

A tutorial of Bayesian beta regressions with brms in R

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Abstract

This is the abstract. Lorem ipsum dolor sit amet, consectetur adipiscing elit. Vestibulum augue turpis, dictum non malesuada a, volutpat eget velit. Nam placerat turpis purus, eu tristique ex tincidunt et. Mauris sed augue eget turpis ultrices tincidunt. Sed et mi in leo porta egestas. Aliquam non laoreet velit. Nunc quis ex vitae eros aliquet auctor nec ac libero. Duis laoreet sapien eu mi luctus, in bibendum leo molestie. Sed hendrerit diam diam, ac dapibus nisl volutpat vitae. Aliquam bibendum varius libero, eu efficitur justo rutrum at. Sed at tempus elit.

Keywords: keyword1, keyword2

1. Introduction

Phonetic research often involves numeric continuous outcome variables, like durations, frequencies, loudness and ratios. Another commonly employed type of outcome variable are proportions: for example, proportion of voicing during closure, vocal folds contact quotient, gesture amplitude, nasalance. Moreover, virtually any measure can be MIN-MAX normalised, a procedure which transforms values so that they are in the range 0–1.

Regression models are very common, but there is a tendency of using Gaussian distribution families (i.e. probability distributions for the outcome variable) for anything that is numeric. A possible reason is that the base R function for fitting regression models, `lm()`, and the `lme4` function used to fit regression models with varying terms, `lmer()`, both fit Gaussian regressions by default and the user does not have to specify the distribution family. This tacit defaulting to Gaussian models is also reflected in teaching practices, where test and models using the Gaussian distribution are the first to be taught, due to their relative simplicity and the fact that other models are generalisations of Gaussian models.

However, proportion are naturally not Gaussian, since they are limited between 0 and 1. The theoretical distribution that generates values with this characteristics is the beta distribution. Thus, regression models with proportions as the outcome variable should be fitted using a beta distribution as the distribution family. This tutorial introduces researchers to beta regression models in R using the package `brms`. Familiarity with regression modelling in R with a package like `lme4` is assumed, but no prior knowledge of Bayesian statistics is necessary.

2. The beta distribution

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3. Case study 1: voicing within consonant closure

For the first case study, we will model the proportion of voicing within consonant closure. The measurements come from a data set of audio and electroglottographic (EGG) recordings of 19 speakers of North-western Italian. The participants read frame sentences which included target words of the form /CVC_o/, where /C/ was either /k, t, p/ in all permutations and /V/ was either /i, e, a, , u/ (two resulting words, /peto/ and /kako/ were excluded because they are profanities), for a total of 43 target words. There were 4 different frame sentence, with a total of 172 trials per participant (3,268 grand total). The actual observation count is 2,419, after removing speech errors, EGG measurement errors, and cases in which voicing ceased before the closure onset/after the closure offset of the second /C/.

The proportion of voicing during the closure of the second /C/ was calculated as the proportion of contiguous voicing duration after closure onset to total duration of closure. The following code chunk attaches the tidyverse packages (for reading and wrangling data) and loads the `ita_egg` tibble (data frame). The tibble is filtered so as to remove voicing proportions (`voi_clo_prop`) that are smaller than 0 and greater than 1. The variables `vowel` and `c2` are converted to factors to specify the order of the levels.

```
# attach tidyverse and set light theme for plots
library(tidyverse)
theme_set(theme_light())

# load tibble
load("data/coretta2018/ita_egg.rda")

# filter and mutate data
ita_egg <- ita_egg |>
  filter(voi_clo_prop > 0, voi_clo_prop < 1) |>
  mutate(
    vowel = factor(vowel, levels = c("i", "e", "a", "o", "u")),
    c2 = factor(c2, levels = c("k", "t", "p"))
  )
```

Here is what the tibble looks like.

`ita_egg`

```
# A tibble: 2,419 x 53
  speaker ipu stimulus sentence_ons sentence_off word_ons word_off v1_ons
  <chr> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
1 it01 ipu_1 Ripete 'po~ 13.2 14.9 13.7 14.1 13.9
2 it01 ipu_2 Ripete 'to~ 16.9 18.6 17.4 17.9 17.5
3 it01 ipu_3 Ripete 'pa~ 20.2 21.9 20.7 21.1 20.8
4 it01 ipu_4 Sentivo 't~ 23.5 25.1 24.0 24.4 24.1
5 it01 ipu_5 Sentivo 't~ 26.3 27.8 26.8 27.2 26.9
6 it01 ipu_6 Scrivete '~ 29.2 30.9 29.7 30.1 29.8
7 it01 ipu_7 Sentivo 'c~ 32.1 33.6 32.6 33.1 32.8
8 it01 ipu_8 Scrivete '~ 35.0 36.6 35.5 35.9 35.6
9 it01 ipu_9 Ha detto '~ 41.9 43.5 42.3 42.7 42.4
10 it01 ipu_10 Sentivo 'p~ 47.4 48.9 47.9 48.4 48.1
# i 2,409 more rows
# i 45 more variables: c2_ons <dbl>, v2_ons <dbl>, voice_ons <dbl>,
```

```
# voice_off <dbl>, c1_rel <dbl>, c2_rel <dbl>, stimulus_id <dbl>,
# sentence <chr>, word <chr>, c1 <chr>, vowel <fct>, c2 <fct>,
# backness <chr>, height <fct>, c1_place <fct>, c2_place <fct>,
# v1_duration <dbl>, c2_clos_duration <dbl>, rel_voff <dbl>,
# sent_duration <dbl>, speech_rate <dbl>, speech_rate_c <dbl>, ...
```

Figure 1 shows the raw voicing duration proportion values split by vowel /i, e, a, , u/ and second consonant /k, t, p/ in the /CVCo/ target words. The plot suggests that, on average, the voicing proportion is slightly lower with /k/ than with /t, p/. Moreover, there is greater variability between vowels in /t, p/ than in /k/. We will use a beta regression model to assess these patterns. [“expectations” XXX]

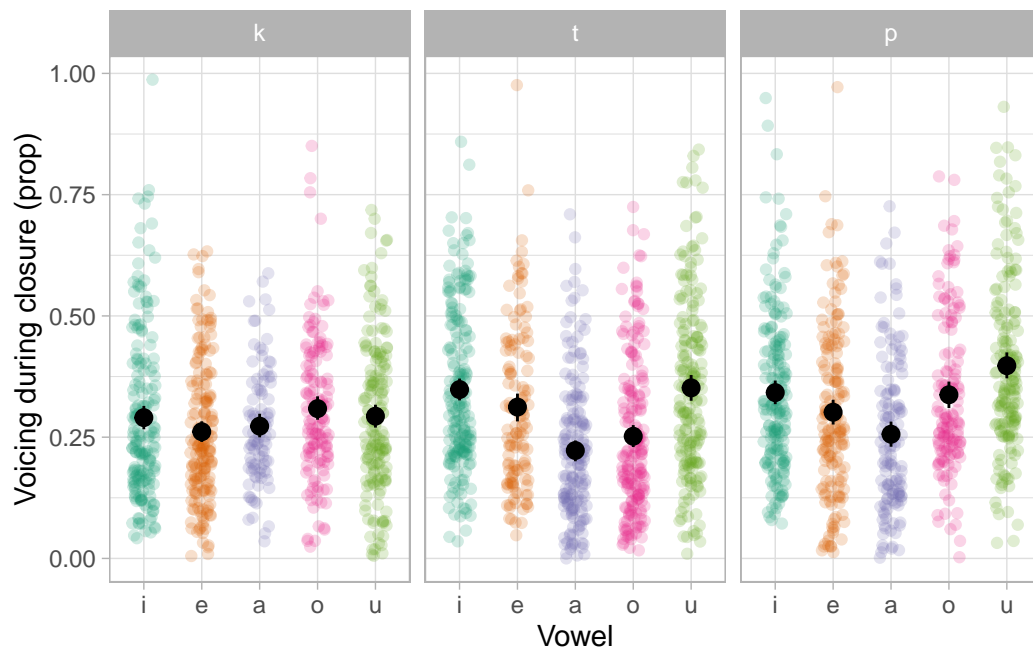


Figure 1: Proportion of voicing during the closure of the second consonant in /CVCo/ words by vowel and the second consonant.

We will use brms to fit Bayesian beta regressions. [XXX why Bayesian]. The model has voicing proportion as the outcome variable and the following terms: an interaction between vowel (/i, e, a, , u/) and second consonant C2 (/k, t, p/), centred speech rate (number of syllables per second); as varying (aka random) terms, by-speaker varying coefficients for the vowel/consonant interaction and for centred speech rate.² The categorical predictors vowel and C2 are coded using indexing rather than traditional R contrasts: in R, this corresponds to suppressing the model’s intercept with the 0 + syntax; using indexing instead of contrasts makes it easier to specify priors. For pedagogical simplicity, the model will use the default priors, but note that in real data analyses contexts, priors should be specified by the user. I refer the readers to XXX.

```
# attach brms
library(brms)

# fit the model
# Takes 3 minutes on MacBook Pro 2020, M1
```

²Footnote about Gelman’s terminology for random effects.

```

voi_prop_bm <- brm(
  # model formula
  voi_clo_prop ~
    # constant terms
    0 + vowel:c2 + speech_rate_c +
    # varying terms
    (0 + vowel:c2 + speech_rate_c | speaker),
  # uses the beta family for the outcome
  family = Beta,
  data = ita_egg,
  cores = 4,
  seed = 3749,
  file = "data/cache/voi_prop_bm"
)

```

The `summary()` function prints the full model summary. For conciseness, we will use the `fixef()` function which prints the regression coefficients. [EXPLAIN EXPECTED PREDICTIONS XXX]. The full summary with an explanation of each part can be found in XXX. For each coefficient in the model, `fixef()` prints the name of the coefficient, the mean estimate, the estimate error and the lower and upper limits of a Bayesian Credible interval (CrI). Here, we print an 80% CrI. There is nothing special about 95% CrI within Bayesian inference and instead experts recommend to check and report a variety of CrIs. Bayesian CrIs indicate that at a certain probability levels the “true” estimate lies within that interval: so, for example, a 90% CrI [A, B] indicates that there is a 90% probability that the “true” estimate is between A and B. Different probability levels correspond to different levels of confidence: the higher the probability the higher the confidence (always conditional on data and model). Obtaining CrIs at different probability levels allows researchers to make more fine-grained inferential statements than the frequentist significance dichotomy affords. For simplicity of exposition, we will use 80% CrIs in this case study but we strongly recommend researchers to always obtain CrIs at different levels of probability and base their inferences on all and not one in particular. To reiterate, in Bayesian inference, an 80% CrI indicates the range of values within which the true estimate falls at 80% probability or confidence. We round all values to the nearest 2 digits for clarity.

```

round(
  fixef(voi_prop_bm, prob = c(0.1, 0.9)),
  digits = 2
)

```

	Estimate	Est.Error	Q10	Q90
speech_rate_c	0.08	0.06	0.01	0.15
voweli:c2k	-0.91	0.14	-1.08	-0.74
vovela:c2k	-1.08	0.11	-1.22	-0.94
vowelo:c2k	-0.99	0.12	-1.14	-0.84
vowelu:c2k	-0.79	0.14	-0.96	-0.62
vowelu:c2k	-1.00	0.16	-1.20	-0.80
voweli:c2t	-0.66	0.11	-0.79	-0.53
vovela:c2t	-0.84	0.14	-1.02	-0.66
vowelu:c2t	-1.43	0.13	-1.60	-1.26
vowelu:c2t	-1.15	0.13	-1.31	-0.99
vowelu:c2t	-0.68	0.12	-0.83	-0.54
voweli:c2p	-0.68	0.11	-0.81	-0.54
vovela:c2p	-0.88	0.15	-1.07	-0.68

vowela:c2p	-1.14	0.13	-1.31	-0.98
vowelo:c2p	-0.66	0.11	-0.80	-0.53
vowelu:c2p	-0.44	0.12	-0.59	-0.28

The coefficients of a beta regression are estimated on the log-odds scale, as in Bernoulli/binomial (aka logistic) regressions. From the summary, we see that speech rate (number of syllables per second) has a positive effect on voicing proportion: the 80% CrI is between 0.01 and 0.15 log-odds [$\beta = 0.8$, $SD = 0.06$]. Log-odds can be converted to odd ratios by exponentiating the value: 0.01-0.15 log odds correspond to an odd ratio of 1.01 to 1.16, or as percentages, to an increase of voicing of 1 to 16% for every increase of one syllable per second. Since this is an 80% CrI, we can be 80% confident that the true effect of speech rate is between 1-16% increase of voicing proportion, conditional on the data and model. Note that transforming measures this way is appropriate *only* with quantile-based measures (like CrIs) but not with moments like the mean and standard deviation: to correctly get mean and SDs in the transformed scale, you must first extract the posterior draws (see below), convert them and then take moments such as mean and SD (for a more detailed explanation, see XXX).

Turning now to the coefficients for vowel and C2, given the indexing approach of coding these variables the model summary and the output of `fixef()` reports the *predictions* in log-odds for each combination of vowel and C2, rather than differences between levels. The CrIs of the vowel/C2 coefficients span all negative log-odds values: these correspond to proportions that are lower than 0.5 (which is 0 in log-odds). This matches the general trends in the raw data, which we plotted in Figure 1.

Next, we will plot the predicted proportions of each vowel/C2 combination at mean speech rate (i.e. centred speech rate = 0) and then calculate the average pair-wise difference in voicing proportion between /k, t, p/. Finally, we will assess whether there is greater between-vowel variability in /t, p/ relative to /k/.

Before being able to plot the predictions, it's important to get familiar with the so-called posterior draws. [Bayesian MCMC XXX]. Posterior draws can be conveniently obtained with the `as_draws_df()`. For the moment, we will extract only the draws of the constant regression coefficients (model variables starting with `b_`). To check which coefficients are available in a model, use `get_variables()` from the tidybayes package. `as_draws_df()` returns a tibble where each column contains the drawn values of a coefficient. The probability distribution of the drawn values of each coefficient is the posterior probability distribution of that coefficient. Note that, due to the indexing coding of vowel and C2, all coefficient except `b_speech_rate_c` are *predicted log-odds* for each vowel/C2 combination (the drawn values for `b_speech_rate_c` are drawn *differences* in log-odds for each unit increase of speech rate). The drawn values are in log-odds, but we can convert them to proportions with `plogis()` (we will do this when plotting below).

```
# extract only coefficient variables starting with "b_"
voi_prop_bm_draws <- as_draws_df(voi_prop_bm, variable = "^b_", regex = TRUE)
voi_prop_bm_draws
```

```
# A draws_df: 1000 iterations, 4 chains, and 16 variables
  b_speech_rate_c b_voweli:c2k b_vowele:c2k b_vowela:c2k b_vowelo:c2k
1          0.159         -0.72         -1.05         -1.12         -1.02
2          0.035         -0.75         -1.39         -1.06         -0.89
3          0.126         -0.85         -0.98         -1.10         -0.64
4          0.064         -0.70         -1.07         -1.05         -0.83
5          0.032         -0.77         -1.18         -0.94         -0.70
6          0.073         -0.85         -1.23         -1.06         -0.77
7          0.101         -0.95         -1.07         -1.14         -0.86
8          0.074         -1.02         -1.07         -1.17         -0.83
9          0.087         -1.04         -1.07         -1.26         -0.79
```

```

10      0.092      -1.20      -1.04      -0.92      -0.64
   b_vowelu:c2k b_voweli:c2t b_vowele:c2t
1      -1.05      -0.62      -0.80
2      -1.04      -0.67      -0.99
3      -0.91      -0.66      -0.80
4      -1.07      -0.53      -0.87
5      -1.06      -0.63      -0.87
6      -1.00      -0.69      -0.73
7      -1.22      -0.74      -1.08
8      -1.22      -0.73      -1.04
9      -1.14      -0.66      -0.91
10     -0.84      -0.63      -0.61
# ... with 3990 more draws, and 8 more variables
# ... hidden reserved variables {'.chain', '.iteration', '.draw'}

```

We can now wrangle this tibble and plot the posterior distributions for each vowel/C2 combination.

```

voi_prop_bm_draws_long <- voi_prop_bm_draws |>
  # drop b_speech_rate_c before pivoting
  select(-b_speech_rate_c) |>
  # pivot vowel:c2 columns
  pivot_longer(`b_voweli:c2k`:`b_vowelu:c2p`, names_to = "coeff") |>
  # separate "coeff" labels into type ("b"), vowel and c2
  separate(coeff, into = c("type", "vowel", "c2"))

```

Warning: Dropping 'draws_df' class as required metadata was removed.

```
voi_prop_bm_draws_long
```

```

# A tibble: 60,000 x 7
  .chain .iteration .draw type vowel c2 value
  <int>    <int> <int> <chr> <chr> <chr> <dbl>
1      1      1      1 1 b voweli c2k -0.721
2      1      1      1 1 b vowele c2k -1.05
3      1      1      1 1 b vowela c2k -1.12
4      1      1      1 1 b vowelo c2k -1.02
5      1      1      1 1 b vowelu c2k -1.05
6      1      1      1 1 b voweli c2t -0.625
7      1      1      1 1 b vowele c2t -0.795
8      1      1      1 1 b vowela c2t -1.40
9      1      1      1 1 b vowelo c2t -1.10
10     1      1      1 1 b vowelu c2t -0.668
# i 59,990 more rows

```

For plotting, we can use ggplot2 statistics layers from the ggdist package. `stat_halfeye()` plots the density of the posterior probability (in grey), its median (point) and CrIs (lines). Let's use 60 and 80% CrIs and transform the log-odds values to proportions with `plogis()`.

```
# attach ggdist package
library(ggdist)
```

Attaching package: 'ggdist'

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

```
dstudent_t, pstudent_t, qstudent_t, rstudent_t
```

```
voi_prop_bm_draws_long |>
  ggplot(aes(plogis(value), vowel)) +
  stat_halfeye(.width = c(0.6, 0.8)) +
  facet_grid(rows = vars(c2))
```

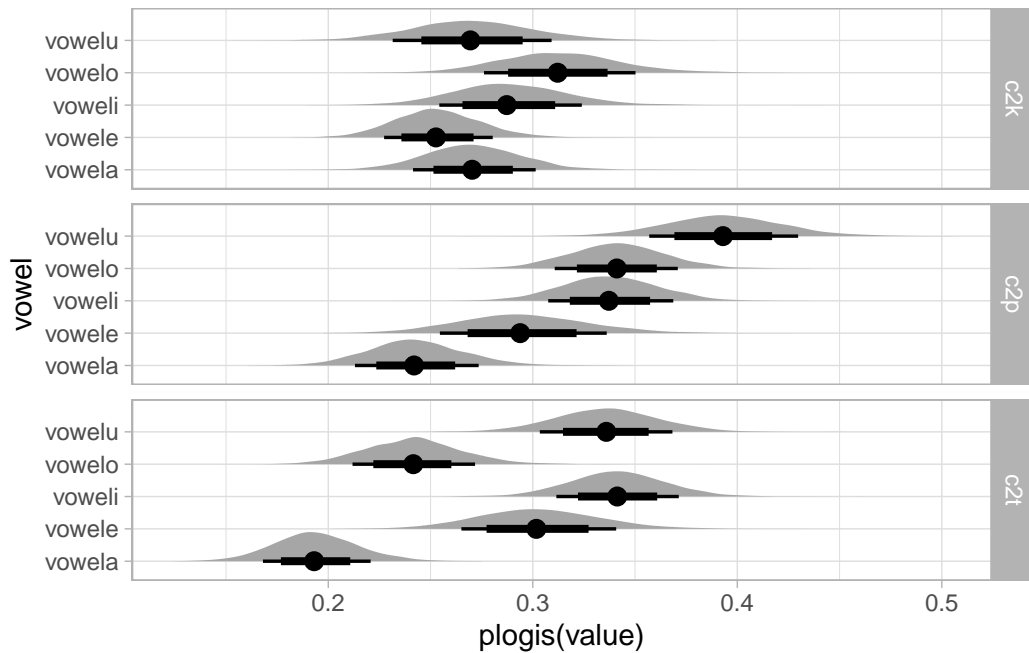


Figure 2

What if we want to plot the average predicted voicing proportion for the three consonants /k, t, p/? One approach is to take the mean across vowels within each consonant for each posterior draw, and the posterior distribution of the resulting list of values is the predicted posterior distribution of voicing proportion for each consonant, assuming an “average” vowel.

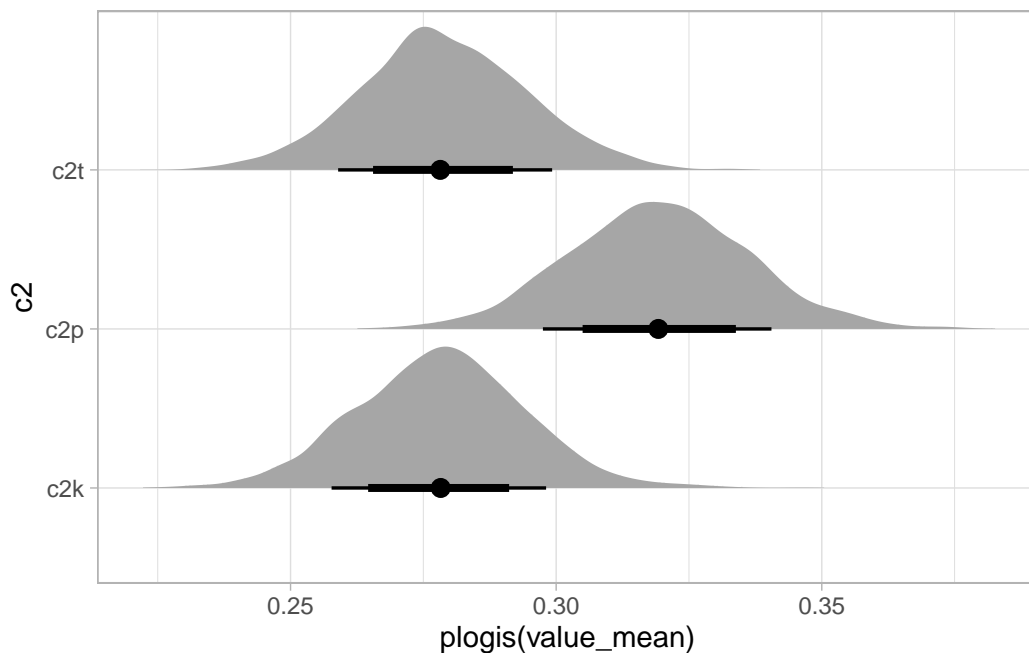
```
voi_prop_bm_draws_long_c2 <- voi_prop_bm_draws_long |>
  # grouping by .draw and c2 ensures that averaging applies only within draw and c2
  group_by(.draw, c2) |>
  # calculate the mean value within draw/c2
  summarise(
```

```

    value_mean = mean(value), .groups = "drop"
  )

voi_prop_bm_draws_long_c2 |>
  ggplot(aes(plogis(value_mean), c2)) +
    stat_halfeye(.width = c(0.6, 0.8))

```



Based on the posterior distributions of the mean voicing proportion by consonant, /p/ has a somewhat higher voicing proportion than /k/ and /t/. The real question is: how much higher? We can quantify this by taking the difference of the drawn values for /p/ and those for /t, k/. Since we want to compare /t, k/ to /p/, we should first average the draws of /t, k/ and then take the difference of the averaged draws and the draws of /p/.

```

voi_prop_bm_diff <- voi_prop_bm_draws_long_c2 |>
  # pivot data to create one column per consonant with the mean drawn values,
  # with one draw per row
  pivot_wider(names_from = c2, values_from = value_mean) |>
  mutate(
    # calculate the mean of /k/ and /t/, for each draw
    c2tk = mean(c(c2k, c2t)),
    # calculate the difference of /p/ and /t, k/
    c2p_tk_diff = c2p - c2tk
  )

voi_prop_bm_diff

```

```

# A tibble: 4,000 x 6
  .draw    c2k    c2p    c2t    c2tk c2p_tk_diff
  <int>  <dbl>  <dbl>  <dbl>  <dbl>      <dbl>

```



```

1      1 -0.992 -0.745 -0.917 -0.953      0.208
2      2 -1.02  -0.790 -1.03  -0.953      0.163
3      3 -0.895 -0.687 -0.890 -0.953      0.266
4      4 -0.944 -0.814 -0.910 -0.953      0.140
5      5 -0.928 -0.791 -0.920 -0.953      0.162
6      6 -0.983 -0.728 -0.926 -0.953      0.225
7      7 -1.05  -0.873 -1.08  -0.953      0.0802
8      8 -1.06  -0.875 -1.07  -0.953      0.0782
9      9 -1.06  -0.974 -1.05  -0.953     -0.0206
10     10 -0.929 -0.829 -0.953 -0.953      0.125
# i 3,990 more rows

```

```

voi_prop_bm_diff |>
  ggplot(aes(c2p_tk_diff)) +
  stat_halfeye(.width = c(0.6, 0.8, 0.9)) +
  geom_vline(xintercept = 0)

```

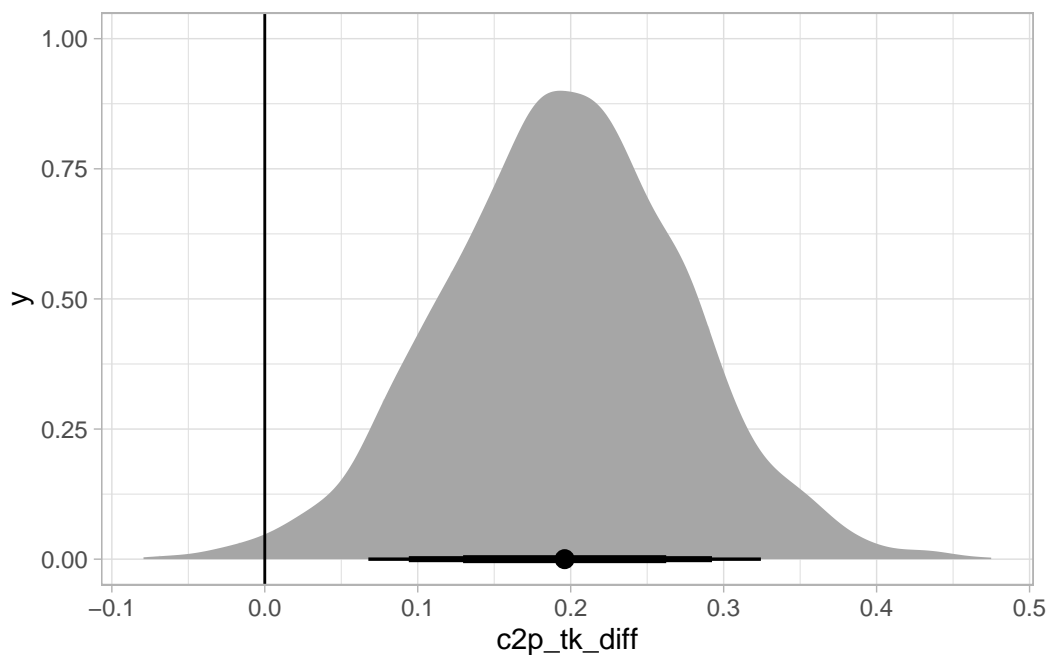


Figure 3

Once we have the posterior difference, we can obtain CrIs of the difference using `quantile2()` from the `posterior` package. Beware that the values of the difference are in log-odds! We can convert these into odd ratios with `exp()`.

```
library(posterior)
```

This is posterior version 1.6.0

Attaching package: 'posterior'

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

mad, sd, var

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

%in%, match

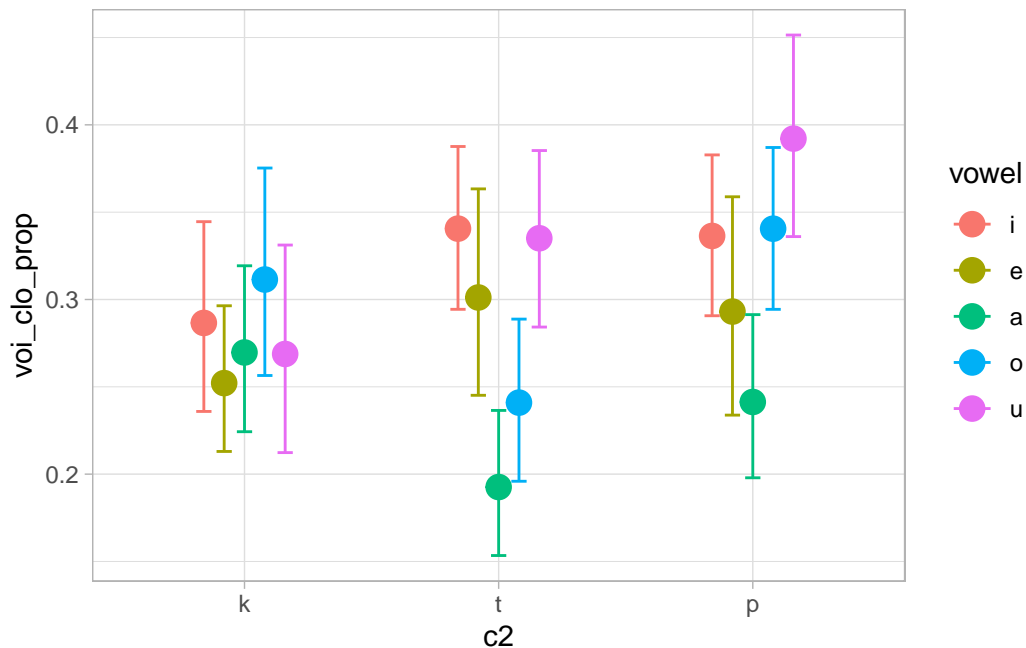
```
voi_prop_bm_diff |>
  reframe(
    # 90% CrI
    q90 = quantile2(c2p_tk_diff, probs = c(0.05, 0.95)),
    # 80% CrI
    q80 = quantile2(c2p_tk_diff, probs = c(0.1, 0.9)),
    # 60% CrI
    q60 = quantile2(c2p_tk_diff, probs = c(0.2, 0.8)),
  ) |>
  # exponentiate to get odd ratios and round to 2 digits
  mutate(across(everything(), ~round(exp(.x), 2)))
```

```
# A tibble: 2 x 3
  q90    q80    q60
<dbl> <dbl> <dbl>
1  1.07  1.1    1.14
2  1.38  1.34   1.3
```

So, based on the model and data, there is a 90% probability that the voicing proportion in /p/ is 1.07-1.38 times longer (or 7-38% increase) than in /t, k/. At 80% confidence, the change ratio is 1.10-1.34 (or 10-34% increase) while at 60% confidence is 1.14-1.30 (14-30% increase). In other words we can be quite confident that the voicing proportion in /p/ is longer than in /t, k/ and that the increase is less than 35%.

brms comes with a convenient function, `conditional_effects()`, to plot posterior means and CrIs based on predictors in the model. In the following example, we plot the predicted proportion of voicing by consonant and vowel.

```
conditional_effects(voi_prop_bm, "c2:vowel")
```



Finally, the package `marginalEffects` [XXX] has two other convenience functions that return CrIs of comparisons across predictor levels (`avg_comparisons()`) and CrIs of posterior predictions across predictor levels (`avg_predictions()`). [XXX]

```
library(marginalEffects)
```

```
avg_comparisons(voi_prop_bm, variables = list(c2 = "pairwise"), conf_level = 0.8, type = "link")
```

	Contrast	Estimate	10.0 %	90.0 %
mean(t) - mean(k)		0.0348	-0.00418	0.0738
mean(p) - mean(k)		0.2176	0.17837	0.2558
mean(p) - mean(t)		0.1829	0.14474	0.2192

Term: c2

Type: link

Columns: term, contrast, estimate, conf.low, conf.high, predicted_lo, predicted_hi, predicted, tmp_id

```
avg_predictions(voi_prop_bm, variables = "vowel", conf_level = 0.8)
```

vowel	Estimate	10.0 %	90.0 %
i	0.331	0.325	0.338
e	0.300	0.293	0.307
a	0.245	0.238	0.252
o	0.305	0.298	0.312
u	0.348	0.341	0.354

Type: response

Columns: vowel, estimate, conf.low, conf.high

4. Case study 2: coarticulatory vowel nasalisation

For the second case study we will use data from [Carignan et al. \(2021\)](#). The study looked at properties of nasality in German VNC sequences. Here, we will focus on the effect of C voicing (voiceless /t/ vs voiced /d/) on the proportion of nasalisation within the vowel in the VNC sequence. Previous work on coarticulatory nasalisation in English has suggested that vowels followed by an NC sequence where C is voiceless (NT) should show earlier coarticulatory nasalisation than vowels followed by an NC sequence where C is voiced (ND, see review in [Carignan et al., 2021](#)). This pattern has been suggested to be driven by the articulatory and acoustic incompatibility of voicelessness and nasalisation, by which the velum opening gesture of the nasal consonant is pushed away (i.e. earlier) when the consonant following the nasal is voiceless. Everything else being equal, a greater proportion of vowel nasalisation (from the perspective of time) should be found in vowels followed by NT than in vowels followed by ND.

We will model the proportion of coarticulatory nasalisation in the German short vowels /i, e, a, o, u/ when followed by /nt/ or /nd/, using a Bayesian beta regression model. The proportion was calculated as the proportion of the nasal interval to the duration of the vowel. The nasal interval was defined thus: the interval between the time of peak velocity of velum opening to the offset of the vowel.

First, let's read and plot the data.

```
nasal <- read_csv("data/carignan2021/nasal.csv")
```

```
Rows: 705 Columns: 6
-- Column specification -----
Delimiter: ","
chr (5): speaker, label, vowel, NC, voicing
dbl (1): nas_prop

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
nasal
```

```
# A tibble: 705 x 6
  speaker label          vowel NC voicing nas_prop
  <chr>   <chr>          <chr> <chr> <chr>    <dbl>
1 S03    b__U_nt_@___N_B17/s u    nt   voiceless 0.367
2 S03    b__a_nd_@___N_B19/s a    nd    voiced 0.195
3 S03    b__a_nt_@___N_B15/s a    nt   voiceless 0.279
4 S03    f__I_nt_@___N_B05/s i    nt   voiceless 0.764
5 S03    l__I_nd_@___N_B06/s i    nd    voiced 0.00529
6 S03    p__E_nt_@___N_B09/s e    nt   voiceless 0.335
7 S03    r__a_nt_@___N_B06/s a    nt   voiceless 0.243
8 S03    v__I_nd_@___N_B07/s i    nd    voiced 0.0248
9 S03    v__I_nt_6___N_B15/s i    nt   voiceless 0.135
10 S03    z__E_nd_@___N_B17/s e    nd    voiced 0.538
# i 695 more rows
```

- `speaker` indicates the speaker ID.
- `label` is the word label as given in the original data.

- `vowel` is the target vowel in the VNC sequence.
- `NC` is the NC sequence.
- `voicing` indicates the voicing of C.
- `nas_prop` is the proportion of coarticulatory nasalisation of the vowel.

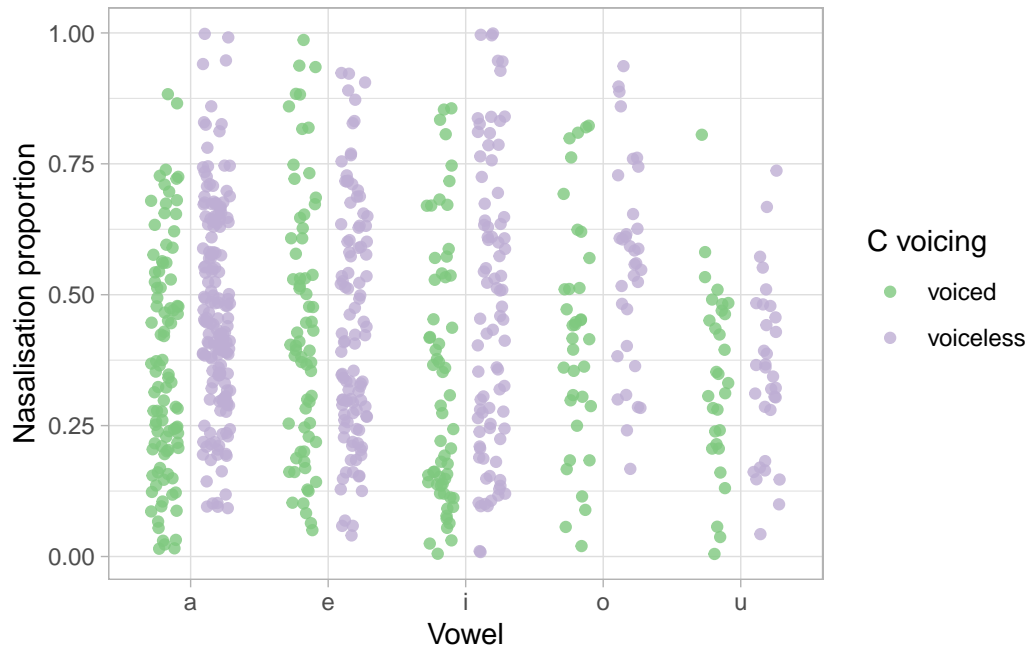


Figure 4: Proportion of coarticulatory nasalisation during the vowel in VNC sequences in German, depending on C voicing.

Figure 4 shows the proportion of coarticulatory nasalisation in vowels followed by /nd/ (voiced) vs /nt/ (voiceless) sequences, for the short vowels /i, e, a, o, u/. We can see a pattern of higher nasalisation proportion in vowels followed by /nt/, at least in the vowels /a, i, o/. For /e, u/, the distribution of nasalisation proportion seems to be similar between the voiced and voiceless contexts.

Now onto modelling with a beta regression. Note that a full appropriate model would include further predictors (both constant and varying), but for simplicity here we include only the following predictors: voicing (voiced /nd/ vs voiceless /nt/), vowel (/i, e, a, o, u/), including an interaction between them. As varying terms, we include a varying intercept by speaker and a by-speaker varying slope for voicing and vowel in interaction. As with the model from the first case study, voicing and vowel are coded using indexing, by suppressing the intercept with 0 +. Here's the code of the model.

```
nas_prop_bm <- brm(
  nas_prop ~ 0 + voicing:vowel + (0 + voicing:vowel | speaker),
  data = nasal,
  family = Beta,
  cores = 4,
  seed = 3749,
  file = "data/cache/nas_prop_bm"
)
```

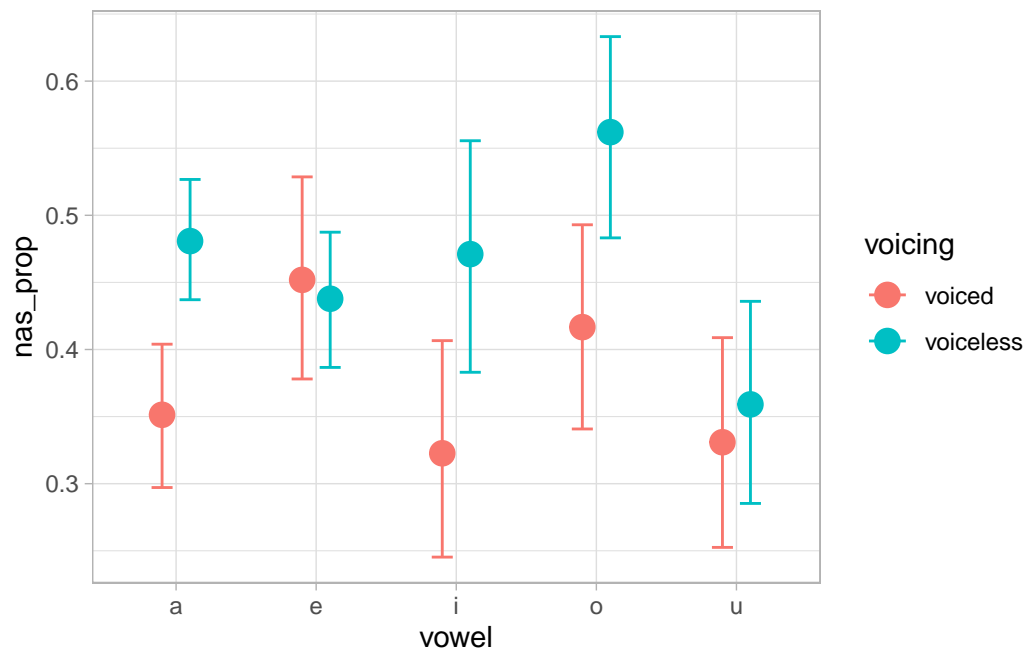
Let's inspect the output of `fixef()`.

```
round(
  fixef(nas_prop_bm, prob = c(0.1, 0.9)),
  digits = 2
)
```

	Estimate	Est.Error	Q10	Q90
voicingvoiced:vowela	-0.61	0.12	-0.77	-0.46
voicingvoiceless:vowela	-0.08	0.09	-0.19	0.04
voicingvoiced:vowe	-0.19	0.16	-0.38	0.01
voicingvoiceless:vowe	-0.25	0.10	-0.38	-0.12
voicingvoiced:vowel	-0.74	0.19	-0.98	-0.51
voicingvoiceless:vowel	-0.12	0.18	-0.35	0.10
voicingvoiced:vowel	-0.34	0.16	-0.54	-0.14
voicingvoiceless:vowel	0.25	0.15	0.05	0.44
voicingvoiced:vowel	-0.71	0.18	-0.94	-0.49
voicingvoiceless:vowel	-0.58	0.16	-0.78	-0.38

Negative log-odds indicate a proportion that is smaller than 50%, while positive log-odds a proportion that is greater than 50%. Generally, the expected log-odd predictions are negative, indicating an overall tendency for the nasalisation to take less than 50% of the duration of the vowel. Moreover, the predictions are higher for voiceless NC sequences than for voiced NC sequences, indicating a greater proportion of nasalisation in the former. However there is vowel-specific variation, and there doesn't seem to be much of a difference in nasalisation proportion in /e/ and /u/. Plotting the expected predictions with `conditional_effects()` should make this clearer.

```
conditional_effects(nas_prop_bm, "vowel:voicing")
```



Now that we fitted the model we can use the draws to answer two questions:

1. Is the nasalisation proportion, on average across vowels, greater in voiceless NC sequences?
2. Is there individual speaker variation?

To answer question 1, we can calculate the average difference in nasalisation proportion by first calculating the average nasalisation across all vowels for voiced and voiceless sequences and then take the difference of those, similarly to what we have done in the Case Study 1 above.

```
# extract only coefficient variables starting with "b_"
nas_prop_bm_draws <- as_draws_df(nas_prop_bm, variable = "^b_", regex = TRUE)

nas_prop_bm_draws_long <- nas_prop_bm_draws |>
  # pivot vowel:c2 columns
  pivot_longer(`b_voicingvoiced:vowela`:`b_voicingvoiceless:vowelu`, names_to = "coeff") |>
  # separate "coeff" labels into type ("b"), vowel and c2
  separate(coeff, into = c("type", "voicing", "vowel"))
```

Warning: Dropping 'draws_df' class as required metadata was removed.

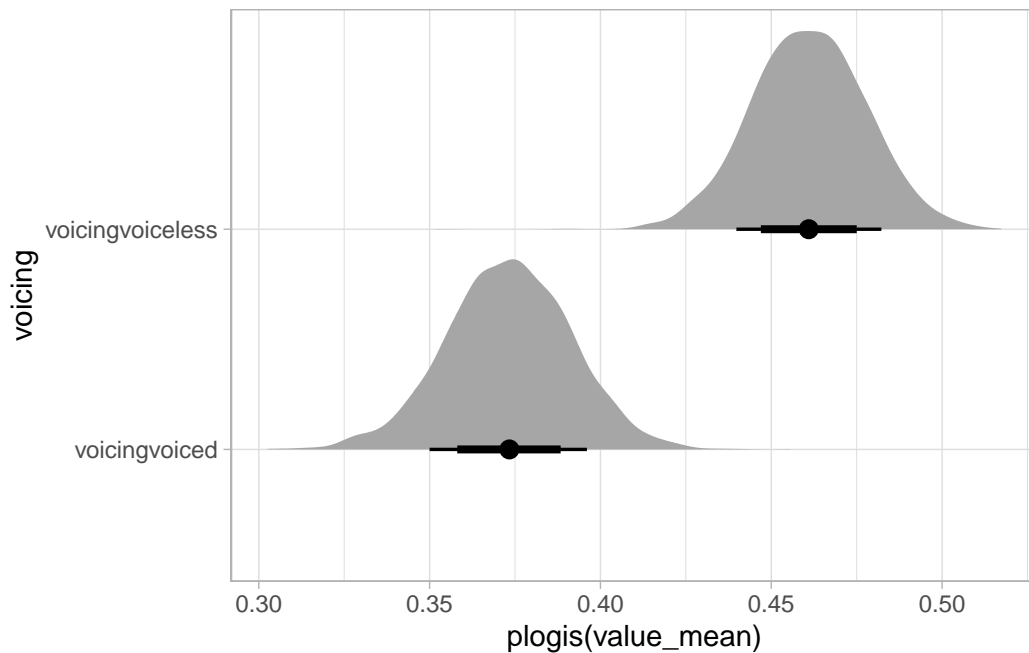
```
nas_prop_bm_draws_long
```

```
# A tibble: 40,000 x 7
  .chain .iteration .draw type voicing vowel value
  <int>    <int>    <int> <chr> <chr>    <chr> <dbl>
1      1      1      1 1 b voicingvoiced vowela -0.463
2      1      1      1 1 b voicingvoiceless vowela -0.0944
3      1      1      1 1 b voicingvoiced vowel e -0.155
4      1      1      1 1 b voicingvoiceless vowel e -0.208
5      1      1      1 1 b voicingvoiced vowel i -0.481
6      1      1      1 1 b voicingvoiceless vowel i -0.0529
7      1      1      1 1 b voicingvoiced vowel o -0.310
8      1      1      1 1 b voicingvoiceless vowel o 0.321
9      1      1      1 1 b voicingvoiced vowel u -0.620
10     1      1      1 1 b voicingvoiceless vowel u -0.368
# i 39,990 more rows
```

Now let's calculate the mean nasalisation proportion within each draw by voicing, and plot the resulting posterior distributions.

```
nas_prop_bm_draws_long_voicing <- nas_prop_bm_draws_long |>
  # grouping by .draw and voicing ensures that averaging applies only within draw and voicing
  group_by(.draw, voicing) |>
  # calculate the mean value within draw/voicing
  summarise(
    value_mean = mean(value), .groups = "drop"
  )

nas_prop_bm_draws_long_voicing |>
  ggplot(aes(plogis(value_mean), voicing)) +
  stat_halfeye(.width = c(0.6, 0.8))
```



The plot suggests an overall greater nasalisation proportion in voiceless NC sequences. Let's quantify how greater as we did in Case Study 1.

```
nas_prop_bm_diff <- nas_prop_bm_draws_long_voicing |>
# pivot data to create one column per voicing with the mean drawn values,
# with one draw per row
pivot_wider(names_from = voicing, values_from = value_mean) |>
mutate(
  # calculate the difference of voiceless and voiced
  voicing_diff = voicingvoiceless - voicingvoiced
)

nas_prop_bm_diff |>
  reframe(
    # 90% CrI
    q90 = quantile2(exp(voicing_diff), probs = c(0.05, 0.95)),
    # 80% CrI
    q80 = quantile2(exp(voicing_diff), probs = c(0.1, 0.9)),
    # 60% CrI
    q60 = quantile2(exp(voicing_diff), probs = c(0.2, 0.8)),
  ) |>
  mutate(across(everything(), ~round(.x, 2)))
```

```
# A tibble: 2 x 3
  q90  q80  q60
<dbl> <dbl> <dbl>
1  1.23  1.27  1.33
2  1.69  1.63  1.56
```

The CrIs of the ratio difference in nasalisation proportion in voiceless vs voiced NC sequences suggest a

robust increase of nasalisation in the voiceless NC sequences, with a 90% probability that the increase is between 23% and 69% of the proportion in voiced NC sequences.

Moving onto question 2: is there individual speaker variation? [TAMMINGA XXX] For this, we will use the `spread_draws()` function from tidybayes [XXX] to extract the draws of the varying terms (in brms these are the coefficients that start with `r_`). There is quite a few steps of processing to get from the raw draws to the estimand we need: while we have commented the following code, we encourage readers to test each line sequentially and inspect the intermediate output to fully understand the process.

```
library(tidybayes)
```

Attaching package: 'tidybayes'

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

```
dstudent_t, pstudent_t, qstudent_t, rstudent_t
```

```
nas_prop_r <- nas_prop_bm |>
# extract draws from model, only `r_speaker` varying terms
spread_draws(r_speaker[speaker,voicingvowel]) |>
# separate the column voicingvowel to two columns
separate(voicingvowel, c("voicing", "vowel")) |>
# join the draws with the `b_` terms
left_join(y = nas_prop_bm_draws_long) |>
# get the expected log-odd value of each speaker, in each draw
# this is the sum of the `value` from the b_ terms and the value from the
# r_speaker term.
mutate(r_speaker_value = value + r_speaker) |>
# group the data for summarise
group_by(.draw, speaker, voicing) |>
# get mean expected log-odds by draw, speaker and voicing (averaging across vowel)
summarise(r_speaker_value_mean = mean(r_speaker_value)) |>
# make the data wider: two columns, one for voiced and one for voiceless
pivot_wider(names_from = voicing, values_from = r_speaker_value_mean) |>
# finally, calculate the difference in expected log-odds of voiceless and voiced
mutate(voicing_diff = voicingvoiceless - voicingvoiced)
```

Joining with ``by = join_by(voicing, vowel, .chain, .iteration, .draw)``

``summarise()`` has grouped output by `'draw', 'speaker'`. You can override using the ``groups`` argument.

```
nas_prop_r
```

```
# A tibble: 140,000 x 5
# Groups:   .draw, speaker [140,000]
  .draw speaker voicingvoiced voicingvoiceless voicing_diff
  <int> <chr>          <dbl>          <dbl>          <dbl>
1     1 1 S03         -1.42          0.0676         1.49
```

2	1	S04	0.209	0.185	-0.0238
3	1	S05	-0.284	-0.0546	0.229
4	1	S06	0.00669	-0.324	-0.331
5	1	S07	-0.446	-0.147	0.299
6	1	S08	-0.610	-0.127	0.483
7	1	S09	-0.473	0.0497	0.523
8	1	S10	-0.556	-0.311	0.245
9	1	S11	0.201	-0.426	-0.628
10	1	S12	-0.0812	-0.0856	-0.00439

i 139,990 more rows

Figure 5 plots the posterior distributions of the expected log-odd difference of coarticulatory nasalisation in voiceless vs voiced NC sequences (x -axis), for each speaker in the data (y -axis), as predicted by the model. The red solid vertical line indicates the constant (overall) expected log-odd difference based on the (constant) b_{\cdot} terms. The black dashed vertical line marks log-difference 0 (i.e., no difference in proportion of nasalisation between voiceless and voiced NC).

```
nas_prop_r |>
  ggplot(aes(voicing_diff, reorder(speaker, voicing_diff))) +
  stat_halfeye() +
  geom_vline(xintercept = mean(nas_prop_bm_diff$voicing_diff), colour = "red") +
  geom_vline(xintercept = 0, linetype = "dashed") +
  lims(x = c(-1, 1.5))
```

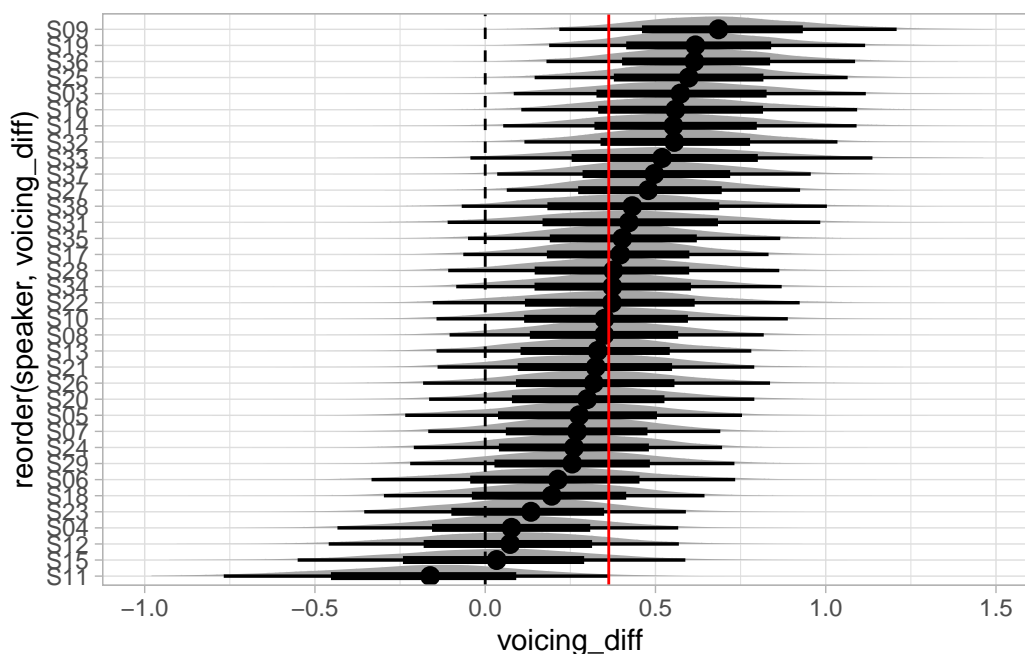


Figure 5

There is a lot of uncertainty within and between speakers: while the distributions of most speakers are located in the positive range, some expected distributions (see bottom of figure) do span both negative and

positive values. In other words, while most speakers are expected to have a larger nasalisation proportion in voiceless NC sequences, a few in fact might have the opposite pattern. Even among those speakers that do have a positive difference, there is a lot of uncertainty as to the magnitude of the difference.

References

Carignan, C., Coretta, S., Frahm, J., Harrington, J., Hoole, P., Joseph, A., Kunay, E., Voit, D., 2021. Planting the seed for sound change: Evidence from real-time MRI of velum kinematics in German. *Language* 97, 333–364. doi:[10.1353/lan.2021.0020](https://doi.org/10.1353/lan.2021.0020).