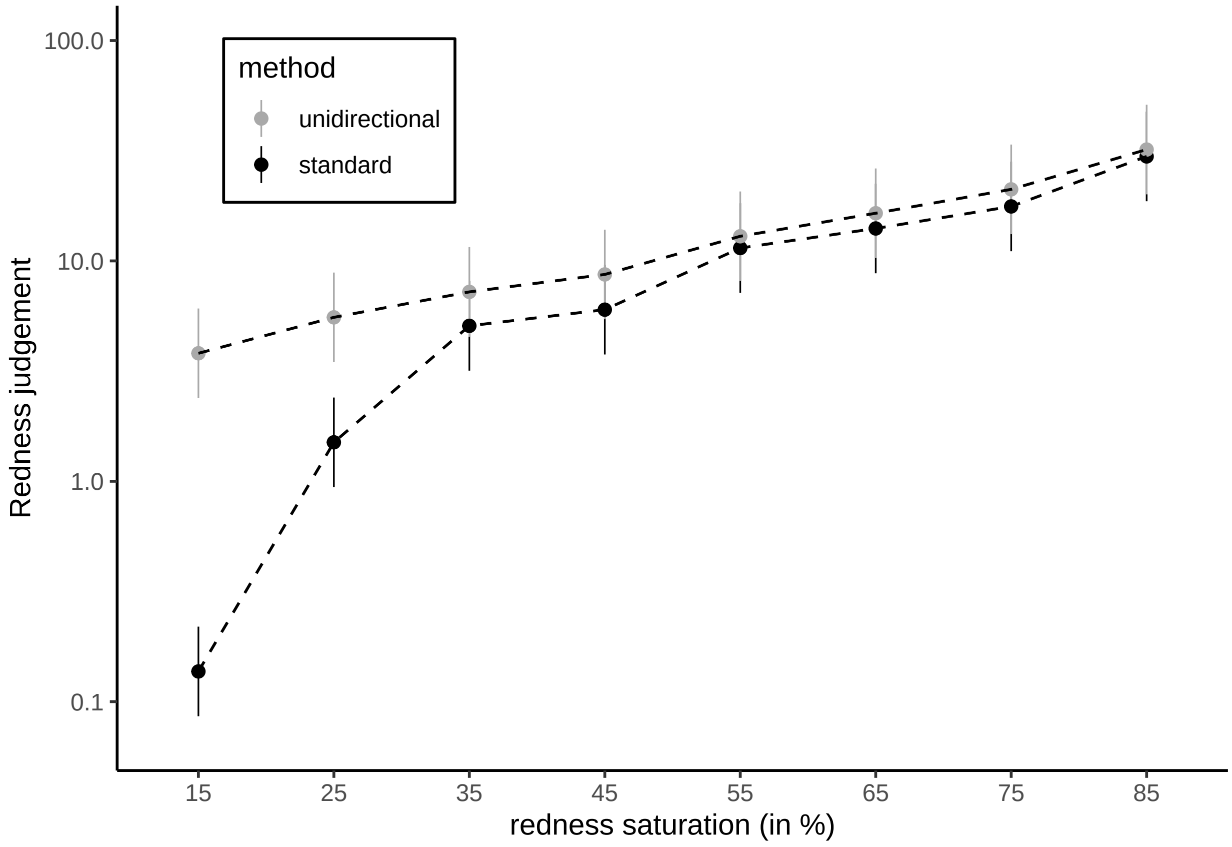


Figure 4

```
ggsave(
  paste0("final_plots/study3_figure3.png"),
  dpi = 600,
  height = 4,
  width = 5,
  units = "in"
)
```

Bayesian mixed effects models (standard condition)

```
prior_settings <- c(set_prior('normal(0, 5)', nlpar = "a"),
                    set_prior('normal(1.0, 0.5)', nlpar = "b", lb = 0))
```

```
(formula = bf(
      redness_rating_comparable ~ a * saturation ^ b ,
      a ~ (1 | File),
      b ~ (1 | File),
      nl = TRUE
    ))
```

Fit power law

```
## redness_rating_comparable ~ a * saturation^b
## a ~ (1 | File)
## b ~ (1 | File)
```

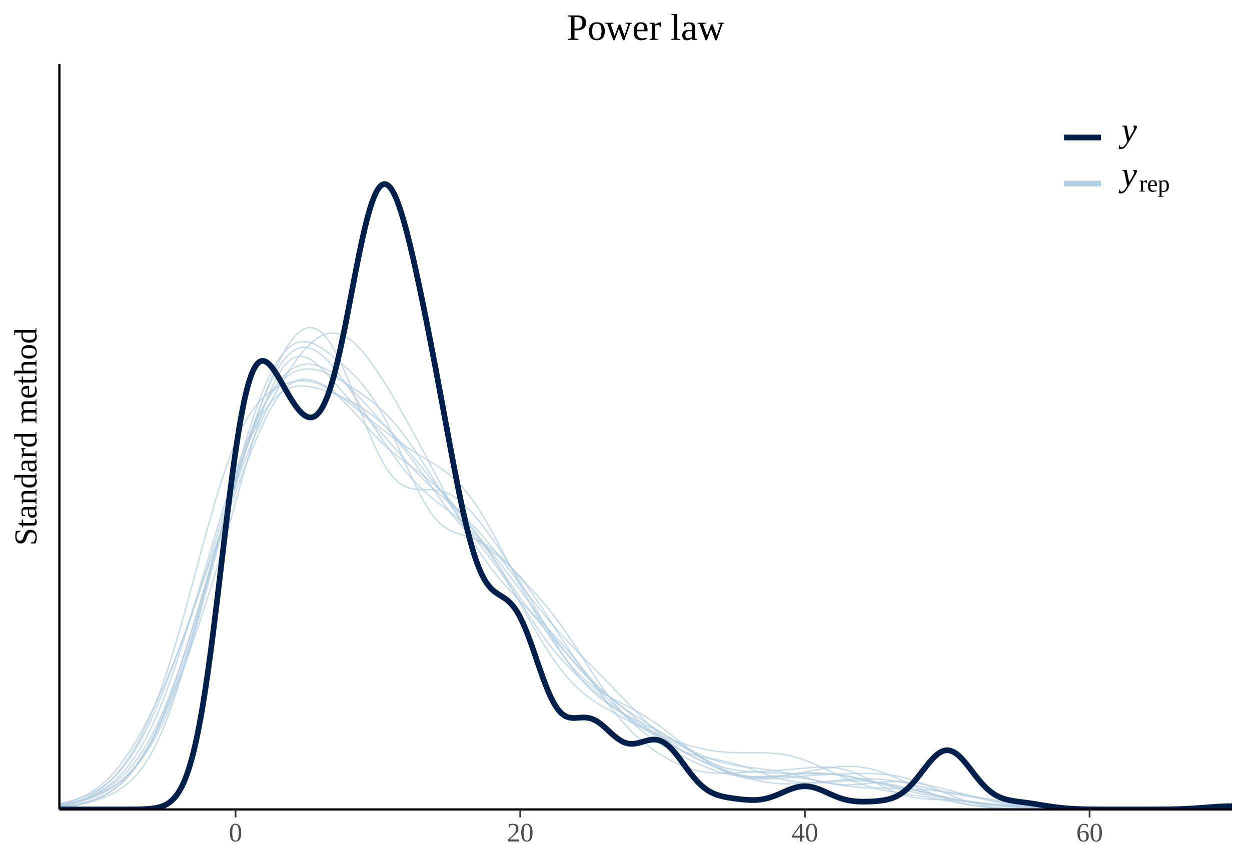
```
# make_stancode(formula, data = df[df$condition == 'standard', ], prior = prior_settings)
```

```
(
  power_law_standard <-
    brm(
      formula,
      data = df[df$condition == 'standard',],
      save_all_pars = T,
      sample_prior = 'yes',
      warmup = 2000,
      iter = 7000,
      cores = 4,
      control = list(adapt_delta = 0.96, max_treedepth = 15),
      prior = prior_settings,
      file = 'study3_power_standard_x'
    )
)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: redness_rating_comparable ~ a * saturation^b
##          a ~ (1 | File)
##          b ~ (1 | File)
##    Data: df[df$condition == "standard", ] (Number of observations: 720)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Group-Level Effects:
## ~File (Number of levels: 18)
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(a_Intercept)     0.24      0.05     0.17     0.35 1.00     4279     7324
## sd(b_Intercept)     1.01      0.21     0.69     1.49 1.00     5274     8608
##
## Population-Level Effects:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## a_Intercept     0.45      0.06     0.33     0.56 1.00     3082     5810
## b_Intercept     1.99      0.23     1.52     2.42 1.00     4071     7693
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.04      0.00     0.03     0.04 1.00    25386    14722
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
(
  pow_standard_plot = pp_check(power_law_standard) +
    labs(title = 'Power law', y = 'Standard method') +
    scale_x_continuous(labels=c(0,20,40,60), breaks=c(0,0.2,0.4,0.6)) +
    scale_y_continuous(limits = c(0, 7)) +
    theme(
      plot.title = element_text(hjust = 0.5),
      legend.position = c(0.9, 0.9)
    )
)
```

```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



```
brms::loo(power_law_standard)
```

Model metrics (LOOCV, WAIC, marginal likelihood)

```
## Warning: Found 3 observations with a pareto_k > 0.7 in model
## 'power_law_standard'. It is recommended to set 'moment_match = TRUE' in order to
## perform moment matching for problematic observations.
```

```
##
## Computed from 20000 by 720 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo   1323.4 43.2
## p_loo        68.2 13.4
## looic     -2646.7 86.3
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)     711   98.8%   2210
##  (0.5, 0.7]   (ok)         6    0.8%   715
##    (0.7, 1]   (bad)        2    0.3%   44
##    (1, Inf)   (very bad)   1    0.1%   11
## See help('pareto-k-diagnostic') for details.
```

```
brms::waic(power_law_standard)
```

```
## Warning:
## 34 (4.7%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
##
## Computed from 20000 by 720 log-likelihood matrix
##
##           Estimate   SE
## elpd_waic   1325.1 42.6
## p_waic        66.5 12.8
## waic       -2650.2 85.2
##
## 34 (4.7%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
brms::bridge_sampler(power_law_standard)
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
```

```
## Bridge sampling estimate of the log marginal likelihood: 1269.088
## Estimate obtained in 6 iteration(s) via method "normal".
```

```
prior_settings = c(
  set_prior('normal(0,1)', class = 'b', coef = 'saturation'),
  set_prior('normal(0,5)', class = 'b', coef = 'Intercept')
)
```

```
(formula = redness_rating_comparable ~ 0 + Intercept + saturation + (1 + saturation |File))
```

Fit linear model

```
## redness_rating_comparable ~ 0 + Intercept + saturation + (1 +
##     saturation | File)
```

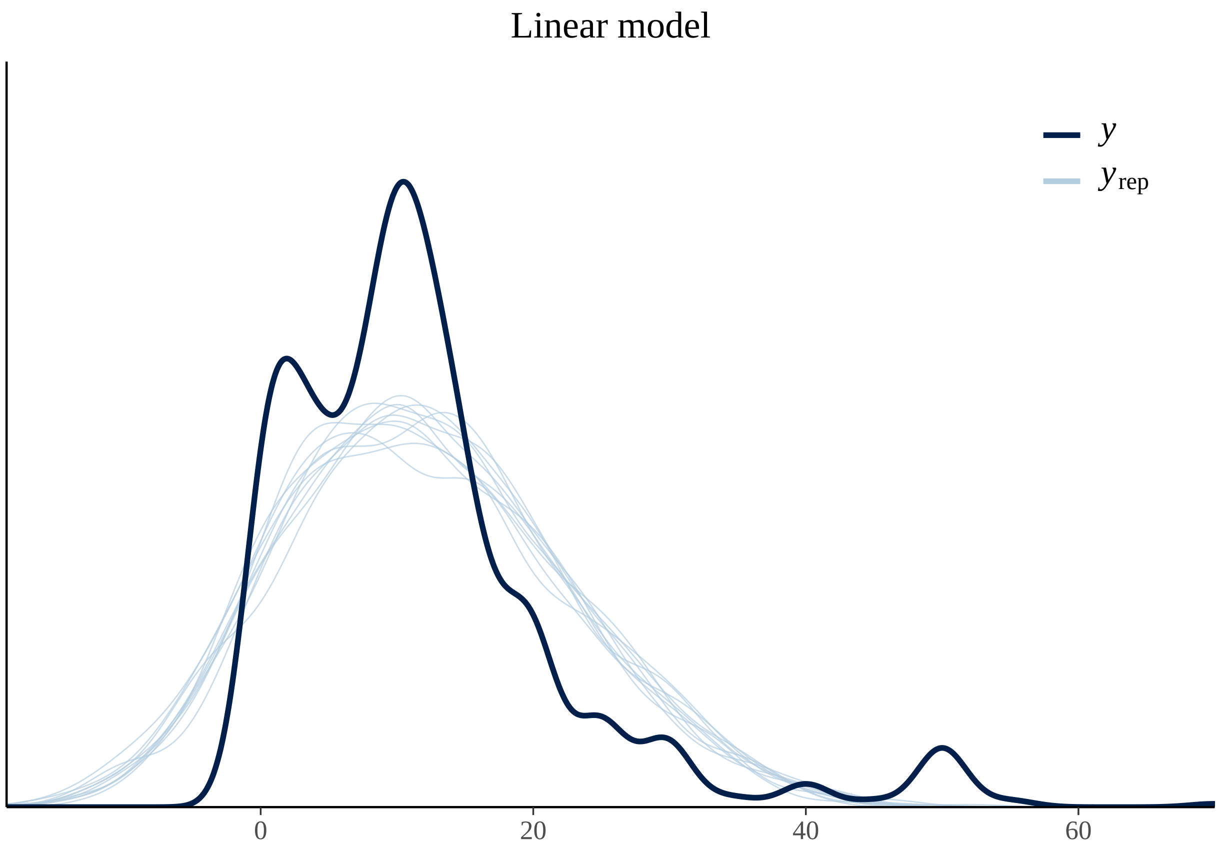
```
# make_stancode(formula, data = df[df$condition == 'standard', ], prior = prior_settings)
```

```
(linear_standard <-
  brm(
    formula,
    data = df[df$condition == 'standard', ],
    save_all_pars = T,
    sample_prior = 'yes',
    warmup = 2000,
    cores = 4,
    prior = prior_settings,
    iter = 7000,
    file = 'study3_linear_standard_x'))
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: redness_rating_comparable ~ 0 + Intercept + saturation + (1 + saturation | File)
##    Data: df[df$condition == "standard", ] (Number of observations: 720)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Group-Level Effects:
## ~File (Number of levels: 18)
##                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                 0.05      0.01     0.03     0.08 1.00     6634
## sd(saturation)                0.14      0.03     0.10     0.21 1.00     5951
## cor(Intercept,saturation)    -0.98      0.02    -1.00    -0.92 1.00     7999
##                           Tail_ESS
## sd(Intercept)                10211
## sd(saturation)                9412
## cor(Intercept,saturation)     9592
##
## Population-Level Effects:
##            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     -0.07      0.01    -0.09    -0.04 1.00     4745     7905
## saturation     0.37      0.04     0.30     0.44 1.00     4667     7078
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.05      0.00     0.05     0.05 1.00    33352    15061
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
(
  lin_standard_plot = pp_check(linear_standard) + labs(title = 'Linear model') +
    scale_x_continuous(labels=c(0,20,40,60), breaks=c(0,0.2,0.4,0.6)) +
    scale_y_continuous(limits = c(0, 7)) +
    theme(
      plot.title = element_text(hjust = 0.5),
      legend.position = c(0.9, 0.9)
  )
)
```

```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



```
brms::loo(linear_standard)
```

Model metrics (LOOCV, WAIC, marginal likelihood)

```
## Warning: Found 1 observations with a pareto_k > 0.7 in model 'linear_standard'.
## It is recommended to set 'moment_match = TRUE' in order to perform moment
## matching for problematic observations.
```

```
##
## Computed from 20000 by 720 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo   1107.0 42.7
## p_loo        46.7  7.5
## looic     -2214.0 85.4
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)     719   99.9%   2469
##  (0.5, 0.7]   (ok)         0    0.0%   <NA>
##    (0.7, 1]   (bad)        1    0.1%   109
##    (1, Inf)   (very bad)   0    0.0%   <NA>
## See help('pareto-k-diagnostic') for details.
```

```
brms::waic(linear_standard)
```

```
## Warning:
## 24 (3.3%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
##
## Computed from 20000 by 720 log-likelihood matrix
##
##           Estimate   SE
## elpd_waic   1107.2 42.7
## p_waic        46.5  7.5
## waic       -2214.4 85.4
##
## 24 (3.3%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
brms::bridge_sampler(linear_standard)
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
```

```
## Bridge sampling estimate of the log marginal likelihood: 1069.355
## Estimate obtained in 6 iteration(s) via method "normal".
```

Model comparison (Bayes factors) Compute logBF in favor of power law. Takes a few minutes to run, hence commented out.

```
bfs_standard = vector('numeric', length = 5)
for (i in 1:5) {
  bfs_standard[i] = log(1 / bayes_factor(linear_standard, power_law_standard)$bf)
}
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
```

```
print(paste0('Mean logBF:', mean(bfs_standard), 'Std logBF:', sd(bfs_standard)))
```

```
## [1] "Mean logBF:199.755857679022Std logBF:0.0423596813878901"
```

Bayesian mixed effects models (unidirectional condition)

```
prior_settings <- c(set_prior('normal(0, 5)', nlpar = "a"),
                    set_prior('normal(1.0, 0.5)', nlpar = "b", lb = 0))
```

```
(formula = bf(
      redness_rating_comparable ~ a * saturation ^ b ,
      a ~ (1 | File),
      b ~ (1 | File),
      nl = TRUE
    ))
```

Fit power law

```
## redness_rating_comparable ~ a * saturation^b
## a ~ (1 | File)
## b ~ (1 | File)
```

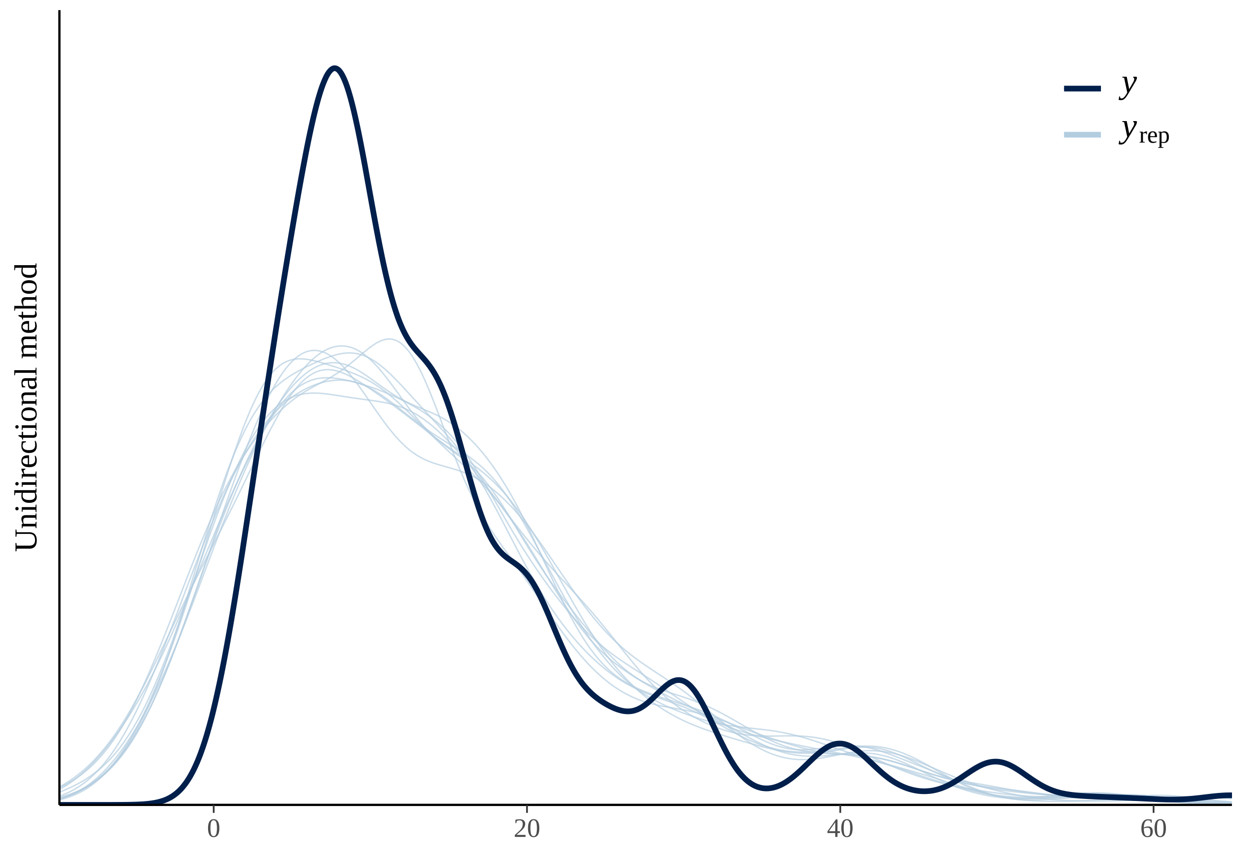
```
# make_stancode(formula, data = df[df$condition == 'unidirectional', ], prior = prior_settings)
```

```
(
  power_law_unidirectional <-
    brm(
      formula,
      data = df[df$condition == 'unidirectional',],
      save_all_pars = T,
      sample_prior = 'yes',
      warmup = 2000,
      iter = 7000,
      cores = 4,
      control = list(adapt_delta = 0.96, max_treedepth = 15),
      prior = prior_settings,
      file = 'study3_power_unidirectional_x'
    )
)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: redness_rating_comparable ~ a * saturation^b
##          a ~ (1 | File)
##          b ~ (1 | File)
##    Data: df[df$condition == "unidirectional", ] (Number of observations: 704)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Group-Level Effects:
## ~File (Number of levels: 18)
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(a_Intercept)     0.24      0.05     0.17     0.35 1.00     4555     7435
## sd(b_Intercept)     0.91      0.18     0.63     1.33 1.00     4553     7719
##
## Population-Level Effects:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## a_Intercept     0.46      0.06     0.34     0.57 1.00     3542     5503
## b_Intercept     1.73      0.21     1.31     2.13 1.00     4438     7068
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.04      0.00     0.03     0.04 1.00    20334    13326
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
(
  pow_unidirectional_plot = pp_check(power_law_unidirectional) +
    scale_x_continuous(labels=c(0,20,40,60), breaks=c(0,0.2,0.4,0.6)) +
    scale_y_continuous(limits = c(0, 7)) +
    labs(y = 'Unidirectional method') +
    theme(legend.position = c(0.9, 0.9))
)
```

```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



```
brms::loo(power_law_unidirectional)
```

Model metrics (LOOCV, WAIC, marginal likelihood)

```
## Warning: Found 1 observations with a pareto_k > 0.7 in model
## 'power_law_unidirectional'. It is recommended to set 'moment_match = TRUE' in
## order to perform moment matching for problematic observations.
```

```
##
## Computed from 20000 by 704 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo   1307.9 36.9
## p_loo        62.5  9.5
## looic     -2615.8 73.8
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)     697   99.0%   1522
##  (0.5, 0.7]   (ok)         6    0.9%   269
##    (0.7, 1]   (bad)        1    0.1%   20
##    (1, Inf)   (very bad)   0    0.0%   <NA>
## See help('pareto-k-diagnostic') for details.
```

```
brms::waic(power_law_unidirectional)
```

```
## Warning:
## 34 (4.8%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
##
## Computed from 20000 by 704 log-likelihood matrix
##
##           Estimate   SE
## elpd_waic   1309.0 36.7
## p_waic        61.4  9.2
## waic       -2617.9 73.3
##
## 34 (4.8%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
brms::bridge_sampler(power_law_unidirectional)
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
```

```
## Bridge sampling estimate of the log marginal likelihood: 1246.294
## Estimate obtained in 6 iteration(s) via method "normal".
```

```
prior_settings = c(
  set_prior('normal(0,1)', class = 'b', coef = 'saturation'),
  set_prior('normal(0,5)', class = 'b', coef = 'Intercept')
)
```

```
(formula = redness_rating_comparable ~ 0 + Intercept + saturation + (1 + saturation |File))
```

Fit linear model

```
## redness_rating_comparable ~ 0 + Intercept + saturation + (1 +
##     saturation | File)
```

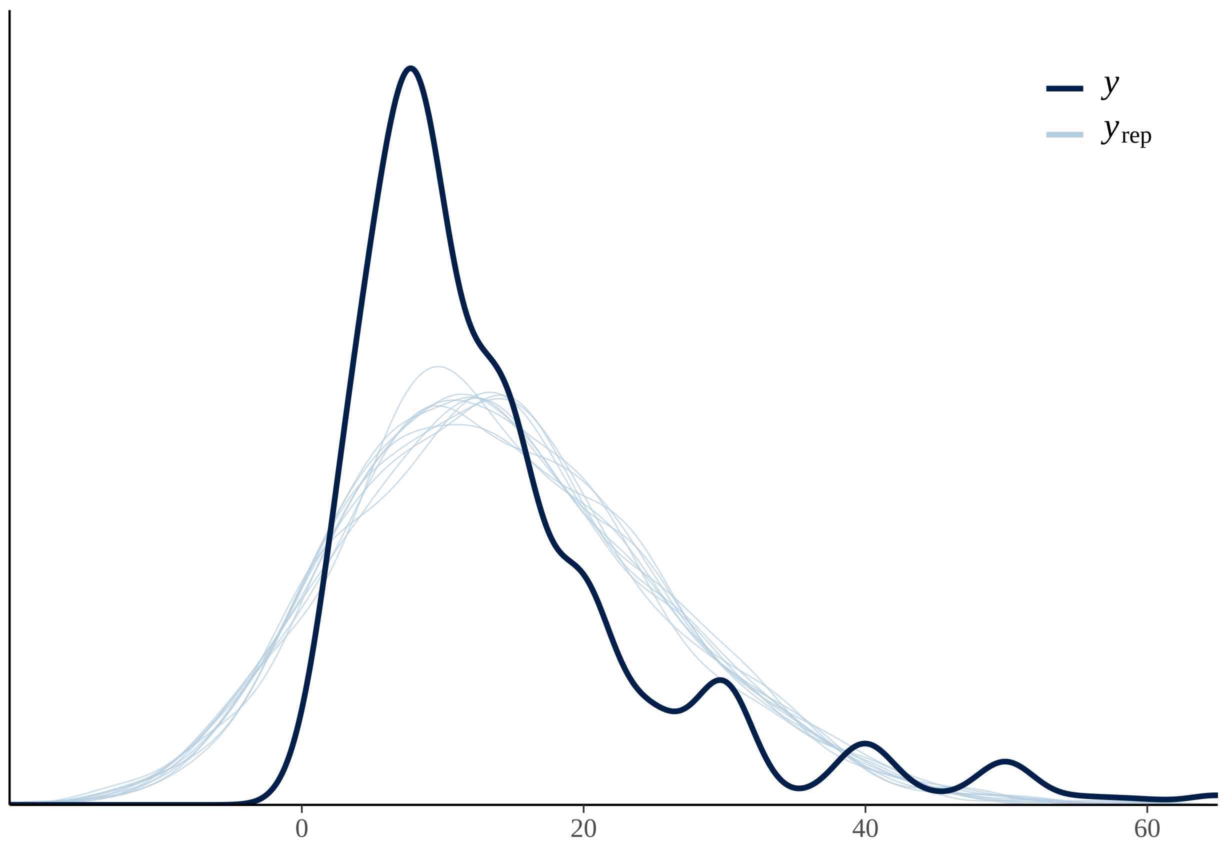
```
# make_stancode(formula, data = df[df$condition == 'unidirectional', ], prior = prior_settings)
```

```
(
  linear_unidirectional <-
    brm(
      formula,
      data = df[df$condition == 'unidirectional',],
      save_all_pars = T,
      sample_prior = 'yes',
      warmup = 2000,
      cores = 4,
      prior = prior_settings,
      iter = 7000,
      file = 'study3_linear_unidirectional_x'
    )
)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: redness_rating_comparable ~ 0 + Intercept + saturation + (1 + saturation | File)
##    Data: df[df$condition == "unidirectional", ] (Number of observations: 704)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Group-Level Effects:
## ~File (Number of levels: 18)
##                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                 0.06      0.01     0.04     0.09 1.00     4600
## sd(saturation)                0.18      0.03     0.12     0.25 1.00     4326
## cor(Intercept,saturation)    -1.00      0.00    -1.00    -0.98 1.00     9694
##                           Tail_ESS
## sd(Intercept)                 9041
## sd(saturation)                8110
## cor(Intercept,saturation)    12046
##
## Population-Level Effects:
##            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     -0.05      0.02    -0.08    -0.02 1.00     3188     5861
## saturation     0.39      0.04     0.30     0.47 1.00     3094     5580
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.05      0.00     0.05     0.05 1.00    29565    15028
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
(lin_unidirectional_plot = pp_check(linear_unidirectional) +
   scale_x_continuous(labels=c(0,20,40,60), breaks=c(0,0.2,0.4,0.6)) +
   scale_y_continuous(limits = c(0, 7)) +
   theme(legend.position = c(0.9, 0.9)))
```

```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



```
brms::loo(linear_unidirectional)
```

Model metrics (LOOCV, WAIC, marginal likelihood)

```
##
## Computed from 20000 by 704 log-likelihood matrix
##
##           Estimate   SE
## elpd_loo    1082.9 35.9
## p_loo         41.1  6.0
## looic      -2165.9 71.8
## ------
## Monte Carlo SE of elpd_loo is 0.1.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)     701   99.6%   1493
##  (0.5, 0.7]   (ok)         3    0.4%   233
##    (0.7, 1]   (bad)        0    0.0%   <NA>
##    (1, Inf)   (very bad)   0    0.0%   <NA>
##
## All Pareto k estimates are ok (k < 0.7).
## See help('pareto-k-diagnostic') for details.
```

```r
brms::waic(linear_unidirectional)
```

```
## Warning:
## 21 (3.0%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
##
## Computed from 20000 by 704 log-likelihood matrix
##
##           Estimate   SE
## elpd_waic   1083.2 35.8
## p_waic        40.8  5.9
## waic       -2166.5 71.7
##
## 21 (3.0%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```r
brms::bridge_sampler(linear_unidirectional)
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
```

```
## Bridge sampling estimate of the log marginal likelihood: 1041.43
## Estimate obtained in 5 iteration(s) via method "normal".
```

Model comparison (Bayes factors) Compute logBF in favor of power law. Takes a few minutes to run, hence commented out.

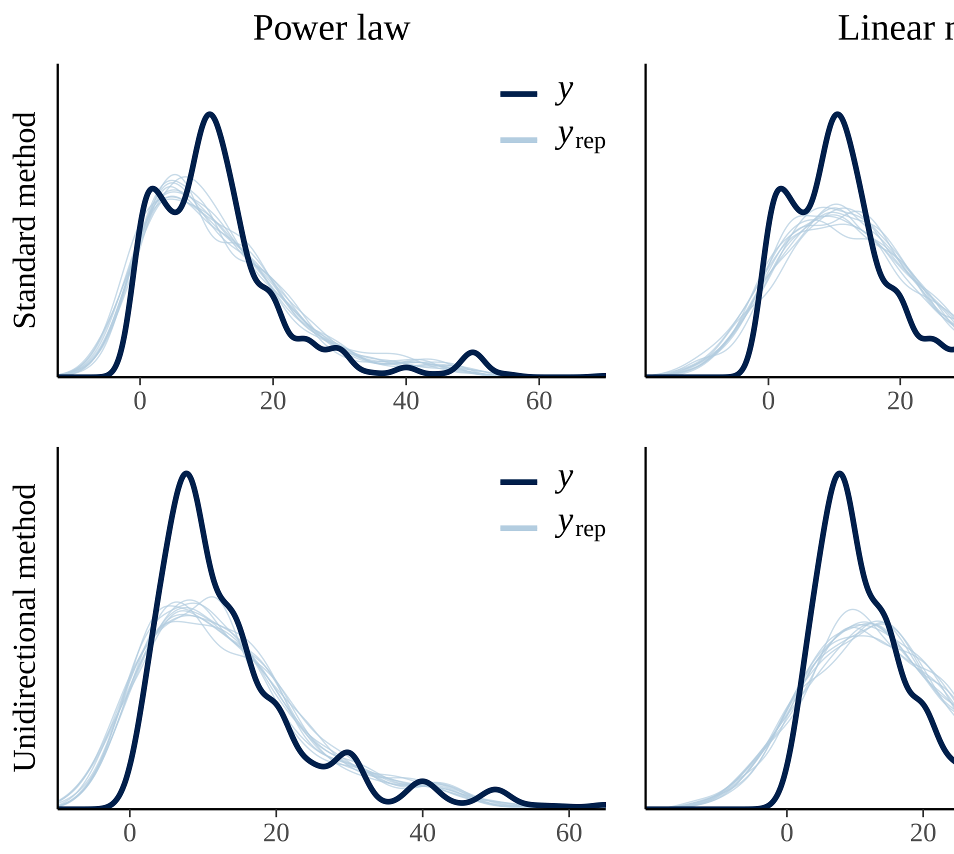
```r
bfs_unidirectional = vector('numeric', length = 5)
for (i in 1:5) {
  bfs_unidirectional[i] = log(1 / bayes_factor(linear_unidirectional, power_law_unidirectional)$bf)
}
```

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 8
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
```

```
print(paste0('Mean logBF:', mean(bfs_unidirectional), 'Std logBF:', sd(bfs_unidirectional)))
```

```
## [1] "Mean logBF:204.796370950875Std logBF:0.0524814192557632"
```

```
pp_grid = (
  grid.arrange(
    pow_standard_plot,
    lin_standard_plot,
    pow_unidirectional_plot,
    lin_unidirectional_plot
  )
)
```



Posterior predictive plot (Figure 5)

```
ggsave(
  paste0("final_plots/study3_pp_plot.png"),
  plot = pp_grid,
  dpi = 600,
  height = 6,
  width = 7,
  units = "in"
)
```

Bayesian mixed-effects models (aggregated data)

```
df_agg = df %>% group_by(saturation,condition) %>% summarise(median_rating = median(redness_rating_compa
```

Fit power law (standard condition)

```
## `summarise()` regrouping output by 'saturation' (override with `.groups` argument)
```

```r
prior_settings <- c(set_prior('normal(0, 5)', nlpar = "a"),
            set_prior('normal(1.0, 0.5)', nlpar = "b", lb = 0))
```

```r
(formula = bf(median_rating ~ a * saturation ^ b , a ~ 1, b ~ 1 , nl = TRUE))
```

```
## median_rating ~ a * saturation^b
## a ~ 1
## b ~ 1
```

```r
# make_stancode(formula, data = df_agg[df_agg$condition == 'standard', ], prior = prior_settings)
```

```r
(
  power_law_standard_agg <-
    brm(
      formula,
      data = df_agg[df_agg$condition == 'standard',],
      save_all_pars = T,
      sample_prior = 'yes',
      warmup = 2000,
      iter = 7000,
      cores = 4,
      control = list(adapt_delta = 0.96, max_treedepth = 20),
      prior = prior_settings,
      file = 'study3_power_standard_agg_x'
    )
)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: median_rating ~ a * saturation^b
##          a ~ 1
##          b ~ 1
##    Data: df_agg[df_agg$condition == "standard", ] (Number of observations: 8)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Population-Level Effects:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## a_Intercept     0.33      0.04     0.25     0.40 1.00     5929     6659
## b_Intercept     1.72      0.28     1.14     2.25 1.00     5903     6051
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.03      0.01     0.01     0.05 1.00     6154     8064
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
prior_settings <- c(set_prior('normal(0, 5)', nlpar = "a"),
            set_prior('normal(1.0, 0.5)', nlpar = "b", lb = 0))
```

```
(formula = bf(median_rating ~ a * saturation ^ b , a ~ 1, b ~ 1 , nl = TRUE))
```

Fit power law (unidirectional condition)

```
## median_rating ~ a * saturation^b
## a ~ 1
## b ~ 1
```

```
# make_stancode(formula, data = df_agg[df_agg$condition == 'unidirectional', ], prior = prior_settings)
```

```
(
  power_law_unidirectional_agg <-
    brm(
      formula,
      data = df_agg[df_agg$condition == 'unidirectional',],
      save_all_pars = T,
      sample_prior = 'yes',
      warmup = 2000,
      iter = 7000,
      cores = 4,
      control = list(adapt_delta = 0.96, max_treedepth = 20),
      prior = prior_settings,
      file = 'study3_power_unidirectional_agg_x'
    )
)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: median_rating ~ a * saturation^b
##          a ~ 1
##          b ~ 1
##    Data: df_agg[df_agg$condition == "unidirectional", ] (Number of observations: 8)
## Samples: 4 chains, each with iter = 7000; warmup = 2000; thin = 1;
##          total post-warmup samples = 20000
##
## Population-Level Effects:
##              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## a_Intercept      0.34      0.04     0.26     0.42 1.00     6117     5750
## b_Intercept      1.56      0.26     1.03     2.08 1.00     6311     5676
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.03      0.01     0.02     0.06 1.00     6197     6391
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```