

# Bayesian Mixed-Effects model of Pulse Pressure Variation by Tidal Volume and Respiratory Rate

This document presents code for fitting, analysing and visualising the Bayesian mixed-effects model presented in the paper. It includes a presentation of model priors, with arguments for why they are considered weakly informative.

## 1 Setup

```
library(tidyverse)
library(patchwork) # For combining plots

library(brms)      # For fitting Stan models
library(tidybayes) # For working with fitted Stan models
options(mc.cores = parallel::detectCores())

source("plot_settings.R") # Plot theme and utility functions
theme_set(theme_paper())
```

## 2 Load data

Data is shared in the data/ folder in the code repository:

<https://doi.org/10.5281/zenodo.6984310>

A codebook is available in the same folder.

```
PPV_df <- read_csv("data/vent_setting_study-vent_protocol.csv") |>
  mutate(
    # Create factors for ventilator settings
    id_f = factor(id),
    vent_rel_vt_f = factor(vent_rel_vt, levels = c(10, 8, 6, 4)),
    vent_RR_f = factor(vent_RR, levels = c(10, 17, 24, 31)),
    vent_setting = interaction(vent_rel_vt, vent_RR, drop = TRUE) |>
      forcats::fct_relevel("10.10", "8.10", "6.10", "4.10",
                          "8.17", "6.17",
                          "8.24", "6.24",
                          "8.31", "6.31")
  ) |>
```

```

# Remove the 13 / 520 rows without a PPV value. PPV is missing either because the
# ventilator setting was not applied or because PPV estimation was infeasible
# because of frequent extra-systoles (≥3 in one window).
drop_na(PPV_gam)

# Labels for vent settings
vent_setting_levels <- c(
  "10.10" = "V<sub>T</sub>=10, RR=10",
  "8.10" = "V<sub>T</sub>=8, RR=10",
  "6.10" = "V<sub>T</sub>=6, RR=10",
  "4.10" = "V<sub>T</sub>=4, RR=10",
  "8.17" = "V<sub>T</sub>=8, RR=17",
  "6.17" = "V<sub>T</sub>=6, RR=17",
  "8.24" = "V<sub>T</sub>=8, RR=24",
  "6.24" = "V<sub>T</sub>=6, RR=24",
  "8.31" = "V<sub>T</sub>=8, RR=31",
  "6.31" = "V<sub>T</sub>=6, RR=31"
)

vt_levels <- c(
  "10" = "V<sub>T</sub>=10",
  "8" = "V<sub>T</sub>=8",
  "6" = "V<sub>T</sub>=6",
  "4" = "V<sub>T</sub>=4"
)

rr_levels <- c(
  "10" = "RR=10",
  "17" = "RR=17",
  "24" = "RR=24",
  "31" = "RR=31"
)

# Pivot PPV data frame to long format with one column for PPV
# and one column indicating the method (Classic or GAM)
PPV_df_long <- PPV_df |>
  pivot_longer(c(PPV_gam, PPV_classic),
    values_to = "PPV",
    names_to = "PPV_method",
    names_prefix = "PPV_") |>
  mutate(PPV_vt = 10*PPV/vent_rel_vt,
    label = vent_setting_levels[as.character(vent_setting)] |>
      factor(levels = vent_setting_levels),
    PPV_method = factor(PPV_method, levels = c("gam", "classic")))

```

### 3 Model specification

The model (m1), fitted with brms, corresponds to the following model in mathematical notation:

$$\begin{aligned}
& \textbf{[Likelihood]} \\
& PPV_{strm} \sim StudentT(\mu_{strm}, \sigma_{trm}, df = 4) \\
& \textbf{[Linear model of } \log(\mu) \textbf{]} \\
& \log(\mu_{strm}) = \beta 0_m + \beta 1_{tm} + \beta 2_{rm} + \alpha_s \\
& \textbf{[Addaptive prior for random effect of subject]} \\
& \alpha_s \sim Normal(0, \sigma_\alpha) \\
& \quad , \text{ for subject } s = 1, \dots, 52 \\
& \textbf{[Prior for SD of subjects]} \\
& \sigma_\alpha \sim truncNormal(0, 1.5, low = 0) \\
& \textbf{[Prior for PPVmethod-specific intercept]} \\
& \beta 0_m \sim Normal(2.3, 1) \\
& \quad , \text{ for PPVmethod } m = (\text{gam}, \text{classic}) \\
& \textbf{[Prior for } \beta \textbf{]} \\
& (\beta 1_{tm}, \beta 2_{rm}) \sim Normal(0, 2) \\
& \quad , \text{ for ventVT } t = (8, 6, 4); \text{ ventRR } r = (17, 24, 31); \text{ PPVmethod } m = (\text{gam}, \text{classic}) \\
& \textbf{[Linear model of } \log(\sigma) \textbf{]} \\
& \log(\sigma_{trm}) = \gamma 0_m + \gamma 1_{tm} + \gamma 2_{rm} \\
& \textbf{[Prior for } \gamma \textbf{]} \\
& (\gamma 0_m, \gamma 1_{tm}, \gamma 2_{rm}) \sim Normal(0, 1.5) \\
& \quad , \text{ for ventVT } t = (8, 6, 4); \text{ ventRR } r = (17, 24, 31); \text{ PPVmethod } m = (\text{gam}, \text{classic})
\end{aligned}$$

All independent variables are categorical. *PPVmethod*, *m*, is one of the categories “GAM” or “Classic”, *ventVT*, *t*, is one of the tidal volumes 10, 8, 6 or 4 ml kg<sup>-1</sup> (10 ml kg<sup>-1</sup> is the reference), *ventRR*, *r*, is one of the respiratory rates 10, 17, 24 or 31 min<sup>-1</sup> (10 min<sup>-1</sup> is the reference). We use categorical, rather than continuous, variables for tidal volume and respiratory rate, because we do not want to assume a linear effect of these settings, and because we want these model parameters to be directly interpretable as relative effects (after exponentiation). The random term ( $\alpha_s$ ) allows a subject specific intercept, reflecting that subjects present with PPVs in different ranges.

Model 2 (m2) is similar, but instead of separate effects of tidal volume (*ventVT*) and respiratory rate (*ventRR*), the two ventilator settings are combined to *ventSetting*, giving estimates of all 10 applied combinations of tidal volume and respiratory rate.

#### 3.1 Priors

First we present the model priors. Generally these are weakly informative and only exclude unreasonably large effects. They simply serve as computational aids for fitting the model.

```

# Population-level terms -----
# Because of the log-link, these terms represent the log of the
# multiplicative effect on the outcome scale.
priors_pterms <- c(
  # Prior for the default population level effects.
  # A normal distribution with SD = 2, means that any effect of ventilator settings
  # different than VT=10, RR=10 is probably (68% interval) between a 7x increase
  # and a 7x decrease in PPV. 95% prior interval exp(c(-4, 4)) ~ 1/50 to 50.
  set_prior("normal(0, 2)", class = "b"),
  # Intercept (median PPV) is probably between 3 and 30 (i.e. exp(c(1.3, 3.3)) )
  # 95% prior interval ~ 1.4 to 73
  set_prior("normal(2.3, 1)", coef = "PPV_methodgam"),
  set_prior("normal(2.3, 1)", coef = "PPV_methodclassic")
)

# Variability terms -----
# Between-subject variability (random effect)
# and within-subject variability (residuals)
priors_ranef <- c(
  # Prior for sd of random effect (half-normal prior).
  # Since this effect is on the log scale, a sd of 1 would mean that
  # 68 % of subjects are within 2.7x below and above the value predicted from
  # the fixed effects.
  set_prior("normal(0,1.5)", class = "sd"),
  # Priors for the linear predictors of log(sigma): The residual variability.
  # This gives 68% prior probability that sigma at VT=10,RR=10 is in the
  # range exp(c(-1.5, 1.5)) = 0.22 to 4.48.
  # The relative effect of VT and RR on sigma is assumed to be less than 4.5x (each).
  set_prior("normal(0,1.5)", dpar = "sigma")
)

priors <- c(priors_pterms,
           priors_ranef)

```

## 3.2 Model sampling

The models are sampled using Stan, via the R interface `brms`. Four chains with 4000 post-warmup draws each were used.

```

m1 <-
  brm(bf(PPV ~
    0 + PPV_method + (vent_rel_vt_f + vent_RR_f):PPV_method +
    (1 | id_f),
    sigma ~ 0 + PPV_method + (vent_rel_vt_f + vent_RR_f):PPV_method,
    # We fix nu (degrees of freedom in T distribution)
    nu = 4
  ),

```

```

prior = priors,
data = PPV_df_long,
seed = 1,
iter = 6000,
warmup = 2000,
family = student(link = "log"),
file = "temp_model_fits/m1",
file_refit = "on_change")

# Model with interaction between VT and RR
m2 <-
  brm(bf(PPV ~
    0 + PPV_method + vent_setting:PPV_method +
    (1 | id_f),
    sigma ~ 0 + vent_setting:PPV_method,
    nu = 4
  ),
  prior = priors,
  data = PPV_df_long,
  seed = 1,
  iter = 6000,
  warmup = 2000,
  family = student(link = "log"),
  file = "temp_model_fits/m2",
  file_refit = "on_change")

```

## 4 Convergence

We consider that models have converged if  $R_{\text{hat}}$  for all parameters are  $< 1.01$  (for details on the  $R_{\text{hat}}$  convergence measure, see [Vehtari et al, 2021](#)).

```

rhat_m1 <- rhat(m1) |> na.omit() # when nu is fixed, Rhat for nu is NaN
rhat_m2 <- rhat(m2) |> na.omit()

stopifnot(max(rhat_m1) < 1.01)
stopifnot(max(rhat_m2) < 1.01)

```

```
m1: max(rhat(m1)) = 1.0028754
```

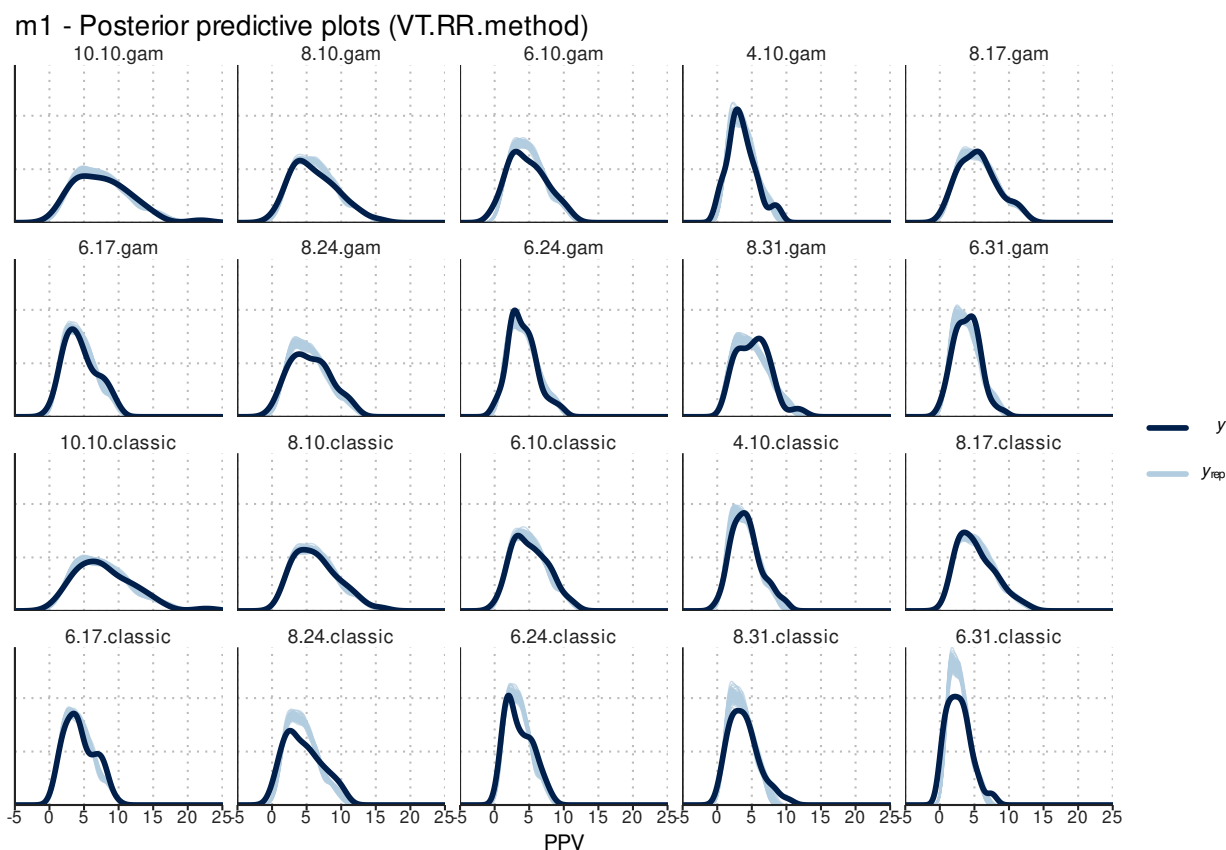
```
m2: max(rhat(m2)) = 1.0027445
```

## 5 Posterior predictive plots

Below are plots showing the posterior prediction of PPV for all 10 ventilator settings (8.10.gam means  $V_T=8$  ml  $\text{kg}^{-1}$ ,  $\text{RR}=10$   $\text{min}^{-1}$  with GAM method). The Student t distribution of the response places a (very) small area of the predictive distribution in negative PPV values. Negative

PPV values are not possible. We also fitted the models with a lower bound of 0 on the response distribution, eliminating negative predictions. That model gave essentially identical results, so we decided to use the non-bounded distribution, as it's location parameter ( $\mu$ ) is equal to the expected value, allowing interpretation of model parameters as conditional effects on the expected value of PPV.

```
bayesplot::ppc_dens_overlay_grouped(
  m1$data$PPV,
  yrep = posterior_epred(m1, ndraws = 50),
  group = with(m1$data, interaction(vent_rel_vt_f, vent_RR_f, PPV_method)) +
  labs(title = "m1 - Posterior predictive plots (VT.RR.method)",
       x = "PPV") +
  scale_x_continuous(limits = c(-5, 25))
```



We only include the posterior predictive distributions for m1. The plots for m2 look practically identical.

## 6 Pareto K diagnostic and comparison of m1 and m2

```
loo(m1, m2)
```

```
## Output of model 'm1':
##
## Computed from 16000 by 1014 log-likelihood matrix
##
##           Estimate      SE
## elpd_loo  -1548.5  33.7
## p_loo      91.4   3.2
## looic      3097.1  67.4
## -----
## Monte Carlo SE of elpd_loo is 0.1.
##
## All Pareto k estimates are good (k < 0.5).
## See help('pareto-k-diagnostic') for details.
##
## Output of model 'm2':
##
## Computed from 16000 by 1014 log-likelihood matrix
##
##           Estimate      SE
## elpd_loo  -1557.8  33.6
## p_loo      105.5   3.6
## looic      3115.6  67.1
## -----
## Monte Carlo SE of elpd_loo is 0.1.
##
## All Pareto k estimates are good (k < 0.5).
## See help('pareto-k-diagnostic') for details.
##
## Model comparisons:
##      elpd_diff se_diff
## m1    0.0        0.0
## m2   -9.3        3.4
```

All Pareto  $k$  are  $< 0.5$  for both models, indicating that we do not have any overly influential data points. The higher elpd of model 1 indicates that this model is probably preferable (it is both simpler and performs better in cross-validation). In the paper we only consider model 1 as it is simpler to interpret. Here, we present both for completeness.

## 6.1 Variation in data explained by the model

```
bayes_R2(m1)
```

```
##      Estimate  Est.Error    Q2.5    Q97.5
## R2  0.8345923  0.004773569  0.8245541  0.8433161
```

Model 1 explains ~83% of the variation in data.

```
bayes_R2(m1, re_formula = NA)
```

```
##      Estimate Est.Error      Q2.5      Q97.5
## R2 0.1490064 0.02120653 0.1101846 0.1941463
```

If we exclude the random effects (between individual variation), we can see that the fixed effects explain ~15% of the variation. I.e. Within individuals, just shy of half the variation in PPV is explained by change in ventilator settings.

```
bayes_R2(m2)
```

```
##      Estimate Est.Error      Q2.5      Q97.5
## R2 0.8355662 0.004910302 0.8252781 0.8445483
```

```
bayes_R2(m2, re_formula = NA)
```

```
##      Estimate Est.Error      Q2.5      Q97.5
## R2 0.1516769 0.02085516 0.1141889 0.1950421
```

## 7 Make figure for m1 - No interaction

The following is the code to produce figure 5 in the paper.

### 7.1 Plot observed PPV

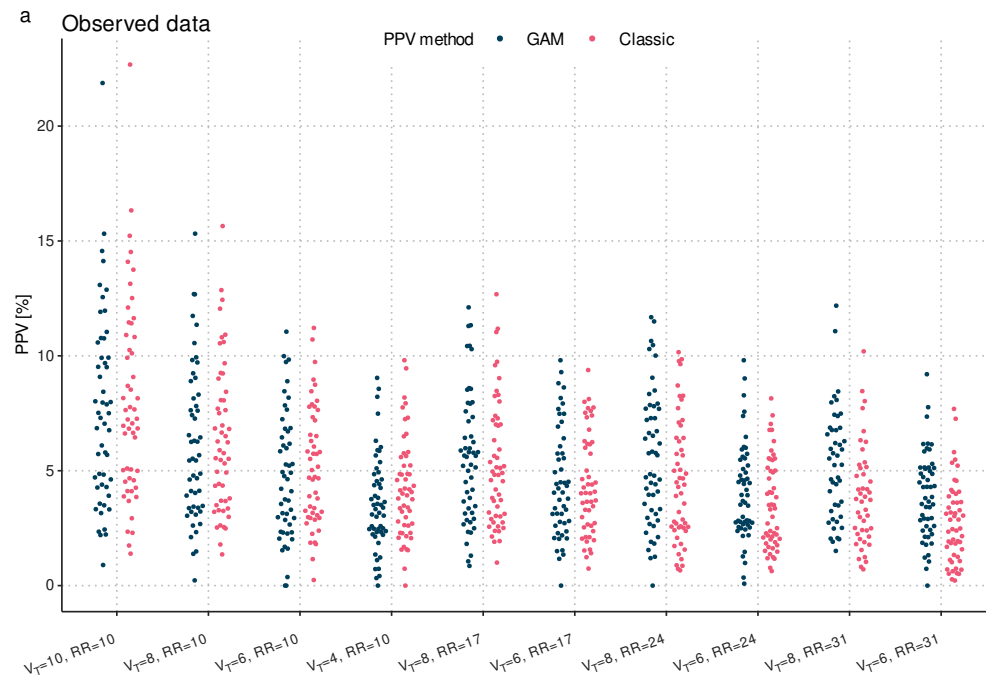
Plot of observed PPV for all ventilator settings and both methods (GAM and Classic)

```
observed_plot <- ggplot(PPV_df_long, aes(label, PPV)) +
  ggbeeswarm::geom_quasirandom(aes(color = PPV_method),
                              dodge.width=.6,
                              width = 0.1,
                              size = 0.7,
                              shape=16) +
  guides(color = guide_legend(override.aes = list(alpha = 1, size = 1))) +
  scale_color_discrete(limits = c("gam", "classic"), labels = c("GAM", "Classic")) +
  labs(title = "Observed data", x="", y="PPV [%]",
       color = "PPV method",
       tag = "a") +
  theme(axis.text.x = ggtext::element_markdown(hjust = 1, angle = 20),
        legend.position = c(0.5, 1),
        legend.direction = "horizontal",
        legend.justification = c(0.5, 0.5),
```



```
legend.box.background = element_rect(color = NA, fill = "white"),
legend.text = element_text(size = rel(1))
```

observed\_plot

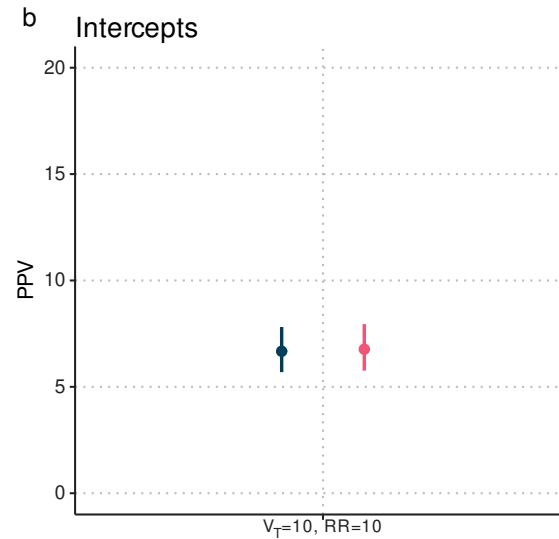


## 7.2 Plot ventilation effects

```
# Intercepts
intercept_draws_m1 <- gather_draws(m1, `b_PPV_method(gam|classic)`, regex = TRUE) |>
  mutate(PPV_method = str_remove(.variable, "b_PPV_method") |>
    factor(levels = c("gam", "classic")),
    intercept = exp(.value),
    label = "V<sub>T</sub>=10, RR=10")

intercept_plot_m1 <- ggplot(intercept_draws_m1, aes(label, intercept, color = PPV_method)) +
  stat_pointinterval(point_size = 1,
    interval_size = 1,
    position = position_dodge(width = 0.4),
    .width = 0.95) +
  coord_cartesian(ylim = c(0, 20)) +
  labs(x="", y="PPV", tag = "b",
    title = "Intercepts") +
  theme(legend.position = "none")

intercept_plot_m1
```



```
# Contrasts
contrast_draws_m1 <- gather_draws(m1, `b_PPV_method(gam|classic):.+`, regex = TRUE) |>
  separate(.variable, into = c("PPV_method", "setting"), sep = ":") |>
  separate(setting, into = c("setting_type", "setting"), sep = "_f") |>
  mutate(PPV_method = str_remove(PPV_method, "b_PPV_method") |>
    factor(levels = c("gam", "classic")),
    rel_effect = exp(.value))

contrast_draws_vt_m1 <- filter(contrast_draws_m1, setting_type == "vent_rel_vt") |>
  mutate(label = vt_levels[setting] |> factor(levels = vt_levels))

contrast_plot_layers <- list(
  stat_pointinterval(point_size = 1,
    interval_size = 1,
    position = position_dodge(width = 0.4),
    .width = 0.95),
  labs(y = "Relative effect", x = ""),
  scale_y_continuous(labels = scales::label_percent(accuracy = 1),
    breaks = seq(0.4, 1, by = 0.2)),
  coord_cartesian(ylim = c(0.4, 1)),
  theme(legend.position = "none")
)

contrast_plot_vt_m1 <- ggplot(contrast_draws_vt_m1,
  aes(label, rel_effect, color = PPV_method)) +
  contrast_plot_layers +
  labs(title = "Effect of tidal volume (V<sub>T</sub>) on PPV",
    subtitle = "Relative to V<sub>T</sub>=10 ml kg<sup>-1</sup>", tag = "c")
```

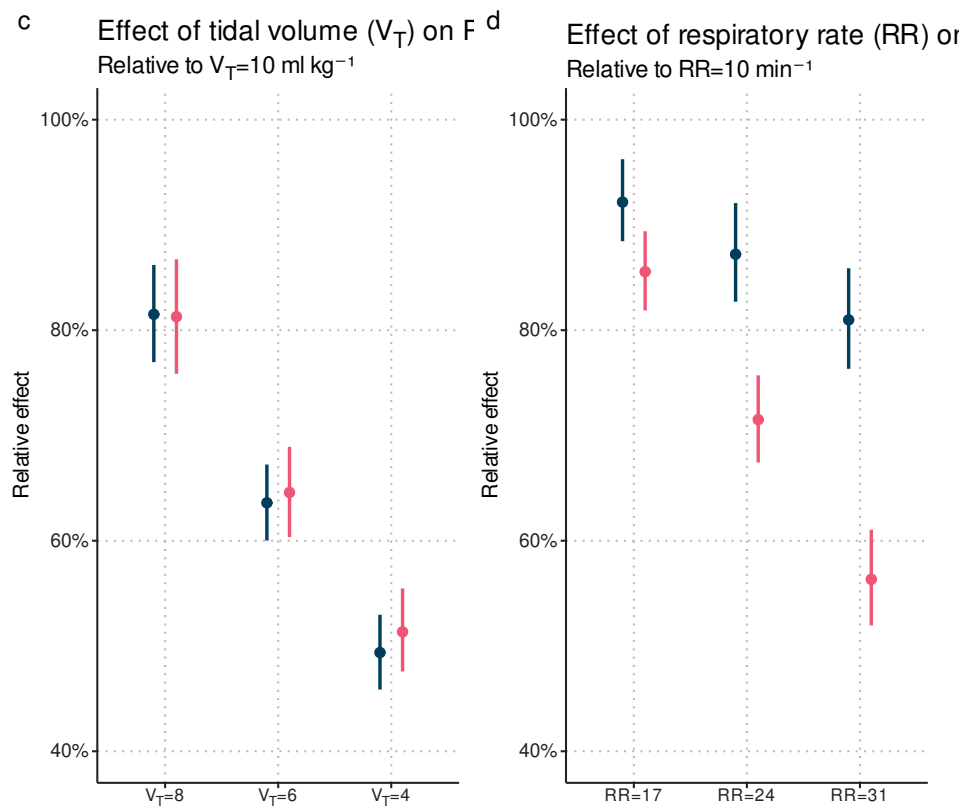
```

contrast_draws_rr_m1 <- filter(contrast_draws_m1, setting_type == "vent_RR") |>
  mutate(label = rr_levels[setting] |> factor(levels = rr_levels))

contrast_plot_rr_m1 <- ggplot(contrast_draws_rr_m1,
                             aes(label, rel_effect, color = PPV_method)) +
  contrast_plot_layers +
  labs(title = "Effect of respiratory rate (RR) on PPV",
       subtitle = "Relative to RR=10 min-1", tag = "d")

contrast_plot_vt_m1 + contrast_plot_rr_m1

```



### 7.3 Make figure 5 (without CV and residuals)

```

param_plot_design_m1_simple <- "
  AAA
  BCD
"

m1_plot_simple <- observed_plot +

```

```

intercept_plot_m1 + contrast_plot_vt_m1 + contrast_plot_rr_m1 +
plot_layout(design = param_plot_design_m1_simple,
             heights = c(2, 3),
             widths = c(1, 3, 3)
            )

save_plot("fig6_mix_model_fig", m1_plot_simple, width = 18, height = 11, scale = 1)

```

```
## [1] "plots/fig6_mix_model_fig.png" "plots/fig6_mix_model_fig.pdf"
```

## 7.4 Plot residuals

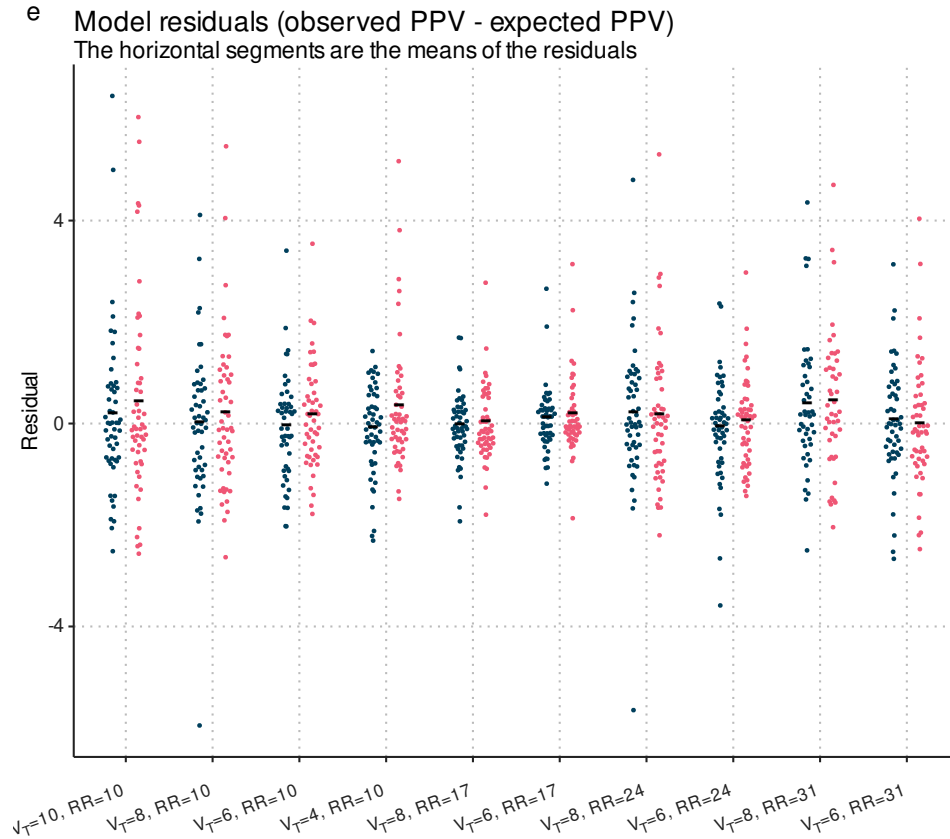
```

# Get mean residuals for both m1 and m2.
PPV_df_long_resid <- PPV_df_long |>
  mutate(
    resid_m1 = residuals(m1, method = "posterior_predict")[, "Estimate"],
    resid_m2 = residuals(m2, method = "posterior_predict")[, "Estimate"]
  )

resid_plot_m1 <- ggplot(PPV_df_long_resid,
                        aes(label, resid_m1, color = PPV_method)) +
  ggbeeswarm::geom_quasirandom(dodge.width=.6,
                              width = 0.1,
                              size = 0.5,
                              shape=16) +
  stat_summary(aes(color = NULL, group = PPV_method), fun = mean, geom = "point",
              shape = "-", size = 5,
              position = position_dodge(width = 0.6)) +
  labs(title = "Model residuals (observed PPV - expected PPV)",
       subtitle = "The horizontal segments are the means of the residuals",
       x="", y="Residual",
       tag = "e") +
  theme(axis.text.x = ggtext::element_markdown(hjust = 1, angle = 20),
        legend.position = "none")

resid_plot_m1

```



## 7.5 Plot residual standard deviation

Since we use a student t distribution for the likelihood, the sigma parameter does not equal the standard deviation (SD). SD of a T distribution is

$$SD = \sqrt{\sigma^2 \frac{\nu}{\nu - 2}}, \text{ for } \nu > 2$$

where  $\nu$  (nu) is the degrees of freedom parameter.

```
sd_t <- function(sigma, nu) {
  stopifnot(nu > 2)
  sqrt( sigma^2 * (nu / (nu-2)) )
}

# Make a data frame with one row for each combination of PPV_method and vent_setting
newdata_method_setting <- PPV_df_long |>
  tidyr::expand(PPV_method, nesting(vent_setting,
    vent_rel_vt, vent_RR,
    vent_rel_vt_f, vent_RR_f))

# Make draws of mean of posterior predictions (epred)
```

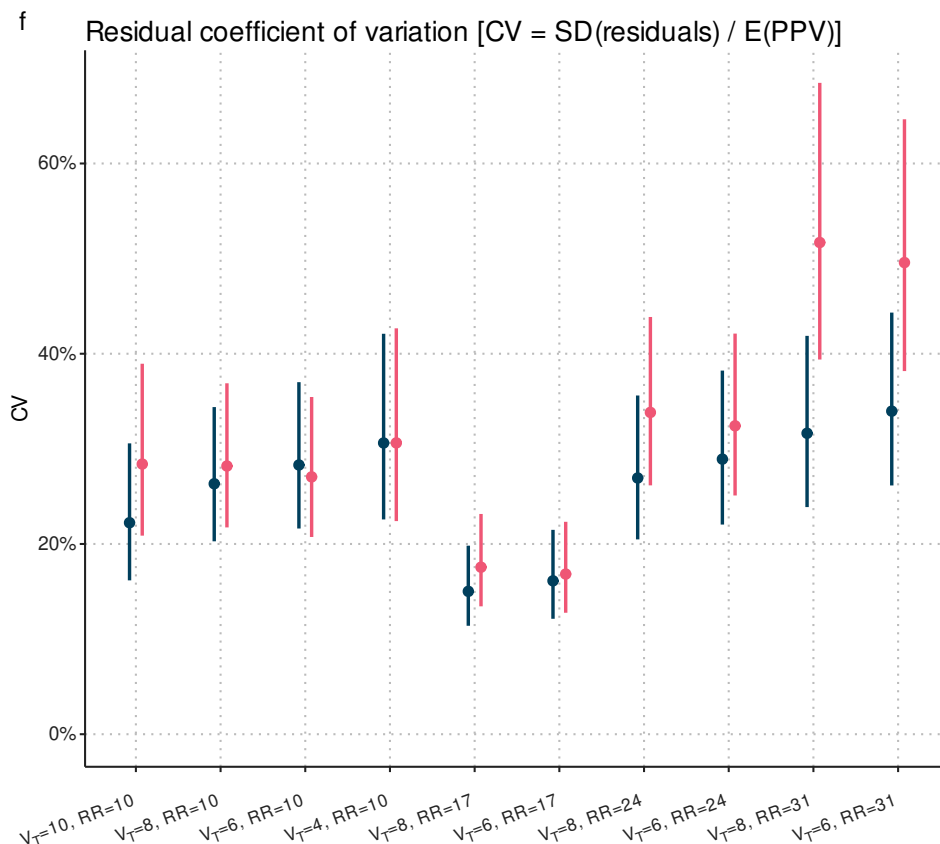
```

# include sigma and nu for each draw (they are used to calculate SD).
vent_setting_epred_m1 <- newdata_method_setting |>
  add_epred_draws(m1, re_formula = NA,
                 dpar = c("sigma", "nu")) |>
  mutate(label = vent_setting_levels[as.character(vent_setting)] |>
         factor(levels = vent_setting_levels),
         SD = sd_t(sigma, nu),
         CV = SD/.epred)

sd_plot_m1 <- ggplot(vent_setting_epred_m1, aes(label,
                                                CV,
                                                color = PPV_method)) +
  stat_pointinterval(position = position_dodge(width = 0.3),
                    .width = 0.95, interval_size = 1,
                    point_size = 1, show.legend = FALSE) +
  scale_y_continuous(limits = c(0, NA), labels = scales::label_percent()) +
  labs(title = "Residual coefficient of variation [CV = SD(residuals) / E(PPV)]",
       x="", y="CV", color = "PPV method",
       tag = "f") +
  theme(axis.text.x = ggtext::element_markdown(hjust = 1, angle = 20))

sd_plot_m1

```



## 7.6 Combine plots in one figure

```
param_plot_design_m1 <- "
  AAA
  BCD
  EEE
  FFF
"

m1_plot <- observed_plot +
  intercept_plot_m1 + contrast_plot_vt_m1 + contrast_plot_rr_m1 +
  resid_plot_m1 +
  sd_plot_m1 +
  plot_layout(design = param_plot_design_m1,
    heights = c(1, 1.5, 1, 1),
    widths = c(1, 3, 3)
  )

save_plot("suppl_m1_plot", m1_plot, width = 18, height = 18, scale = 1)

## [1] "plots/suppl_m1_plot.png" "plots/suppl_m1_plot.pdf"
```

## 8 Make table of relative effects for m1 (relative to $V_T=10 \text{ ml kg}^{-1}$ , $RR=10 \text{ min}^{-1}$ )

These are the estimates that are visualized in panel c and d.

```
contrast_draws_m1 |>
  group_by(PPV_method, setting_type, setting) |>
  median_qi(rel_effect) |>
  mutate(label = sprintf("%.0f [%.0f; %.0f]%%",
    rel_effect * 100,
    .lower * 100,
    .upper * 100)) |>
  select(-c(.width, .point, .interval)) |>
  knitr::kable(booktabs = TRUE, digits = 2)
```

PPV_method	setting_type	setting	rel_effect	.lower	.upper	label
gam	vent_RR	17	0.92	0.88	0.96	92 [88; 96]%
gam	vent_RR	24	0.87	0.83	0.92	87 [83; 92]%
gam	vent_RR	31	0.81	0.76	0.86	81 [76; 86]%
gam	vent_rel_vt	4	0.49	0.46	0.53	49 [46; 53]%
gam	vent_rel_vt	6	0.64	0.60	0.67	64 [60; 67]%
gam	vent_rel_vt	8	0.82	0.77	0.86	82 [77; 86]%
classic	vent_RR	17	0.86	0.82	0.89	86 [82; 89]%
classic	vent_RR	24	0.72	0.67	0.76	72 [67; 76]%
classic	vent_RR	31	0.56	0.52	0.61	56 [52; 61]%
classic	vent_rel_vt	4	0.51	0.48	0.55	51 [48; 55]%
classic	vent_rel_vt	6	0.65	0.60	0.69	65 [60; 69]%
classic	vent_rel_vt	8	0.81	0.76	0.87	81 [76; 87]%

## 9 Compare m1 coefficient of variation (CV) between PPV<sub>Classic</sub> and PPV<sub>GAM</sub> across ventilator settings

```

vent_setting_epred_m1 |>
  ungroup() |>
  pivot_wider(id_cols = c(.draw, vent_setting),
               names_from = PPV_method, values_from = CV, names_prefix = "CV_") |>
  mutate(CV_classic_m_gam = CV_classic - CV_gam) |>
  group_by(vent_setting) |>
  select(vent_setting, CV_classic_m_gam) |>
  median_qi(CV_classic_m_gam) |>
  mutate(label = sprintf("%.0f [%.0f; %.0f]%%-points",
                          CV_classic_m_gam * 100,
                          .lower * 100,
                          .upper * 100)) |>
  select(-c(.width, .point, .interval)) |>
  knitr::kable(booktabs = TRUE, digits = 2)

```

vent_setting	CV_classic_m_gam	.lower	.upper	label
10.10	0.06	-0.03	0.17	6 [-3; 17]%-points
8.10	0.02	-0.06	0.10	2 [-6; 10]%-points
6.10	-0.01	-0.10	0.07	-1 [-10; 7]%-points
4.10	0.00	-0.12	0.13	-0 [-12; 13]%-points
8.17	0.03	-0.03	0.08	3 [-3; 8]%-points
6.17	0.01	-0.05	0.06	1 [-5; 6]%-points
8.24	0.07	-0.02	0.17	7 [-2; 17]%-points
6.24	0.03	-0.06	0.13	3 [-6; 13]%-points
8.31	0.20	0.07	0.36	20 [7; 36]%-points
6.31	0.15	0.03	0.30	15 [3; 30]%-points



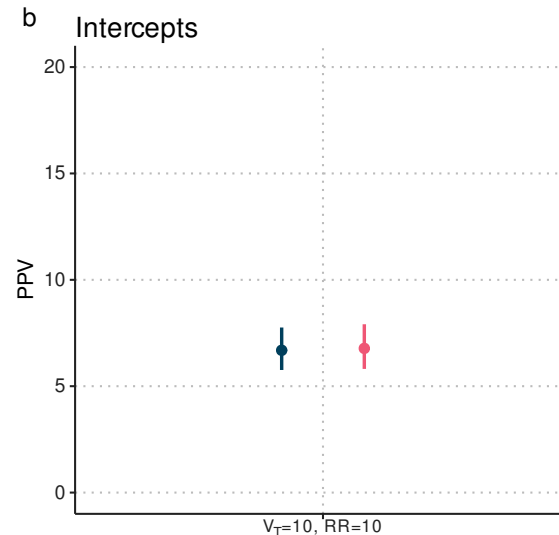
## 10 Make figure for m2 - Model that allows interaction of $V_T$ and RR effects

### 10.1 Plot ventilation effects

```
intercept_draws_m2 <- gather_draws(m2, `b_PPV_method(gam|classic)`, regex = TRUE) |>
  mutate(PPV_method = str_remove(.variable, "b_PPV_method") |>
    factor(levels = c("gam", "classic")),
    intercept = exp(.value),
    label = "V<sub>T</sub>=10, RR=10")

intercept_plot_m2 <- intercept_plot_m1 %>% intercept_draws_m2

intercept_plot_m2
```



```
contrast_draws_m2 <- gather_draws(m2, `b_PPV_method(gam|classic):.+`, regex = TRUE) |>
  separate(.variable, into = c("PPV_method", "vent_setting"), sep = ":") |>
  mutate(PPV_method = str_remove(PPV_method, "b_PPV_method") |>
    factor(levels = c("gam", "classic")),
    vent_setting = str_remove(vent_setting, "vent_setting"),
    label = vent_setting_levels[vent_setting] |>
    factor(levels = vent_setting_levels),
    rel_effect = exp(.value))

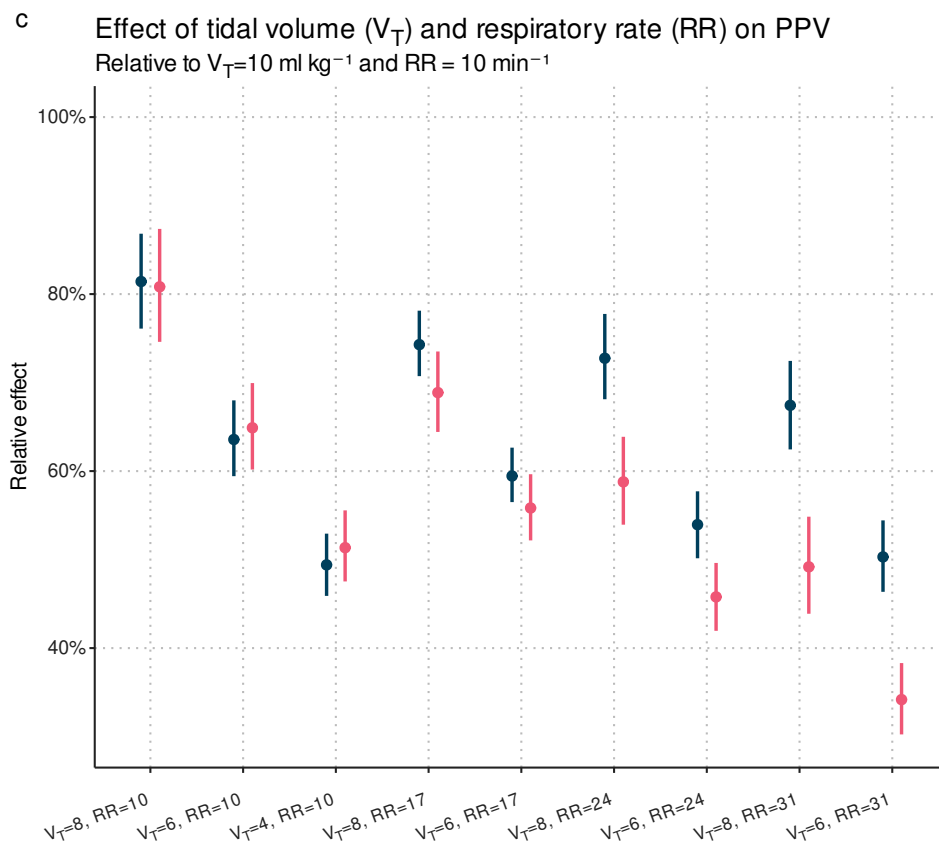
contrast_plot_m2 <- ggplot(contrast_draws_m2,
  aes(label, rel_effect, color = PPV_method)) +
  stat_pointinterval(point_size = 1,
    interval_size = 1,
    position = position_dodge(width = 0.4),
```

```

        .width = 0.95) +
labs(y = "Relative effect", x = "",
     title = "Effect of tidal volume ( $V_T$ ) and respiratory rate (RR) on PPV",
     subtitle = "Relative to  $V_T=10$  ml  $\text{kg}^{-1}$  and RR = 10  $\text{min}^{-1}$ ", tag = "c") +
scale_y_continuous(labels = scales::label_percent(accuracy = 1),
                   breaks = seq(0.4, 1, by = 0.2)) +
coord_cartesian(ylim = c(0.3, 1)) +
theme(legend.position = "none",
      axis.text.x = ggtext::element_markdown(hjust = 1, angle = 20))

```

contrast\_plot\_m2



## 10.2 Plot residuals

```

resid_plot_m2 <- ggplot(PPV_df_long_resid, aes(label, resid_m2)) +
  ggbeeswarm::geom_quasirandom(aes(color = PPV_method),
                               dodge.width=.6,
                               width = 0.1,
                               size = 0.7,

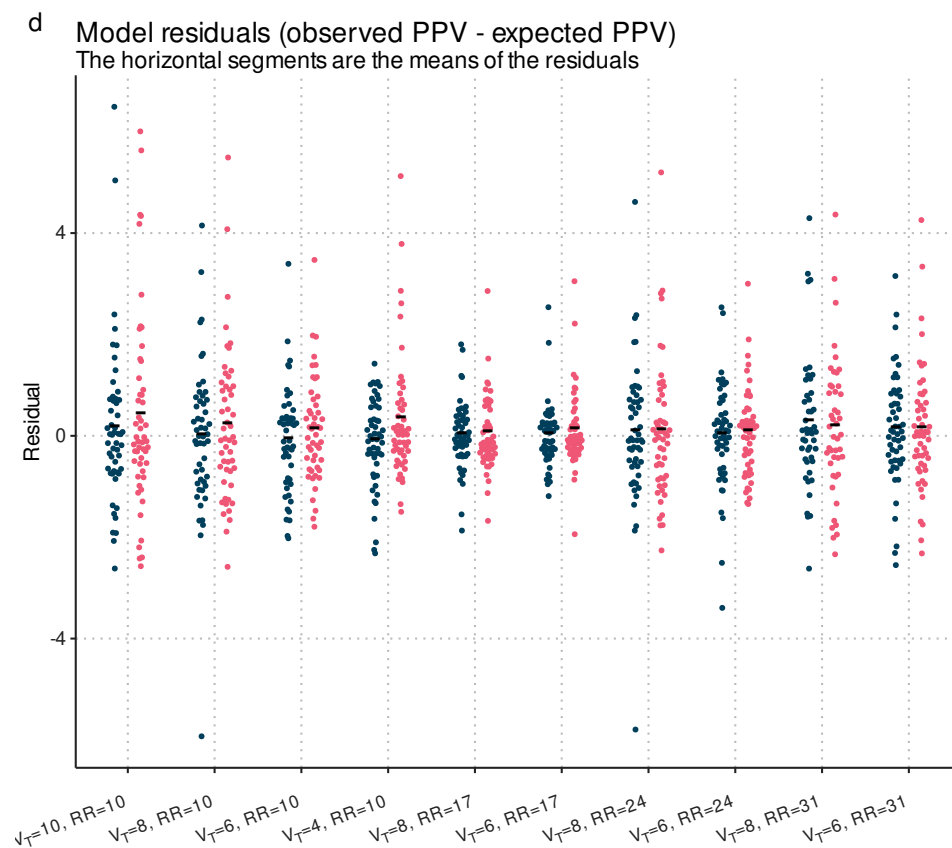
```

```

      shape=16) +
stat_summary(aes(color = NULL, group = PPV_method), fun = mean, geom = "point",
             shape = "-", size = 5,
             position = position_dodge(width = 0.6)) +
labs(title = "Model residuals (observed PPV - expected PPV)",
     subtitle = "The horizontal segments are the means of the residuals",
     x="", y="Residual",
     tag = "d") +
theme(axis.text.x = ggtext::element_markdown(hjust = 1, angle = 20),
     legend.position = "none")

```

resid\_plot\_m2



### 10.3 Plot residual standard deviation

```

# Make draws of mean of posterior predictions (epred)
# include sigma for each draw.

vent_setting_epred_m2 <- newdata_method_setting |>
  add_epred_draws(m2, re_formula = NA,

```

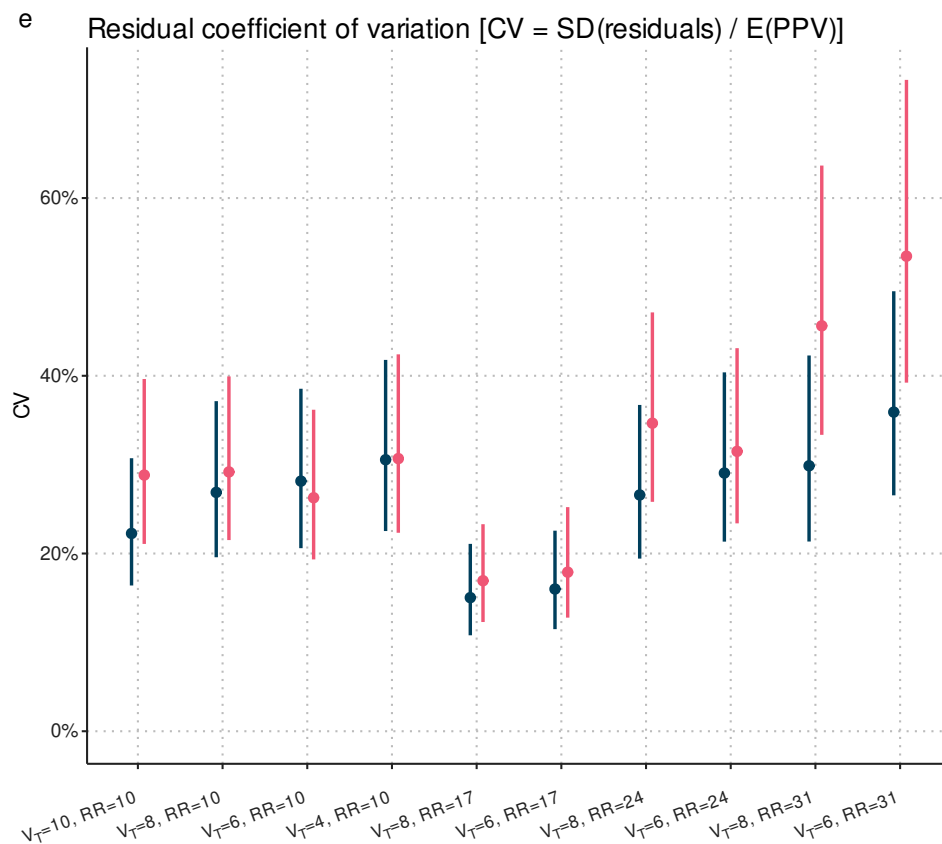
```

      dpar = c("sigma", "nu")) |>
mutate(label = vent_setting_levels[as.character(vent_setting)] |>
      factor(levels = vent_setting_levels),
      SD = sd_t(sigma, nu),
      CV = SD/.epred)

# Reuse the sd plot from model 1, but with new data
sd_plot_m2 <- sd_plot_m1 %>% vent_setting_epred_m2 +
  labs(tag = "e")

sd_plot_m2

```



## 10.4 Combine plots in one figure

```

param_plot_design_m2 <- "
  AA
  BC
  DD
  EE
"

```

```

m2_plot <- observed_plot +
  intercept_plot_m2 +
  contrast_plot_m2 +
  resid_plot_m2 +
  sd_plot_m2 +
  plot_layout(design = param_plot_design_m2,
    heights = c(1, 1.5, 1, 1),
    widths = c(1, 5)
  )

save_plot("extra_m2_plot", m2_plot, width = 18, height = 18, scale = 1)

```

```
## [1] "plots/extra_m2_plot.png" "plots/extra_m2_plot.pdf"
```

```
m2_plot
```

