Statistical re-analysis plan: Predicting body fat proportion using anthropometric measures

Mariana Nold

```r
library(mfp2)
library(rstanarm)
library(projpred)
library(ggplot2)
library(loo)
library(bayesplot)
library(bayesrules)
library(FBMS)
```

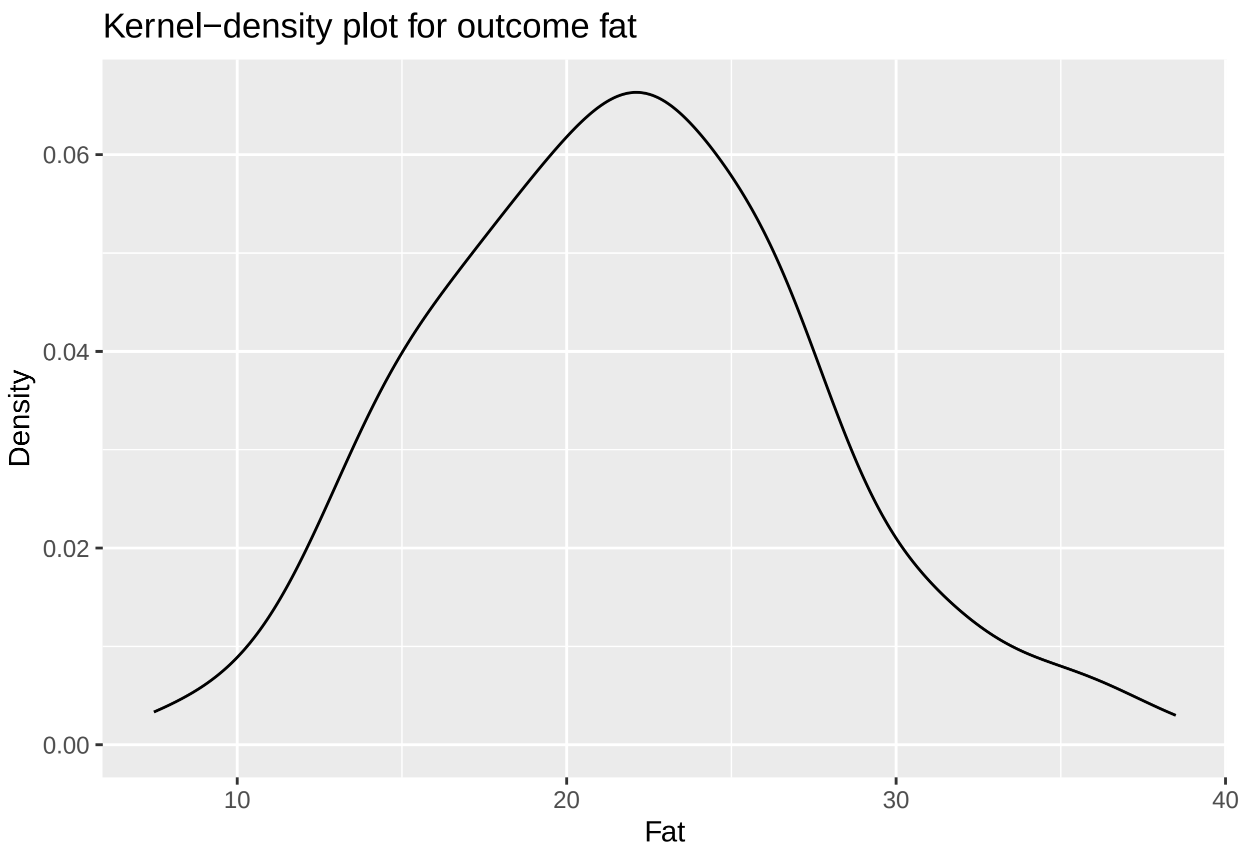
```r
women <- read.delim("C:/Users/zo95yup/Documents/GitHub/Bayes_for_STRATOS/Task Bodyfat/Datafiles/BodyFat
names(women)
```

Load R packages

```
##  [1] "Obs"     "Fat"     "Weight"  "Height"  "BMI"     "Age"     "Neck"
##  [8] "Chest"   "Calf"    "Biceps"  "Hips"    "Waist"   "Forearm" "PThigh"
## [15] "MThigh"  "DThigh"  "Wrist"   "Knee"    "Elbow"   "Ankle"
```

```r
PPath2 <- "C:/Users/zo95yup/Nextcloud/Statistik_SoSe24/Forschung/STRATOS/P6/Code_A/Results"
```

```r
fat_density <- density(women$Fat, na.rm = TRUE)
ggplot(women, aes(x = Fat)) + geom_density() +
  labs(title = "Kernel-density plot for outcome fat", x = "Fat", y = "Density")
```



Prepare data

```
summary(women$Fat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    7.47   17.61   21.64   21.76   25.73   38.49
```

```
summary(women$Age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.00   19.00   20.00   20.39   21.00   25.00
```

```
women<- women[women$Age != 1, ]
women[,3:20] <- scale(women[,3:20])
head(women)
```

```
##   Obs   Fat      Weight     Height        BMI        Age       Neck      Chest
## 1   1 23.07 -1.29458090 -0.9359529 -0.9574982  0.9702795 -1.7434463 -1.3798033
## 2   2 29.50  0.08151288 -1.5820137  1.0776639  0.9702795 -0.1839318  0.3526427
## 3   3 26.99  0.35673163 -0.8498114  0.9208569  0.3269420 -0.4438509 -0.2042149
## 4   4 20.25 -0.85423089  0.2269566 -1.0444077 -0.3163955 -0.9636891 -1.0859062
## 5   5 19.95 -0.08361838  1.0883711 -0.6631153 -0.3163955  0.6608052 -0.1268736
## 6   6 26.02  0.96221290 -0.9359529  1.6864004  2.2569544  1.6355018  1.8530647
##         Calf      Biceps       Hips      Waist    Forearm     PThigh     MThigh
## 1 -0.9068981 -0.66317114 -1.0960084 -1.0337620 -1.5610578 -1.1012185 -0.5462338
## 2 -0.6839428  0.06791512 -0.4770169 -0.2266337 -0.1809922  0.2515874 -0.3492182
## 3 -0.8790287  0.47407415 -0.4770169  0.2390172 -1.0592158 -0.4248155 -0.1029487
## 4 -0.4052487 -1.15056197 -1.0471407 -0.9251101 -1.2474066 -1.1012185 -0.8417572
## 5 -0.1265545 -0.98809836 -0.6073309 -0.6922846 -1.5610578 -0.4248155 -0.3492182
## 6  0.5144420  1.28639220  1.3148007  1.1392756  0.9481524  1.0407242  0.7589945
##        DThigh      Wrist       Knee      Elbow      Ankle
## 1 -0.68363710 -0.6889801 -1.1572958 -1.1260785 -1.2200455
## 2 -0.12699377  0.1614979 -0.4658936 -0.4966577  0.5177452
## 3 -0.40531544 -1.3268386 -0.2930431  0.3215893 -0.9178210
## 4 -0.68363710 -1.2205288 -0.2930431 -0.7484260 -0.9933771
## 5  0.01216707 -0.9015996 -1.1572958  0.3845314 -0.2378160
## 6  0.98629291  1.8624538  1.4354624  1.0139522  0.8955257
```

```
model1_f <- formula(Fat ~ fp(Waist, df = 2) + fp(Height, df = 2) + fp(Weight, df = 2))
model1 <- mfp2(model1_f, data = women, verbose=TRUE)
```

Derive reference model

```
##
## i Initial degrees of freedom:
##    Waist Height Weight
## df     2      2      2
##
## i Visiting order: Weight, Height, Waist
##
## ---------------------
## i Running MFP Cycle 1
## ---------------------
##
## Variable: Weight (keep = FALSE)
##                   Powers    DF    Deviance    Versus           Deviance diff.
## FP1               0.5       6     992.1       .                .
## null              NA        4     1013.6      FP1              21.6
## linear            1         5     989.2       FP1              -2.9
##                   P-value
## FP1               .
## null              0.0000
## linear            1.0000
## Selected: linear
##
## Variable: Height (keep = FALSE)
##                   Powers    DF    Deviance    Versus           Deviance diff.
## FP1               2         6     988.5       .                .
## null              NA        4     1010.0      FP1              21.5
## linear            1         5     989.2       FP1              0.6
##                   P-value
## FP1               .
## null              0.0000
## linear            0.4315
## Selected: linear
##
## Variable: Waist (keep = FALSE)
##                   Powers    DF    Deviance    Versus           Deviance diff.
## FP1               2         6     988.8       .                .
## null              NA        4     999.5       FP1              10.7
## linear            1         5     989.2       FP1              0.4
##                   P-value
## FP1               .
## null              0.0046
## linear           0.5445
## Selected: linear
##
## ---------------------
## i Running MFP Cycle 2
## ---------------------
##
## Variable: Weight (keep = FALSE)
##                  Powers   DF   Deviance   Versus           Deviance diff.
## FP1              0.5      6    992.1      .                .
## null             NA       4    1013.6     FP1              21.6
## linear           1        5    989.2      FP1              -2.9
##                  P-value
## FP1              .
## null             0.0000
## linear           1.0000
## Selected: linear
##
## Variable: Height (keep = FALSE)
##                  Powers   DF   Deviance   Versus           Deviance diff.
## FP1              2        6    988.5      .                .
## null             NA       4    1010.0     FP1              21.5
## linear           1        5    989.2      FP1              0.6
##                  P-value
## FP1              .
## null             0.0000
## linear           0.4315
## Selected: linear
##
## Variable: Waist (keep = FALSE)
##                  Powers   DF   Deviance   Versus           Deviance diff.
## FP1              2        6    988.8      .                .
## null             NA       4    999.5      FP1              10.7
## linear           1        5    989.2      FP1              0.4
##                  P-value
## FP1              .
## null             0.0046
## linear           0.5445
## Selected: linear
##
## i Fractional polynomial fitting algorithm converged after 2 cycles.
```

```
# Summarize the model
summary(model1)
```

```
##
## Call:
## glm(formula = y ~ ., family = family, data = data, weights = weights,
##     offset = offset, x = TRUE, y = TRUE)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  21.7281     0.2698  80.527  < 2e-16 ***
## Weight.1      3.1648     0.6253   5.061 1.03e-06 ***
## Height.1     -1.5464     0.3328  -4.646 6.54e-06 ***
## Waist.1       1.8501     0.5724   3.232  0.00146 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 13.3232)
##
##     Null deviance: 6158.0  on 182  degrees of freedom
## Residual deviance: 2384.9  on 179  degrees of freedom
## AIC: 999.17
##
## Number of Fisher Scoring iterations: 2
```

```r
print(model1)
```

```
## Shifting, Scaling and Centering of covariates
##           shift scale center
## Weight 2.230325     1   TRUE
## Height 2.271145     1   TRUE
## Waist  1.794325     1   TRUE
##
## Final Multivariable Fractional Polynomial for y
##        df_initial select alpha selected df_final power1
## Weight          2   0.05  0.05     TRUE        1      1
## Height          2   0.05  0.05     TRUE        1      1
## Waist           2   0.05  0.05     TRUE        1      1
##
## MFP algorithm convergence: TRUE
##
## Call:  glm(formula = y ~ ., family = family, data = data, weights = weights,
##     offset = offset, x = TRUE, y = TRUE)
##
## Coefficients:
## (Intercept)     Weight.1     Height.1      Waist.1
##      21.728        3.165       -1.546        1.850
##
## Degrees of Freedom: 182 Total (i.e. Null);  179 Residual
## Null Deviance:       6158
## Residual Deviance: 2385  AIC: 999.2
```

```r
# Estimate the model
model2 <- mfp2(Fat ~ fp(Waist, df = 2) + fp(Height, df = 2) + fp(Weight, df = 2)
               + fp(BMI, df = 1), data = women, verbose=TRUE)
```

```
##
## i Initial degrees of freedom:
##    Waist Height Weight BMI
## df     2      2      2   1
##
## i Visiting order: Waist, BMI, Height, Weight
##
## ---------------------
## i Running MFP Cycle 1
## ---------------------
##
## Variable: Waist (keep = FALSE)
##                   Powers    DF    Deviance    Versus            Deviance diff.
## FP1               2         7     986.6       .                 .
## null              NA        5     997.8       FP1               11.2
## linear            1         6     987.5       FP1               0.9
##                   P-value
## FP1               .
## null              0.0036
## linear            0.3309
## Selected: linear
##
## Variable: BMI (keep = FALSE)
##                   Powers    DF    Deviance    Versus            Deviance diff.
## null              NA        5     989.2       .                 .
## linear            1         6     987.5       null              1.6
##                   P-value
## null              .
## linear            0.2005
## Selected: null
##
## Variable: Height (keep = FALSE)
##                   Powers    DF    Deviance    Versus            Deviance diff.
## FP1               2         6     988.5       .                 .
## null              NA        4     1010.0      FP1               21.5
## linear            1         5     989.2       FP1               0.6
##                   P-value
## FP1               .
## null              0.0000
## linear            0.4315
## Selected: linear
##
## Variable: Weight (keep = FALSE)
##                   Powers    DF    Deviance    Versus            Deviance diff.
## FP1               0.5       6     992.1       .                 .
## null              NA        4     1013.6      FP1               21.6
## linear            1         5     989.2       FP1               -2.9
##                   P-value
## FP1               .
## null              0.0000
## linear            1.0000
## Selected: linear
##
## ---------------------
## i Running MFP Cycle 2
## ---------------------
##
## Variable: Waist (keep = FALSE)
##                   Powers    DF    Deviance    Versus            Deviance diff.
## FP1               2         6     988.8       .                 .
## null              NA        4     999.5       FP1               10.7
## linear            1         5     989.2       FP1               0.4
##                   P-value
## FP1               .
## null              0.0046
## linear            0.5445
## Selected: linear
##
## Variable: BMI (keep = FALSE)
##                 Powers    DF    Deviance    Versus            Deviance diff.
## null            NA        5     989.2       .                 .
## linear          1         6     987.5       null              1.6
##                 P-value
## null            .
## linear          0.2005
## Selected: null
##
## Variable: Height (keep = FALSE)
##                 Powers    DF    Deviance    Versus            Deviance diff.
## FP1             2         6     988.5       .                 .
## null            NA        4     1010.0      FP1               21.5
## linear          1         5     989.2       FP1               0.6
##                 P-value
## FP1             .
## null            0.0000
## linear          0.4315
## Selected: linear
##
## Variable: Weight (keep = FALSE)
##                 Powers    DF    Deviance    Versus            Deviance diff.
## FP1             0.5       6     992.1       .                 .
## null            NA        4     1013.6      FP1               21.6
## linear          1         5     989.2       FP1               -2.9
##                 P-value
## FP1             .
## null            0.0000
## linear          1.0000
## Selected: linear
##
## i Fractional polynomial fitting algorithm converged after 2 cycles.
```

```
# Summarize the model
summary(model2)
```

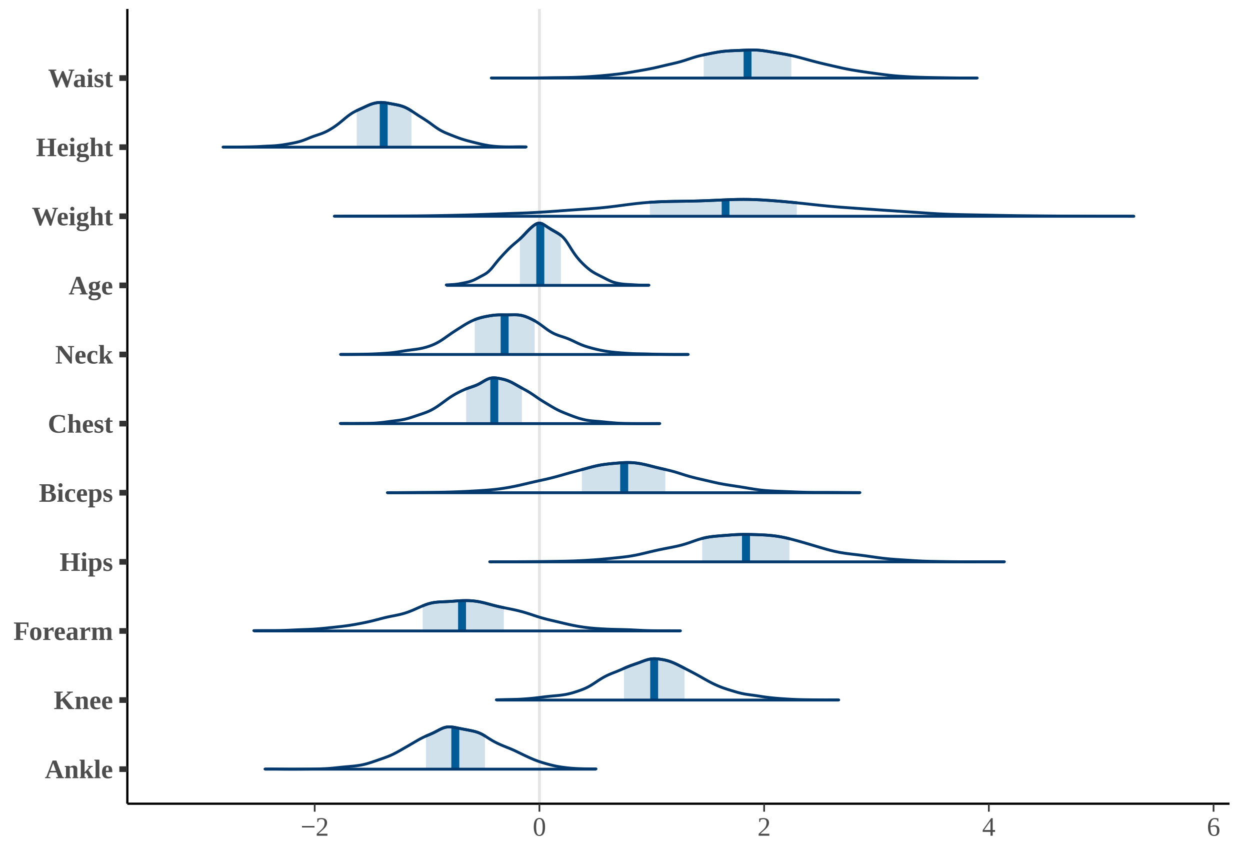
```
##
## Call:
## glm(formula = y ~ ., family = family, data = data, weights = weights,
##     offset = offset, x = TRUE, y = TRUE)
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  21.7281     0.2698  80.527  < 2e-16 ***
## Waist.1       1.8501     0.5724   3.232  0.00146 **
## Height.1     -1.5464     0.3328  -4.646 6.54e-06 ***
## Weight.1      3.1648     0.6253   5.061 1.03e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 13.3232)
##
##     Null deviance: 6158.0  on 182  degrees of freedom
## Residual deviance: 2384.9  on 179  degrees of freedom
## AIC: 999.17
##
## Number of Fisher Scoring iterations: 2
```

```r
print(model2)
```

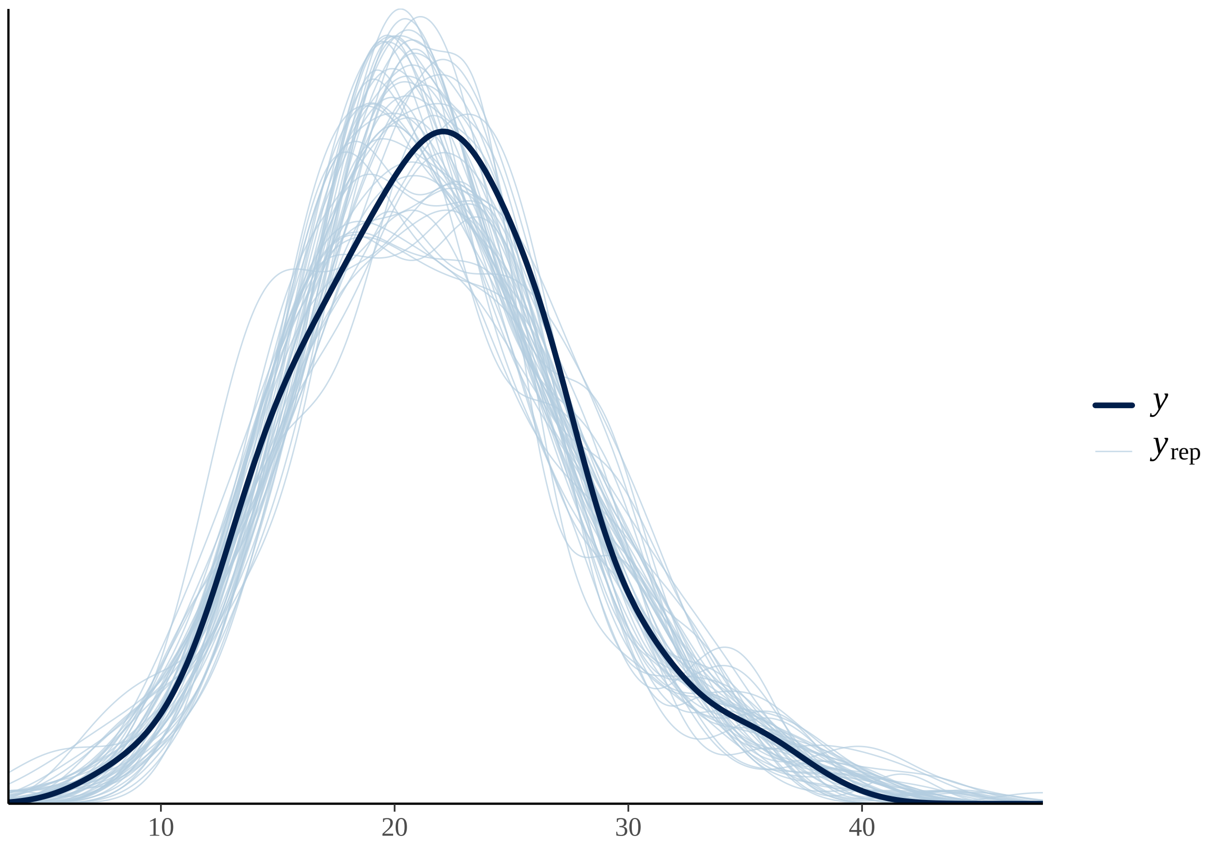
```
## Shifting, Scaling and Centering of covariates
##           shift scale center
## Waist  1.794325     1   TRUE
## BMI    2.143166     1   TRUE
## Height 2.271145     1   TRUE
## Weight 2.230325     1   TRUE
##
## Final Multivariable Fractional Polynomial for y
##        df_initial select alpha selected df_final power1
## Waist           2   0.05  0.05     TRUE        1      1
## BMI             1   0.05  0.05    FALSE        0     NA
## Height          2   0.05  0.05     TRUE        1      1
## Weight          2   0.05  0.05     TRUE        1      1
##
## MFP algorithm convergence: TRUE
##
## Call:  glm(formula = y ~ ., family = family, data = data, weights = weights,
##     offset = offset, x = TRUE, y = TRUE)
##
## Coefficients:
## (Intercept)      Waist.1     Height.1     Weight.1
##      21.728        1.850       -1.546        3.165
##
## Degrees of Freedom: 182 Total (i.e. Null);  179 Residual
## Null Deviance:       6158
## Residual Deviance: 2385  AIC: 999.2
```

```r
#library(rstanarm)
```

```r
# Use the full model after stept 3 in Georgs task, thus model 1 and all predictors but not BMI
# Only use predictors that are available in the man dataset
# Fat = siri, Age = age, Height = height, Weight = weight, Neck = neck, Chest = chest, Waist = abdomen,
rmf <- as.formula(Fat ~ Waist + Height + Weight + Age + Neck + Chest +
                          Biceps + Hips + Forearm +
                        Knee +  Ankle)

# Fit a Bayesian Gaussian regression model using stan_glm
ref_fitf <- stan_glm(rmf, data = women, family = gaussian())
# Check reference model, MCMC check
summary(ref_fitf)
#shinystan::launch_shinystan(ref_fitf)

mcmc_areas(as.matrix(ref_fitf)[,2:12])
```

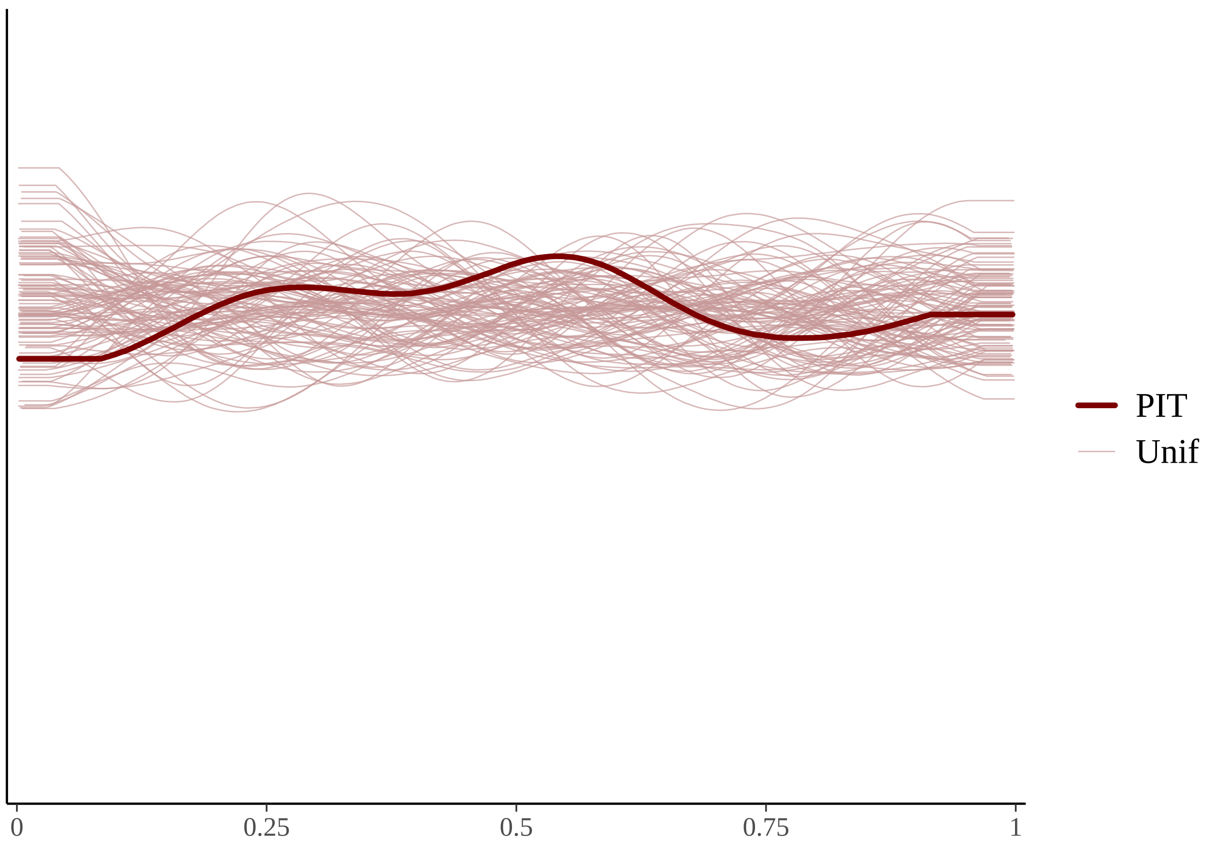


```
pp_check(ref_fitf)
```



```
y_rep_rmf <- posterior_predict(ref_fitf)
loo_rmf <- loo(ref_fitf , save_psis = TRUE, cores = 4)
psis1_rmf <- loo_rmf$psis_object
lw_rmf <- weights(psis1_rmf)
color_scheme_set("red")
#pdf(file.path(PPath2, "/LOOPITrmf.pdf"))
ppc_loo_pit_overlay(y= women$Fat,yrep=y_rep_rmf,lw=lw_rmf)
```

```
## NOTE: The kernel density estimate assumes continuous observations and is not optimal for discrete obs
```



```r
#dev.off()

# Summarize the posterior distributions simple model
summary_rmf_cv <- prediction_summary_cv(model = ref_fitf , data = women, k = 3)

# Print the summary simple model
print(summary_rmf_cv)
```

```
## $folds
##   fold      mae mae_scaled within_50 within_95
## 1    1 2.195283  0.6000621 0.5409836 0.9344262
## 2    2 2.605617  0.7166565 0.4754098 0.9344262
## 3    3 2.540476  0.6754453 0.5245902 0.9672131
##
## $cv
##        mae mae_scaled within_50 within_95
## 1 2.447125  0.6640546 0.5136612 0.9453552
```

```r
pred <- c("Waist" ,"Height" ,"Weight" ,"Age", "Neck" ,"Chest" ,
                          "Biceps" ,"Hips" , "Forearm",
                        "Knee", "Ankle")

# Extract the posterior samples for the estimator
posterior_samples <- as.matrix(ref_fitf, pars = pred)
```

```r
# Define the range
lower_bound <- -0.05
upper_bound <- 0.05

# Apply the condition to each element of the matrix
prob_between <- apply(posterior_samples, 2, function(par) mean(par >= lower_bound & par <= upper_bound)

# Print the result
print(prob_between)
```

Compute the probabilty for each estimator that it is close to zero

```
##   Waist  Height  Weight     Age    Neck   Chest  Biceps    Hips Forearm    Knee
## 0.00025 0.00000 0.00825 0.15400 0.07775 0.05825 0.02800 0.00025 0.03075 0.00575
##   Ankle
## 0.01675
```

```r
print(prob_between[prob_between > 0.25])
```

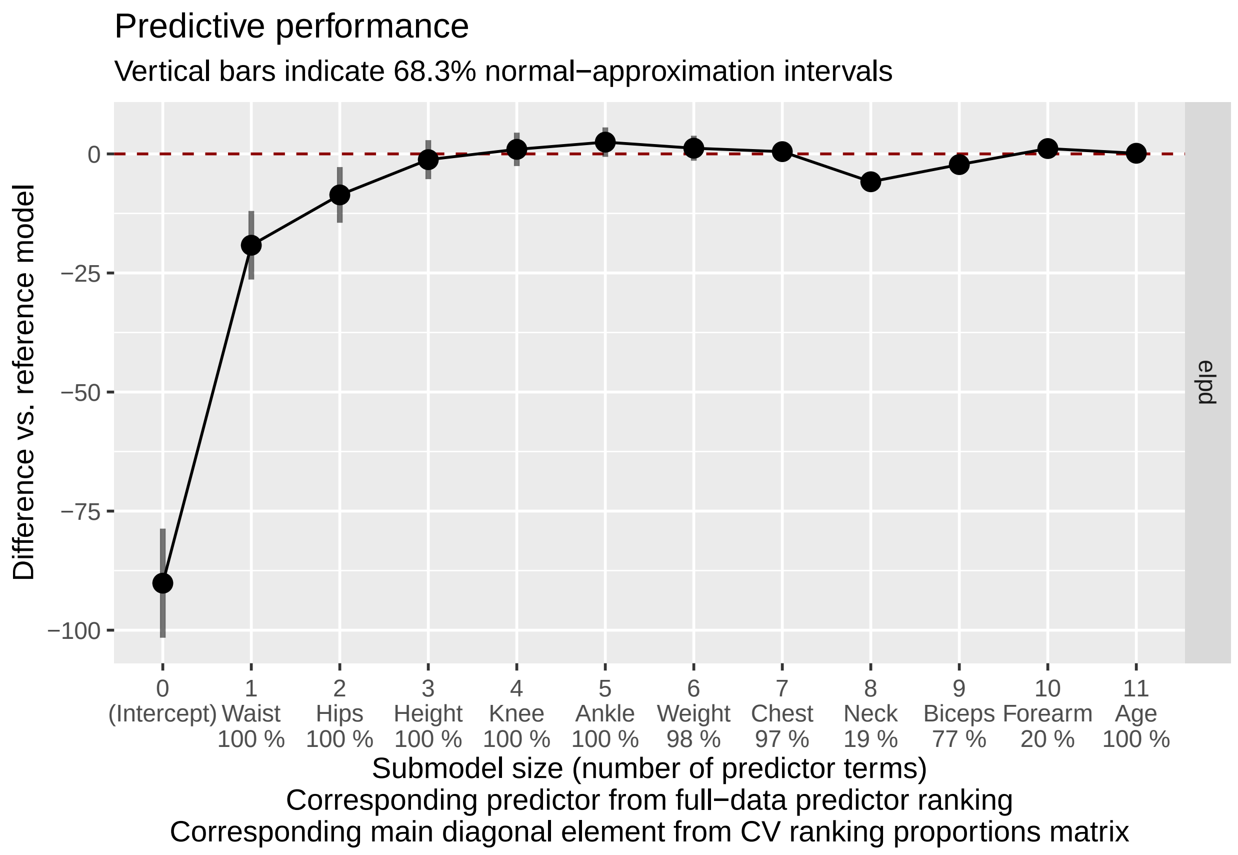
```
## named numeric(0)
```

```r

set.seed(2341)
vs_cvf <- cv_varsel(ref_fitf)
```

Use projpred to downsize model even more

```
## Warning in warn_pareto(n07 = sum(pareto_k > 0.7), n05 = sum(0.7 >= pareto_k & :
## In the calculation of the reference model's PSIS-LOO CV weights, 1 (out of 183)
## Pareto k-values are in the interval (0.5, 0.7]. Moment matching (see the loo
## package), mixture importance sampling (see the loo package), and `reloo`-ing
## (see the brms package) are not supported by projpred. If these techniques (run
## outside of projpred, i.e., for the reference model only; note that `reloo`-ing
## may be computationally costly) result in a markedly different reference model
## ELPD estimate than ordinary PSIS-LOO CV does, we recommend to use K-fold CV
## within projpred.
```

```r
save(vs_cvf,file = file.path(PPath2,"vs_cvf"))
#load(file = file.path(PPath2,"vs_cv"))
nsel <- suggest_size(vs_cvf)
nsel

rank_vs_cvf <- ranking(vs_cvf)
rank_vs_cvf
solterms_final_vs_cvf <- head(rank_vs_cvf$fulldata ,suggest_size(vs_cvf))

solterms_final_vs_cvf

# Print the summary of the variable selection
summary(vs_cvf)

# Plot the variable selection
#pdf(file.path(PPath2, "cv_valsel_plotf.pdf"))
plot(vs_cvf, deltas = TRUE)
```



```r
#dev.off()
#
```

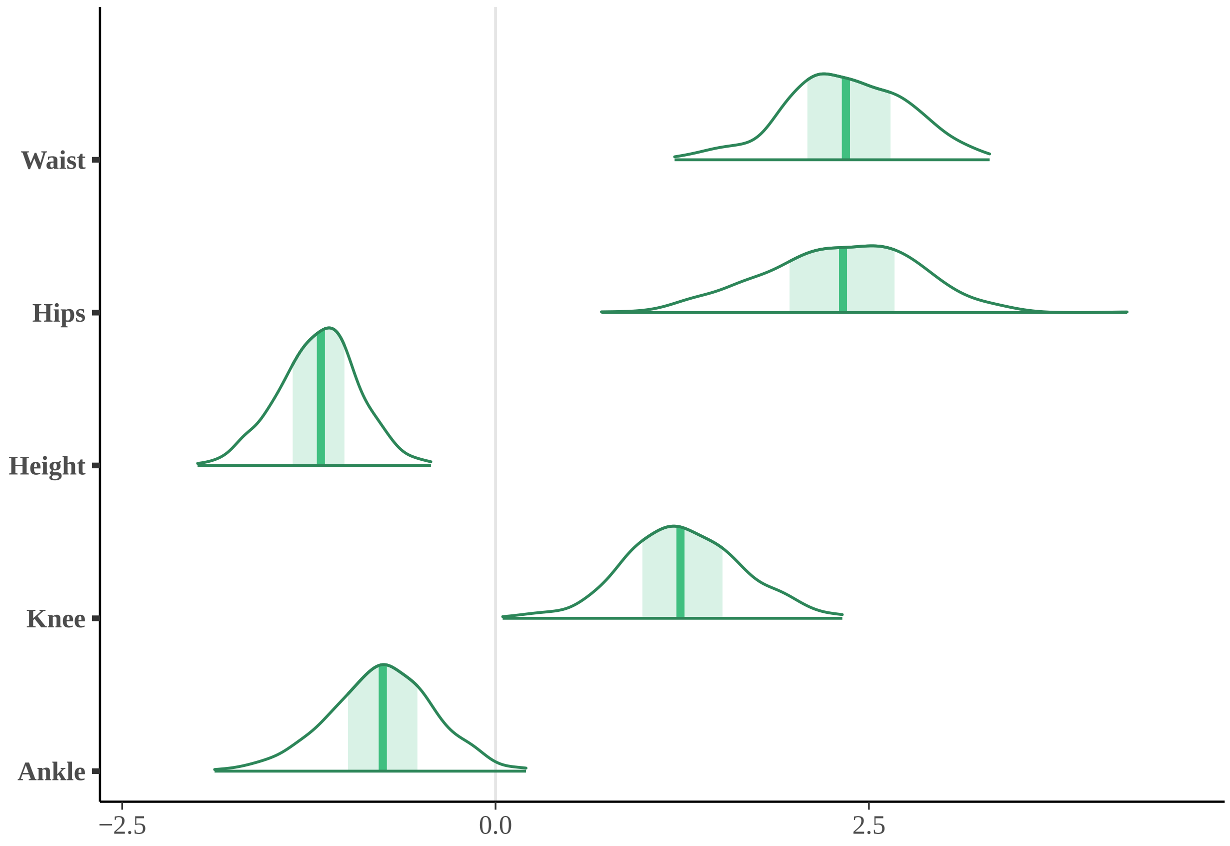
```r
solterms_final_fivef <- head(rank_vs_cvf$fulldata, 5)
solterms_final_fivef
```

```
## [1] "Waist"  "Hips"   "Height" "Knee"   "Ankle"
```

```r
# https://cran.r-project.org/web/packages/projpred/vignettes/projpred.html#post-selection-inference
proj_ref_fitf <- project(vs_cvf, predictor_terms = solterms_final_fivef, ns = 4000)
```

Projected posterior for the selected model

```r
color_scheme_set(scheme = "green")
mcmc_areas(as.matrix(proj_ref_fitf), pars = solterms_final_fivef)#
```



Show results

Derive second reference model based on FBMS: Using BMA, marginal likelihoods inherently account for model complexity, and PIPs derived from them reflect this balance.

```
#Marginal likelihoods inherently account for model complexity by integrating over all possible paramete

transforms <- c("p2","p3")#  transforms planed in my re-sap

probs <- gen.probs.gmjmcmc(transforms)
probs$gen <- c(0,1,0,1) # Only modifications!
params <- gen.params.gmjmcmc(women[,c("Waist","Height","Weight","Age","Neck","Chest","Biceps","Hips","F
params$feat$pop.max <- 20 #set the population size to be 20
params$feat$D <- 1   # Set depth of features to 1
#@ Aliaksandr(1): please decide about this options
params$loglik$r <- exp(-2) # to correspond to AIC complexity that Georg uses in mfp
params$loglik$var <- "unknown"
modelFBMS <- as.formula(Fat ~ Waist + Height + Weight + Age + Neck + Chest +
                          Biceps + Hips + Forearm
                        +  Knee +  Ankle + BMI)

set.seed(1234)

result <- fbms(modelFBMS, data = women, method = "gmjmcmc.parallel",
                family = "gaussian",
               transforms = transforms, probs = probs, params = params, P = 50,
              runs = 40, cores = 10)
```

```
summary(result, labels = c("Waist","Height","Weight","Age","Neck","Chest","Biceps","Hips","Forearm","Kn
```

The final model, which includes five predictors, is identical

```
##                    Importance | Feature
##              #################| Knee
##   #############################| Height
##   #############################| Waist
##   #############################| Hips
##
## Best   population: 31  thread: 1  log marginal posterior: -499.3607
## Report population: 31  thread: 1  log marginal posterior: -499.3607
```

```
##   feats.strings marg.probs
## 1          Hips  0.9977295
## 2         Waist  0.9872543
## 3        Height  0.9713975
## 4          Knee  0.5757139
```

```
formula_male <- as.formula(Fat ~ Waist  + Hips + Height + Knee + Ankle)
```

Fit model to male data set and compare the posterior predictive distributions

```
library(mfp)
```

See Task Bodyfat.qmd

```
## Warning: Paket 'mfp' wurde unter R Version 4.4.2 erstellt
```

```
## Lade nötiges Paket: survival
```

```
##
## Attache Paket: 'mfp'
```

```
## Das folgende Objekt ist maskiert 'package:mfp2':
##
##     fp
```

```
data(bodyfat)

bodyfat_corr <- bodyfat

bodyfat_corr[42,"height"] <- 69.5       # one-digit correction of height
bodyfat_corr[48,"density"] <- 1.0865    # one-digit correction of density
bodyfat_corr[76,"density"] <- 1.0566    # one-digit correction of density
bodyfat_corr[96,"density"] <- 1.0591    # one-digit correction of density

# recompute siri formula based on corrected density

bodyfat_corr[,"siri"]   <- pmax(round(495 / bodyfat_corr$density - 450, 1) , 0)
bodyfat_corr[,"brozek"] <- pmax(round(457/ bodyfat_corr$density - 414.2, 1) , 0)
```

Aligning the two data sets

```
bodyfat_corr$height <- bodyfat_corr$height * 2.54/100
bodyfat_corr$weight <- bodyfat_corr$weight * 0.454592
```

```r
library(tidyverse)
```

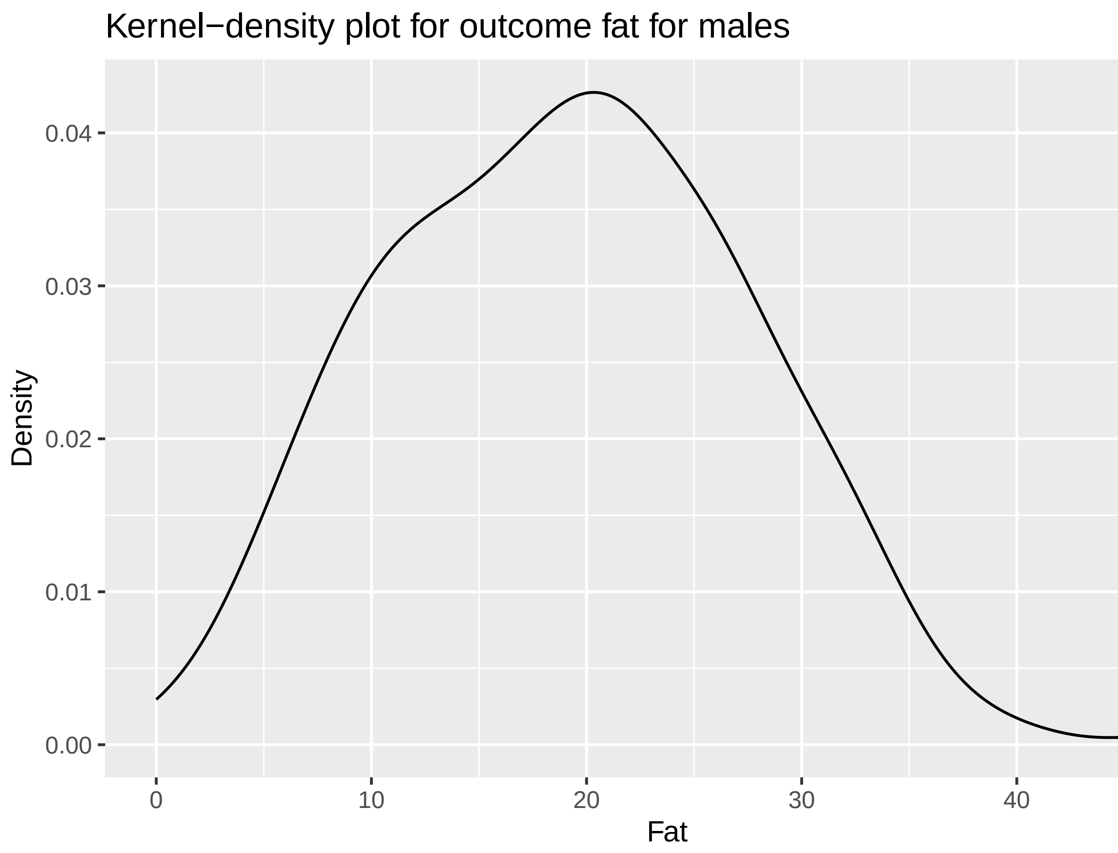
```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v lubridate 1.9.3     v tibble    3.2.1
## v purrr     1.0.2     v tidyr     1.3.1
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```r
men <- bodyfat_corr %>%
  rename(Fat = siri, Age = age, Height = height, Weight = weight,
         Neck = neck, Chest = chest, Waist = abdomen, Hips = hip,
         Knee = knee, Ankle = ankle, Forearm = forearm,
         Biceps = biceps, Thigh = thigh)
names(men)
```

```
##  [1] "case"    "brozek"  "Fat"     "density" "Age"     "Weight"  "Height"
##  [8] "Neck"    "Chest"   "Waist"   "Hips"    "Thigh"   "Knee"    "Ankle"
## [15] "Biceps"  "Forearm" "wrist"
```

```r
# Add BMI
men$BMI <- men$Weight / (men$Height^2)
men[,4:18] <- scale(men[,4:18])
```

```r
fat_density_male <- density(men$Fat, na.rm = TRUE)
ggplot(men, aes(x = Fat)) + geom_density() +
  labs(title = "Kernel-density plot for outcome fat for males", x = "Fat", y = "Density")
```

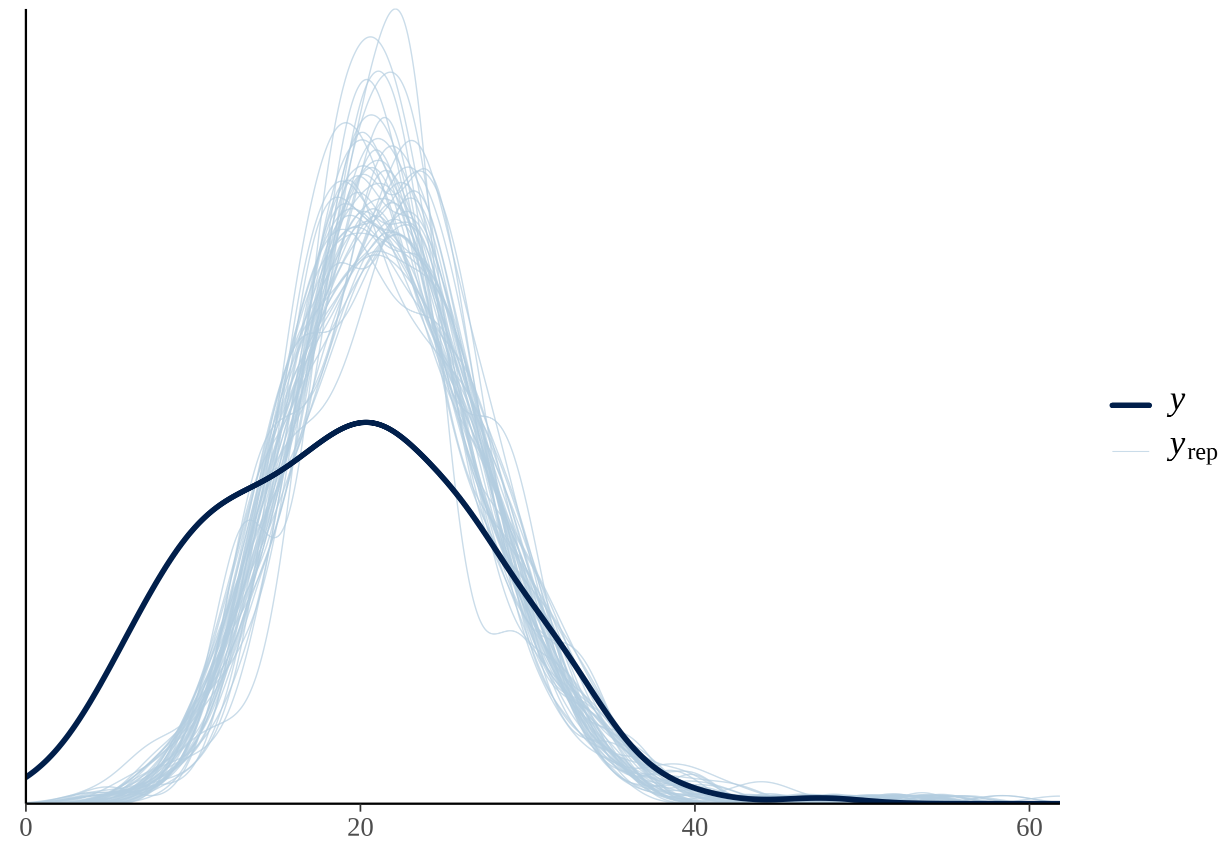


Prepare data for males

```
summary(men$Fat)
```

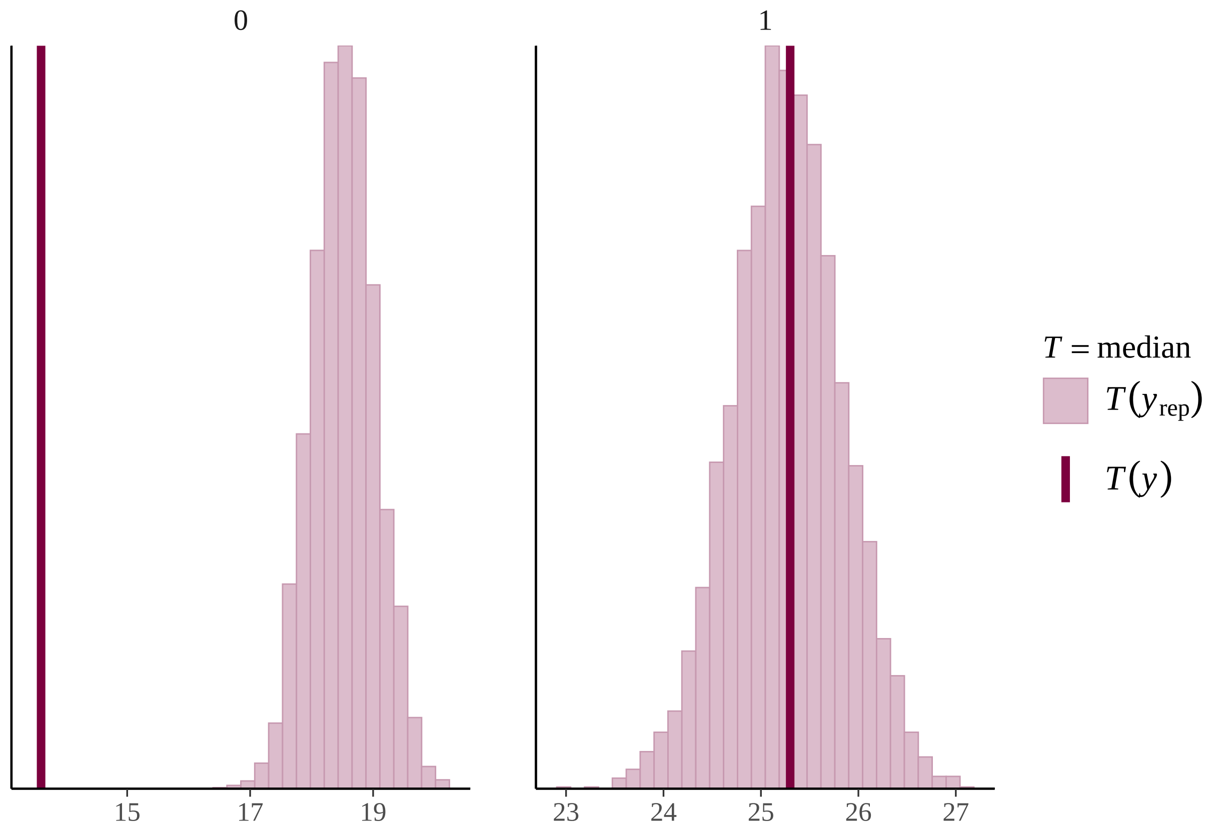
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.00   12.40   19.20   19.16   25.30   47.50
```

```
# LOOPIT and bayesrules summary for male data based on female model
# Prediction for male data based on female model
fit_female <- stan_glm(formula_male, data = women, family = gaussian())
#proj_ref_fitf <- project(vs_cvf, predictor_terms = solterms_final_fivef, ns = 4000)
# https://www.rdocumentation.org/packages/projpred/versions/2.0.2/topics/proj-pred
#y_rep_male <- proj_linpred(vs_cvf, solution_terms= solterms_final_fivef, newdata = men)#
y_rep_male <- posterior_predict(fit_female, newdata = men)
color_scheme_set("blue")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male[1:50,],fun = ppc_dens_overlay)
```



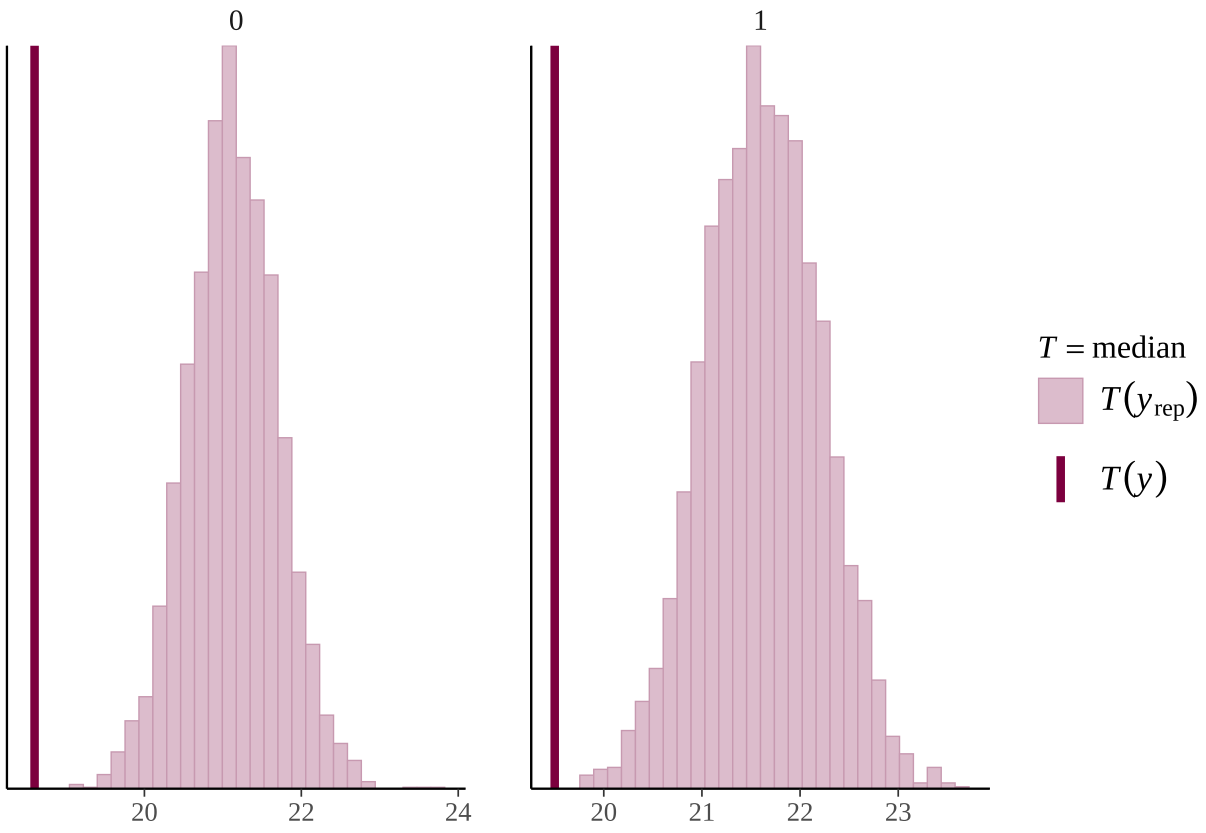
```r
binary_waist_male <- ifelse(men$Waist <= 0, 0, 1)
binary_height_male <- ifelse(men$Height <= 0, 0, 1)
binary_hips_male <- ifelse(men$Hips <= 0, 0, 1)
binary_knee_male <- ifelse(men$Knee <= 0, 0, 1)
binary_ankle_male <- ifelse(men$Ankle <= 0, 0, 1)
color_scheme_set("pink")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_waist_male, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



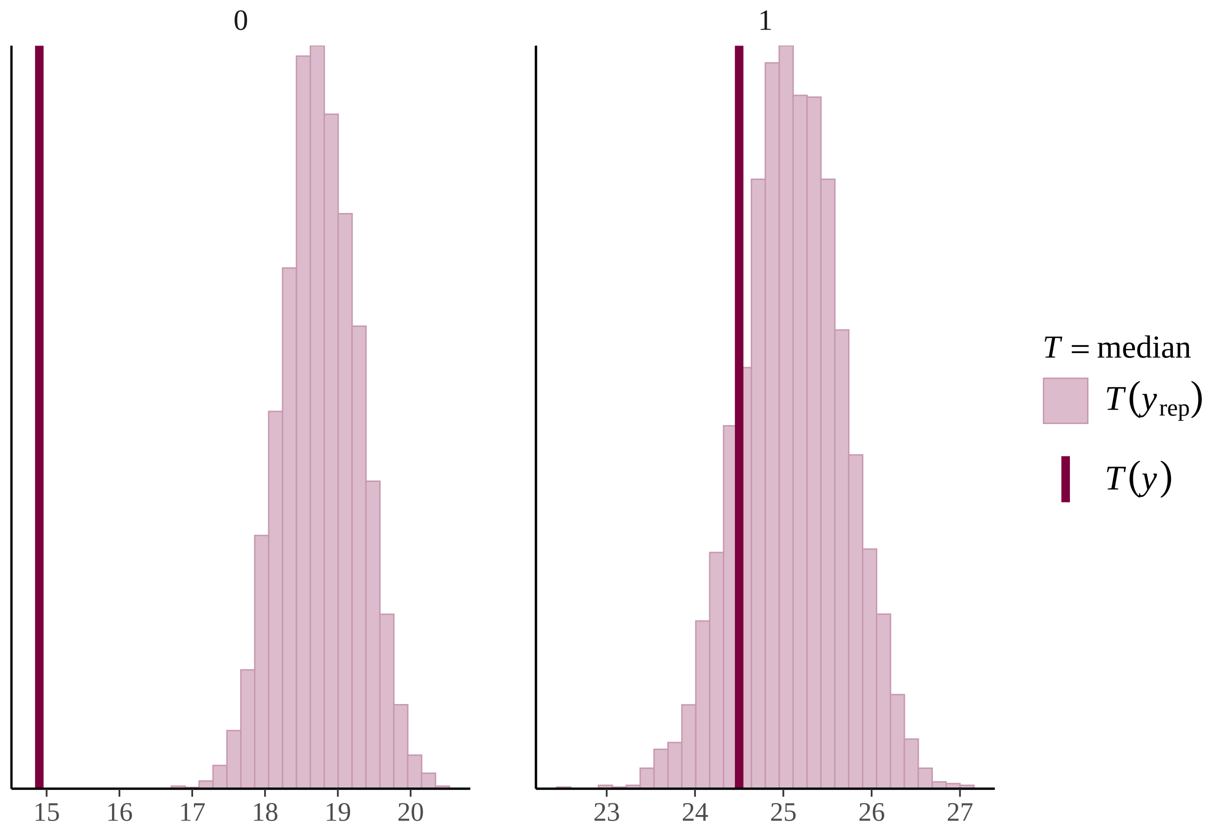
```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_height_male, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



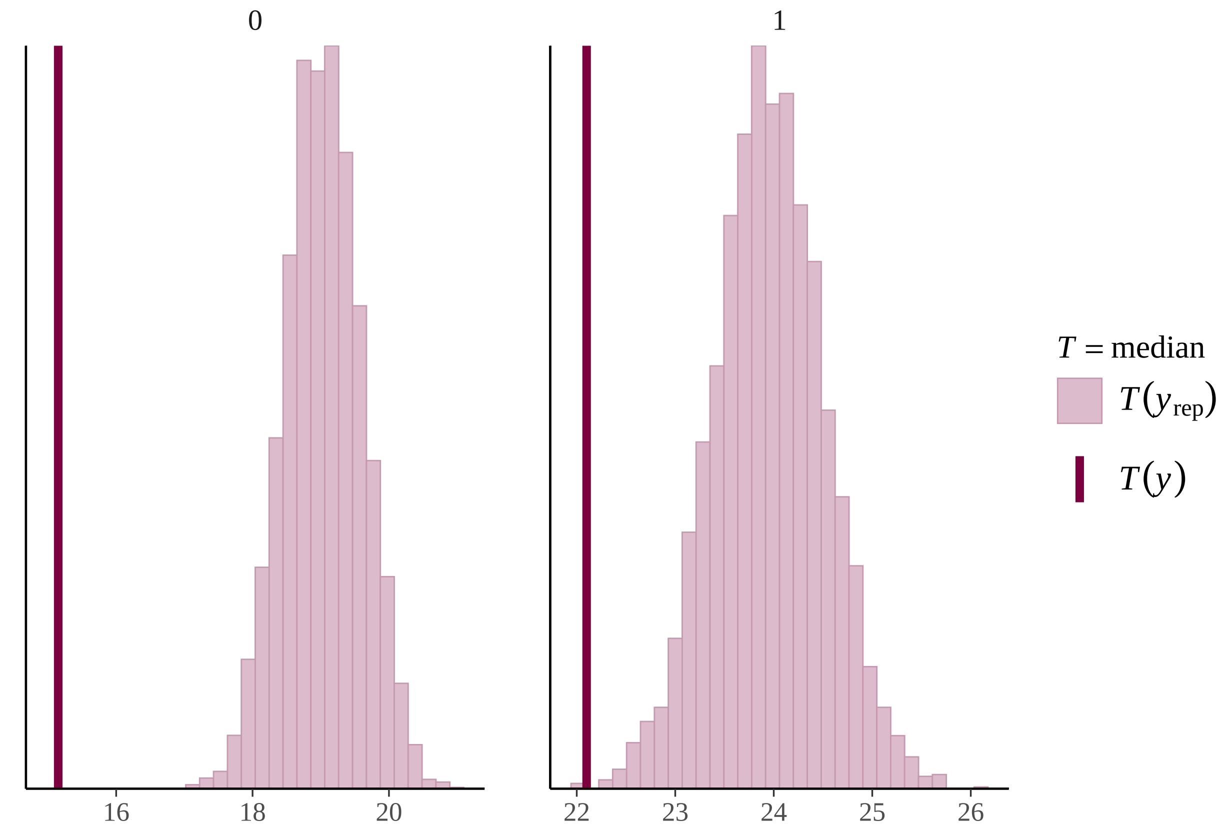
```r
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_hips_male, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



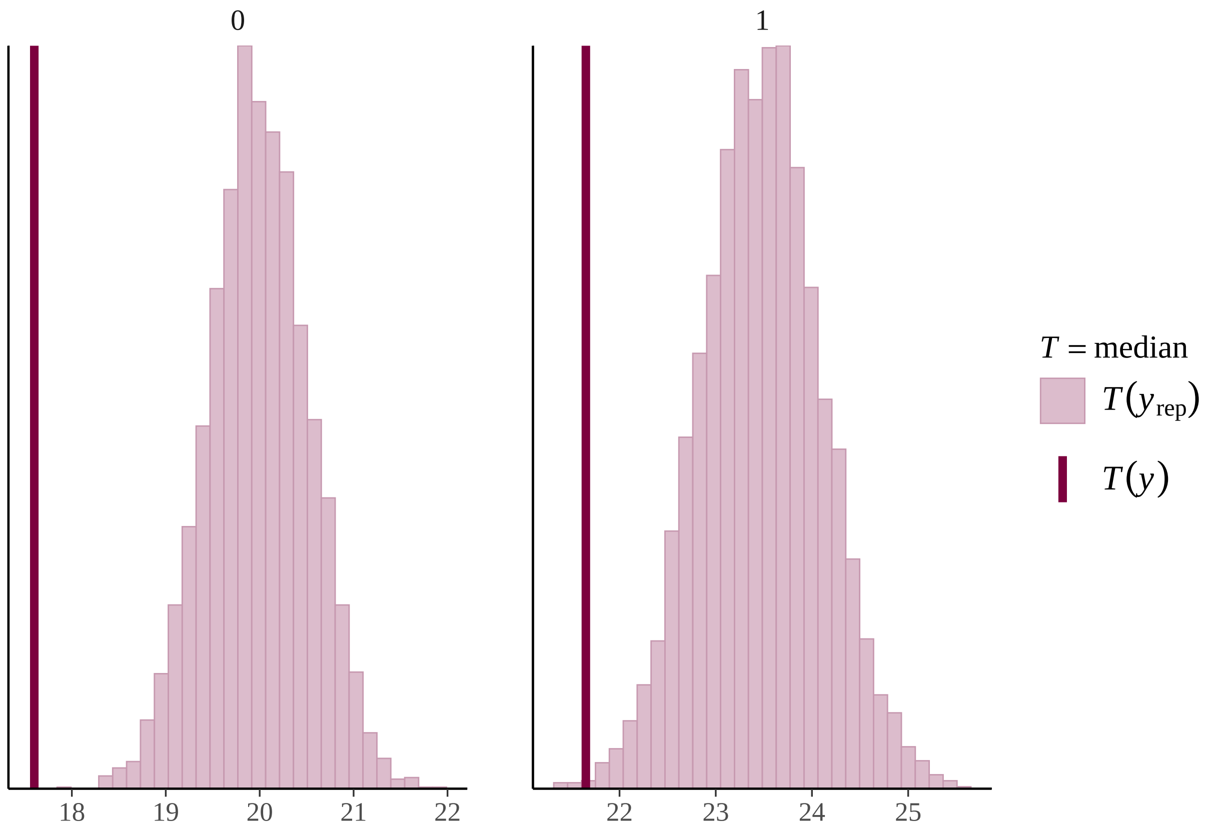
```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,fun = "stat_grouped",
                    group = binary_knee_male, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



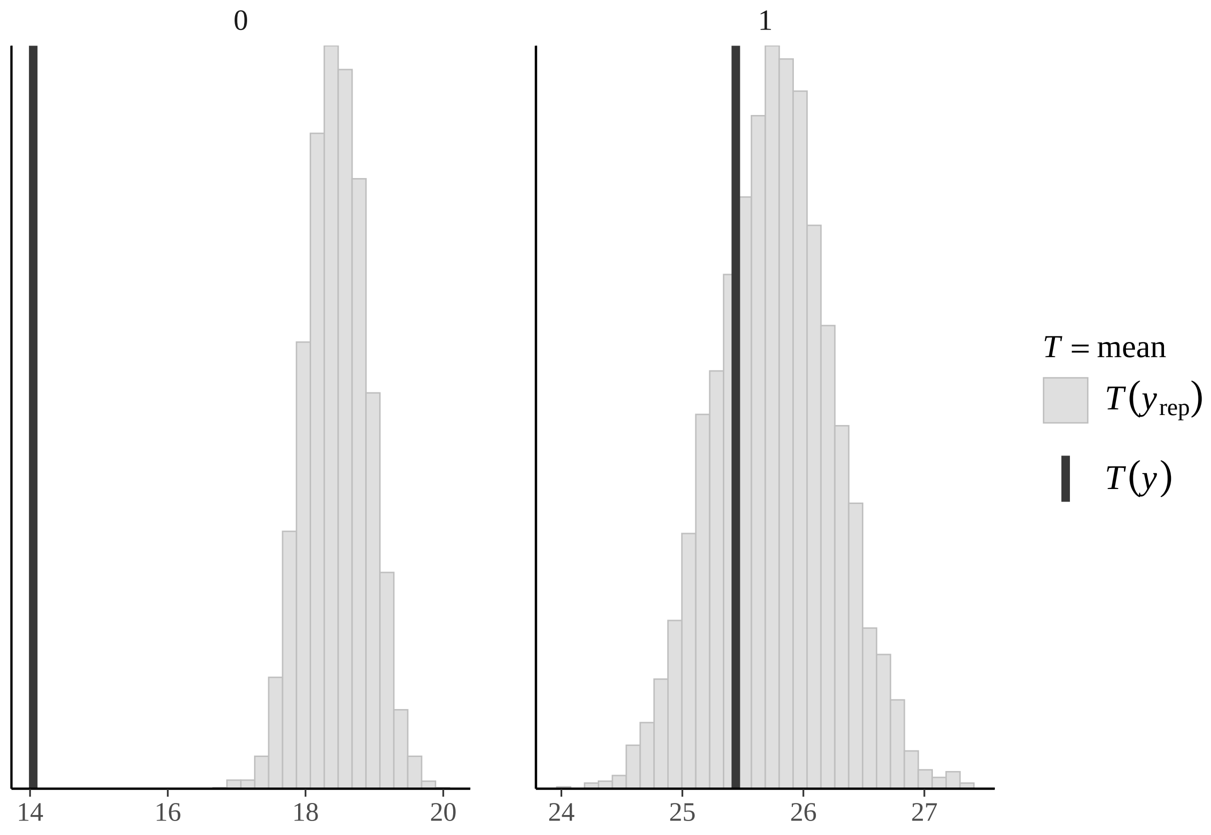
```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,fun = "stat_grouped",
                    group = binary_ankle_male, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



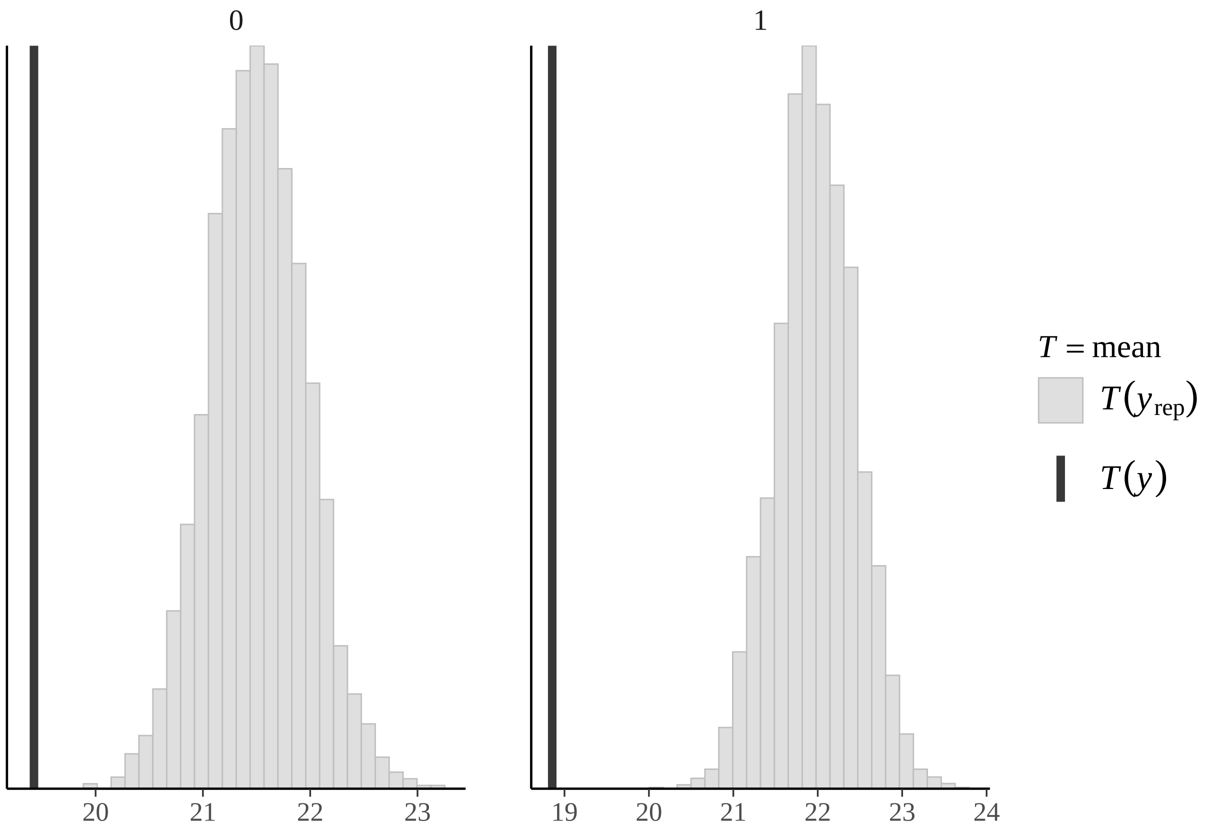
```r
color_scheme_set("gray")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_waist_male, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



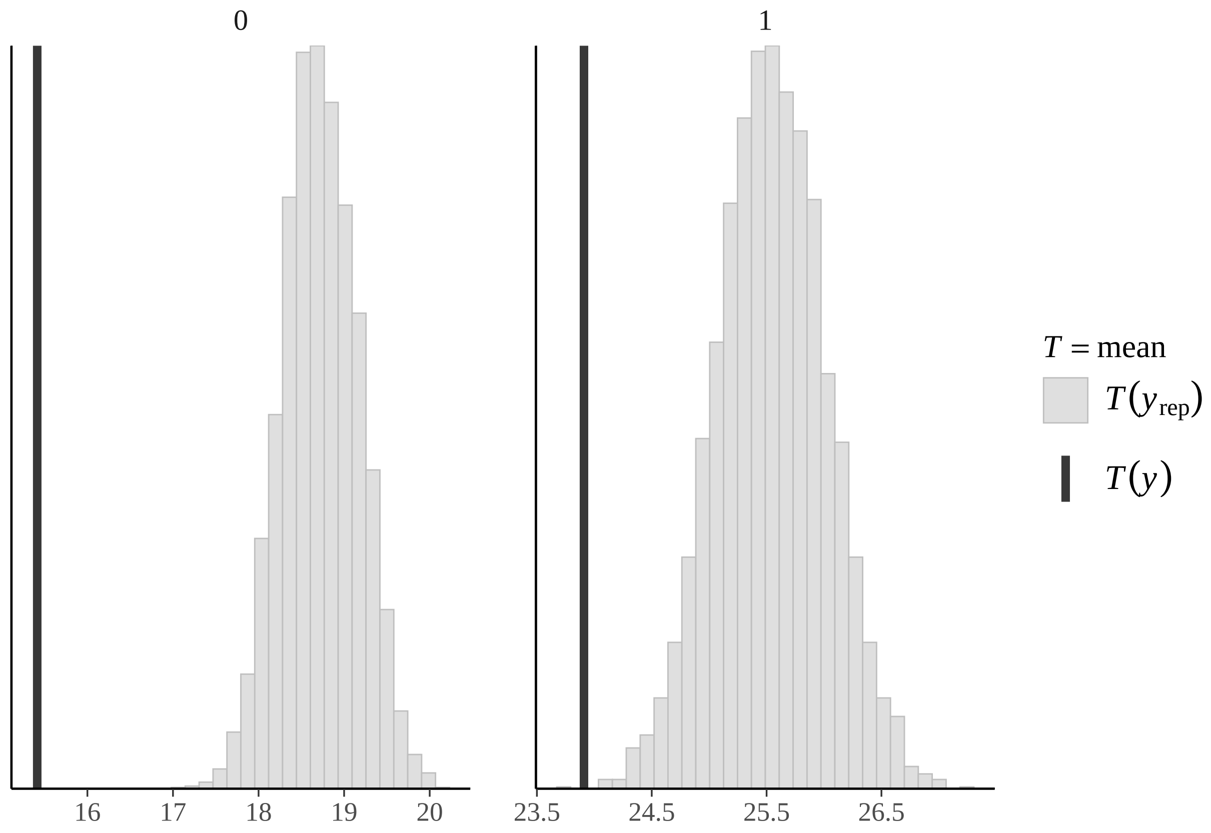
```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_height_male, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



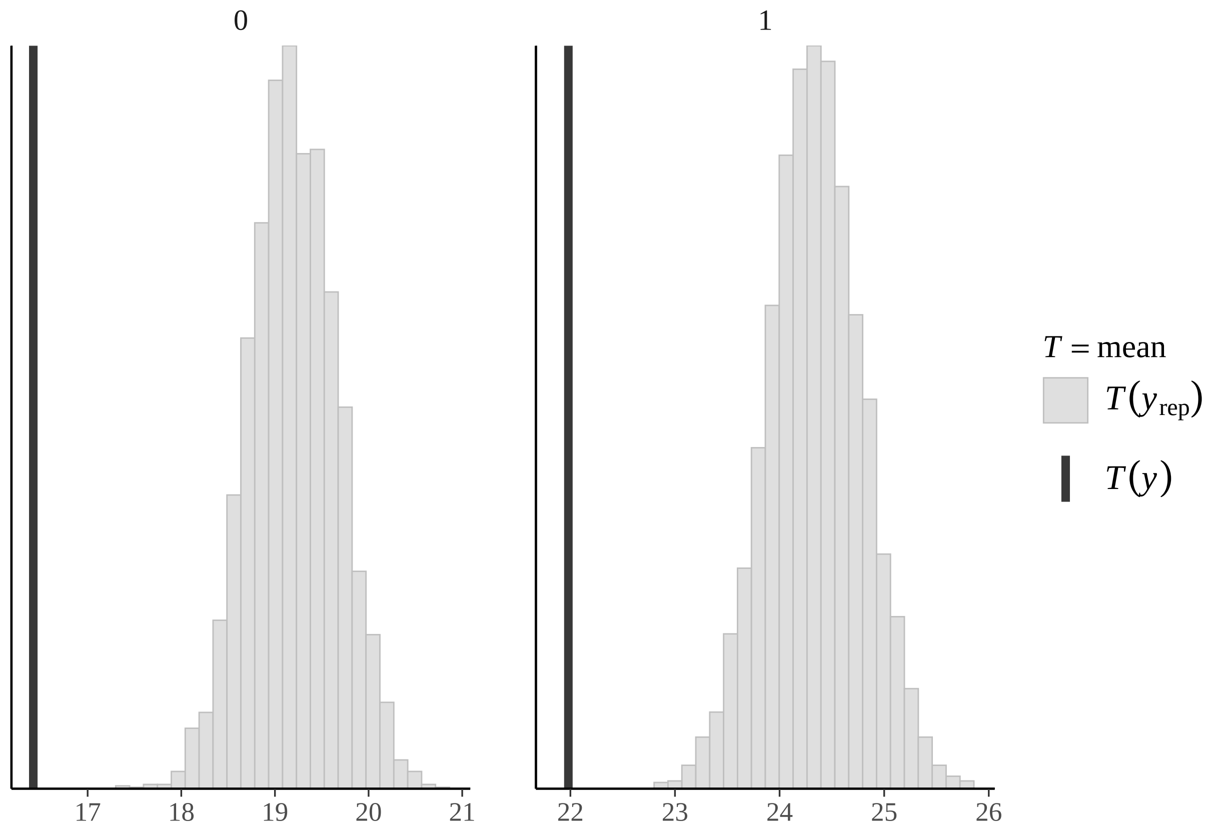
```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = binary_hips_male, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



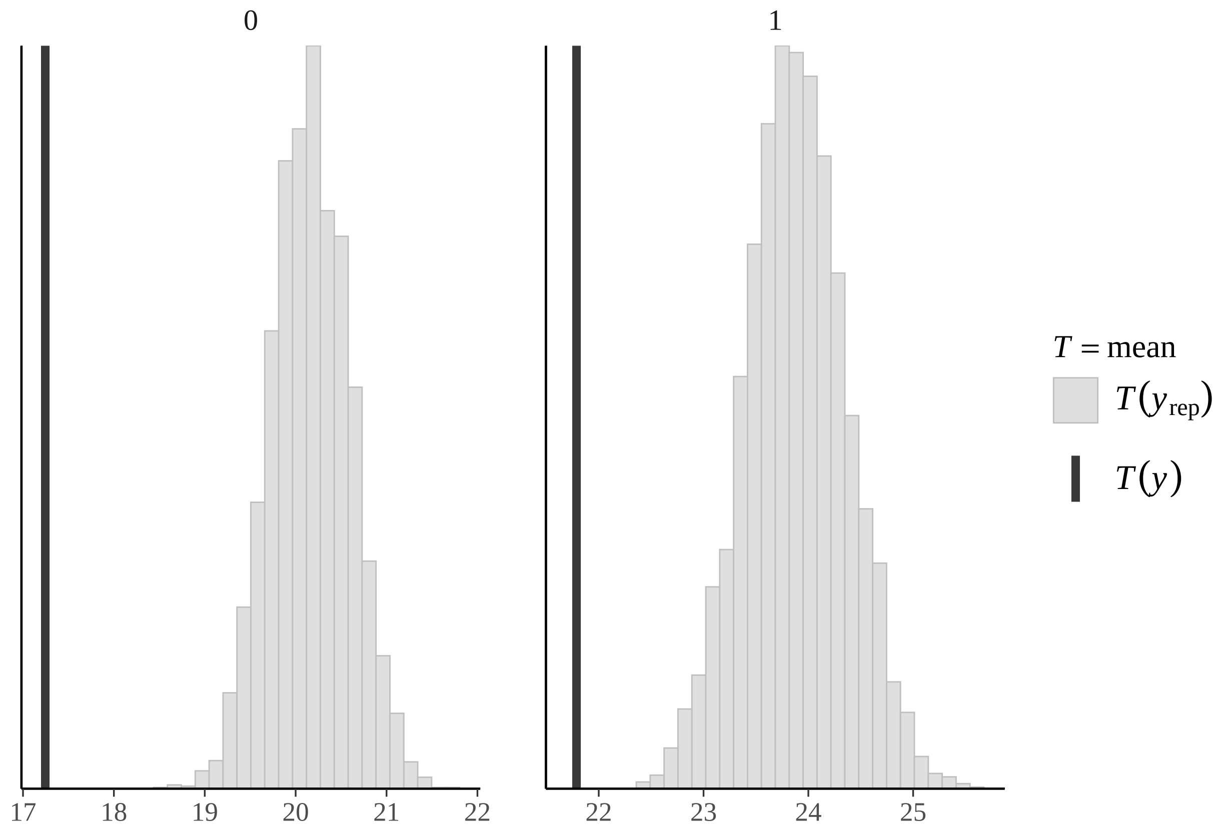
```r
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,fun = "stat_grouped",
                    group = binary_knee_male, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,fun = "stat_grouped",
                    group = binary_ankle_male, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```r
# Summarize the posterior distributions
summary_male_cv <- prediction_summary_cv(model = fit_female, data = men, k = 3)

# Print the summary
print(summary_male_cv)
```

Summarize the posterior distributions

```
## $folds
##   fold      mae mae_scaled within_50 within_95
## 1    1 3.696158  0.7896502 0.4285714 0.9761905
## 2    2 2.835573  0.5887821 0.5714286 0.9642857
## 3    3 3.459173  0.7612981 0.4523810 0.9523810
##
## $cv
##        mae mae_scaled within_50 within_95
## 1 3.330301  0.7132435  0.484127 0.9642857
```

```r
summary_male <- prediction_summary(model = fit_female, data = men)

# Print the summary
print(summary_male)
```

```
##        mae mae_scaled within_50 within_95
## 1 4.316417   1.225886  0.297619 0.7301587
```

```
age_group <- cut(men$Age, breaks = quantile(men$Age, probs = seq(0, 1, by = 0.25)), include.lowest = TRU
table(age_group)
```

Identify the groups where the prediction performs effectively

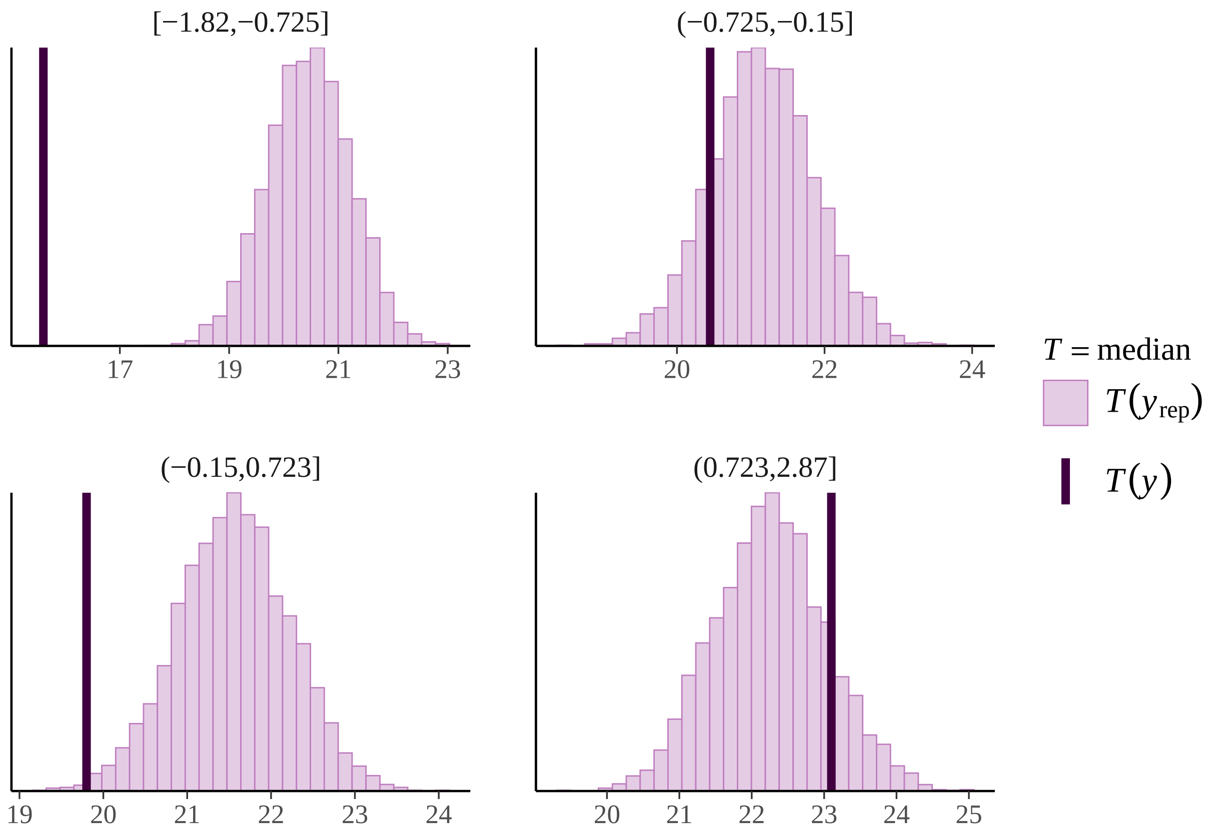
```
## age_group
## [-1.82,-0.725] (-0.725,-0.15]  (-0.15,0.723]   (0.723,2.87]
##             63             64             68             57
```

```
fat_group <- cut(men$Fat, breaks = quantile(men$Fat, probs = seq(0, 1, by = 0.25)), include.lowest = TRU
table(fat_group)
```

```
## fat_group
##    [0,12.4] (12.4,19.2] (19.2,25.3] (25.3,47.5]
##          64          63          64          61
```

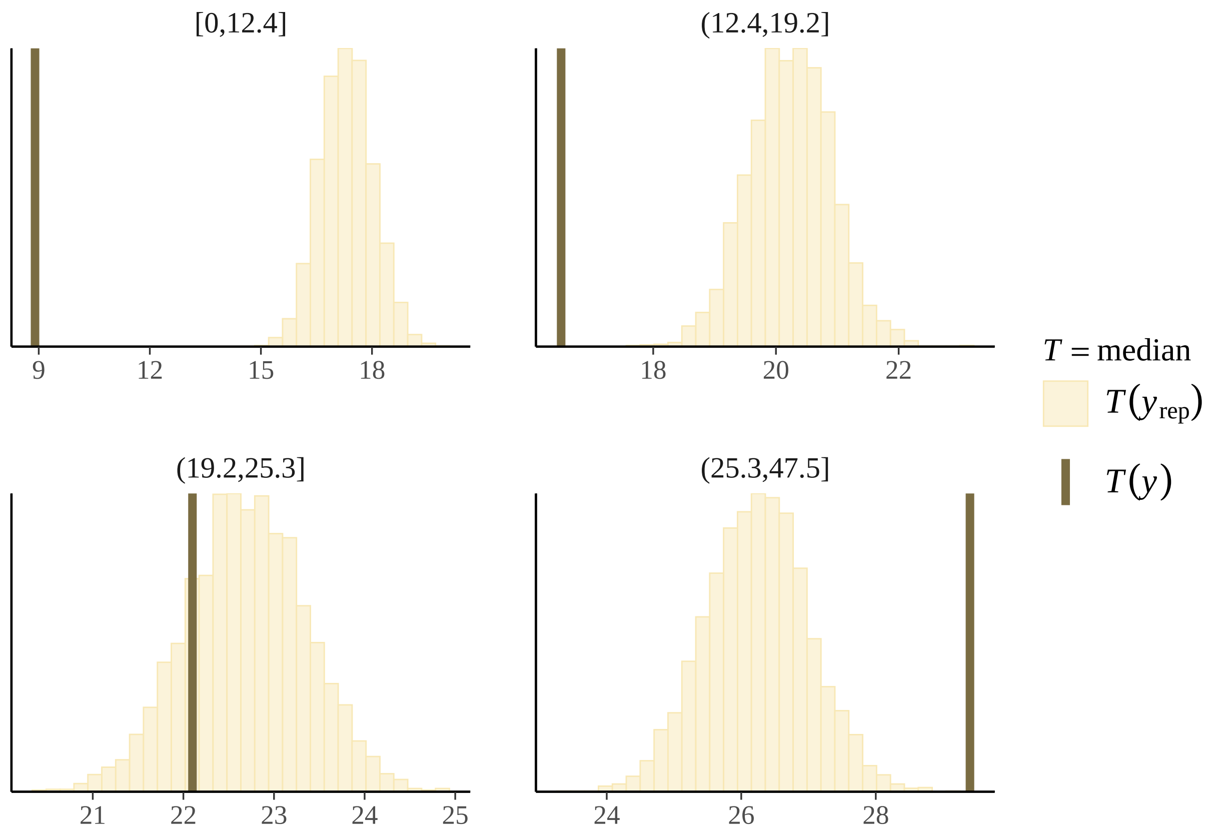
```
waist_group <- cut(men$Waist, breaks = quantile(men$Waist, probs = seq(0, 1, by = 0.25)), include.lowes

color_scheme_set(scheme = "purple")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = age_group, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



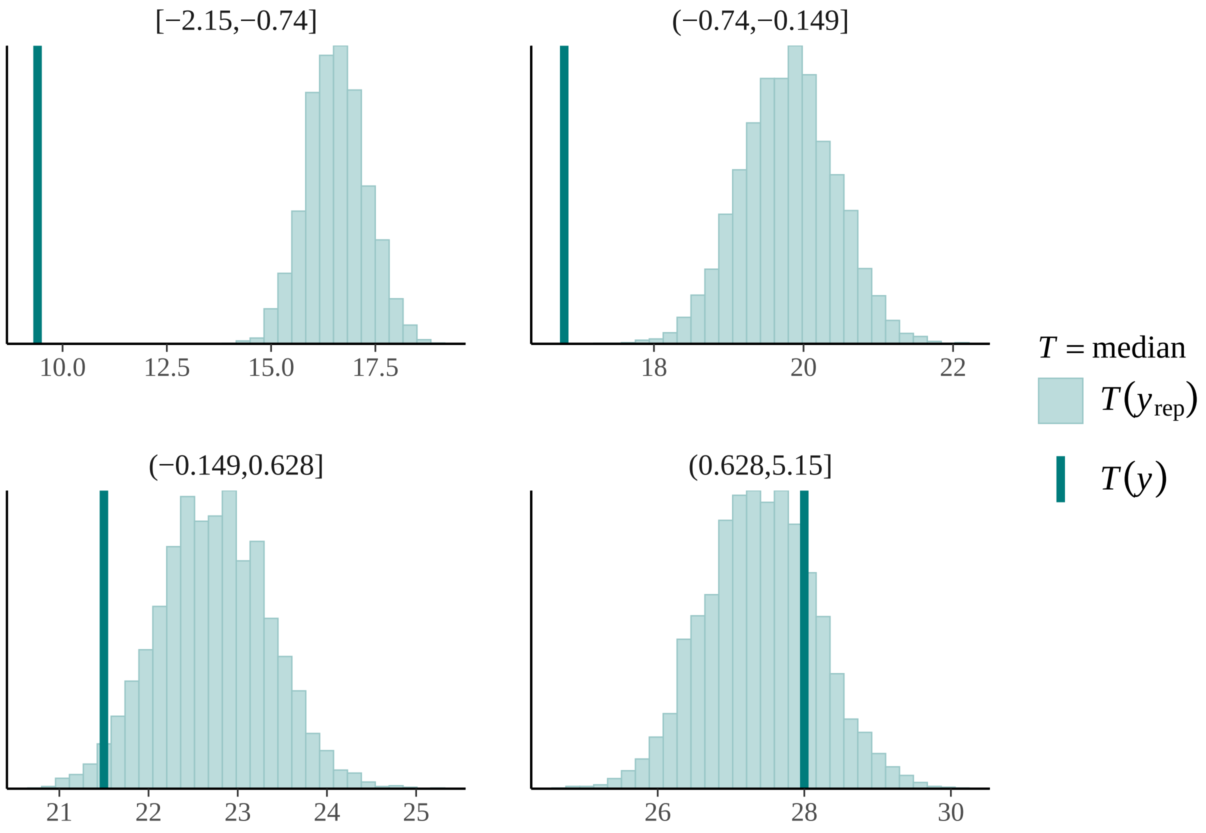
```
color_scheme_set(scheme = "yellow")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = fat_group, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



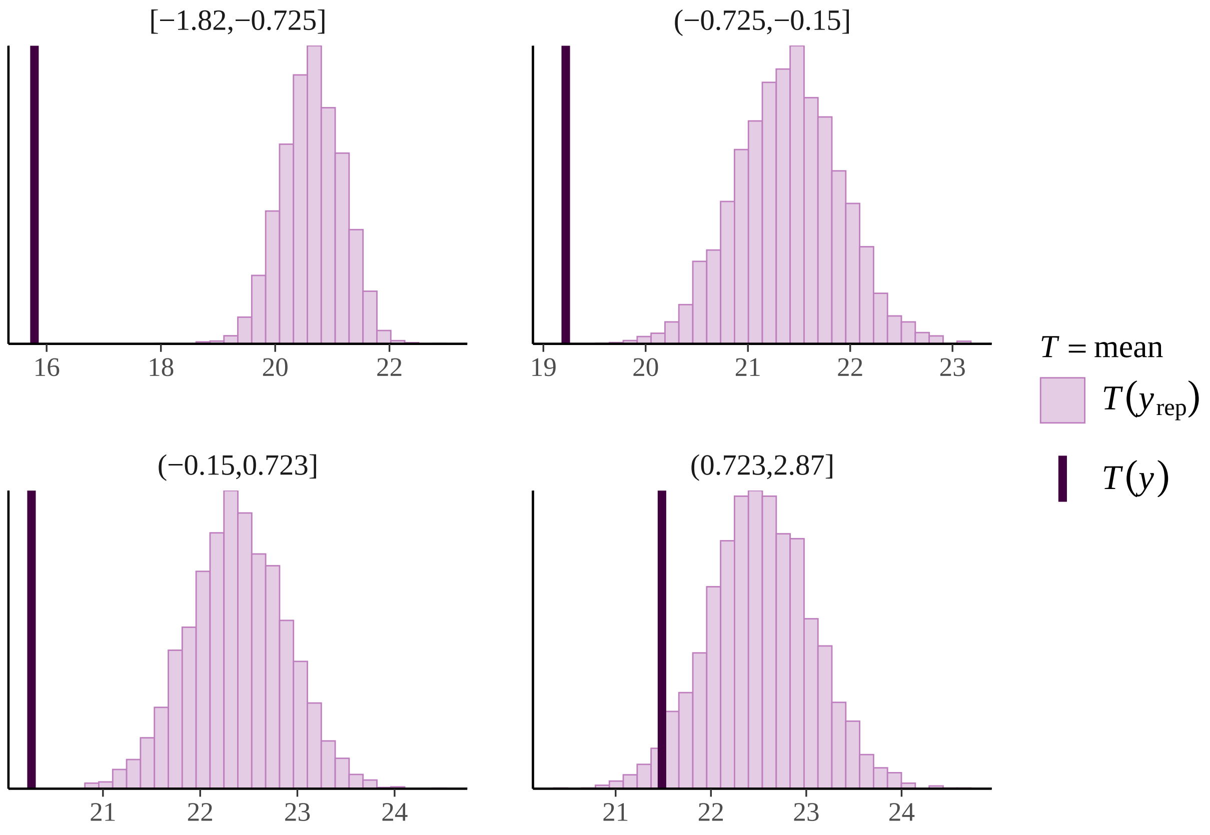
```r
color_scheme_set(scheme = "teal")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = waist_group, stat = "median")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



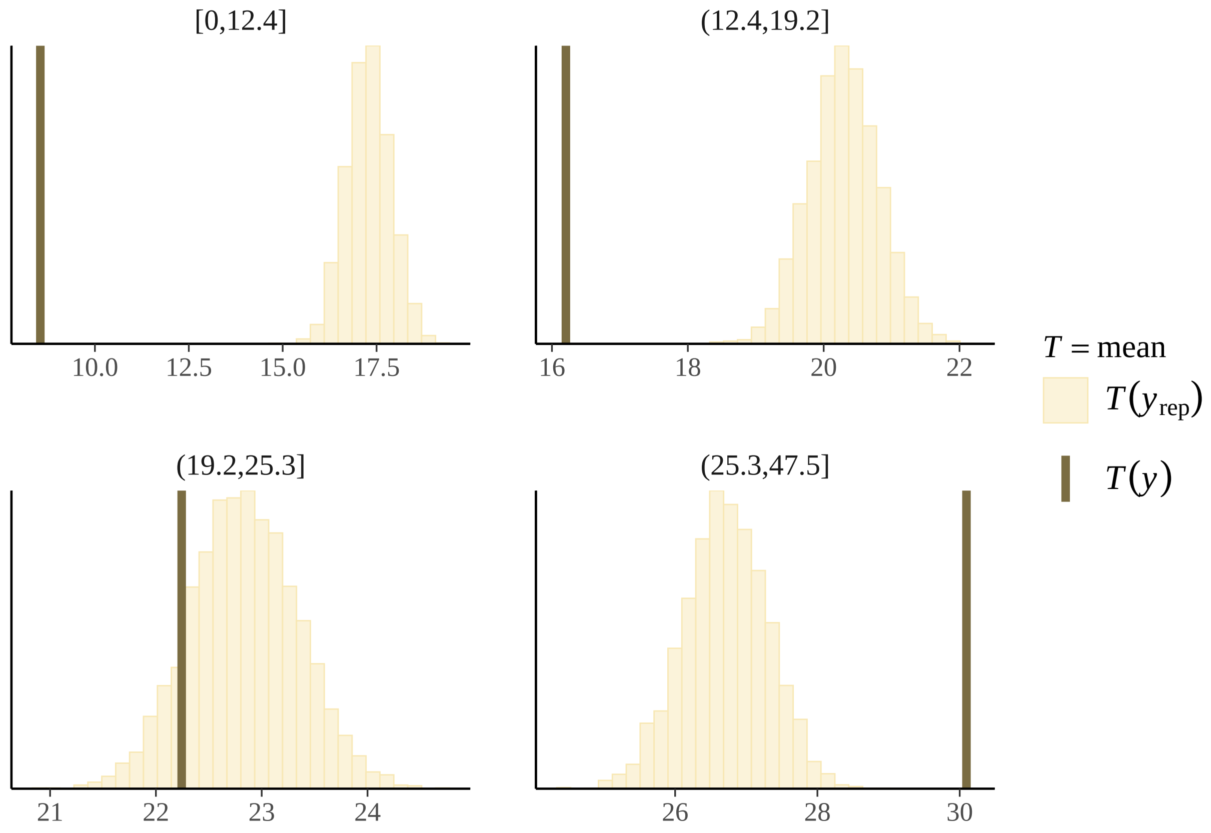
```r
color_scheme_set(scheme = "purple")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = age_group, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



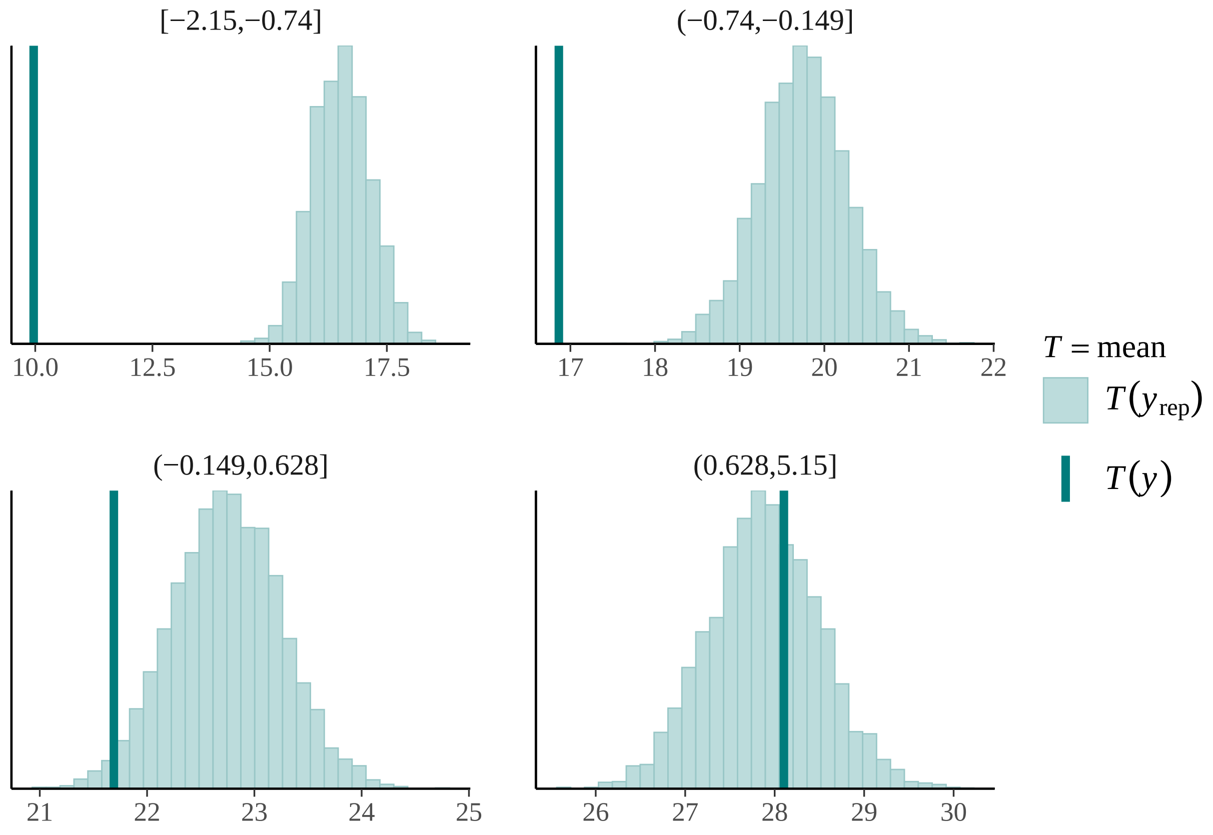
```
color_scheme_set(scheme = "yellow")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = fat_group, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```r
color_scheme_set(scheme = "teal")
bayesplot::pp_check(object = men$Fat, yrep = y_rep_male,
                    fun = "stat_grouped", group = waist_group, stat = "mean")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```


[−2.15,−0.74]
(−0.74,−0.149]
(−0.149,0.628]
(0.628,5.15]
10.0
12.5
15.0
17.5
17
18
19
20
21
22
21
22
23
24
25
26
27
28
29
30
T = mean
$T(y_{\text{rep}})$
$T(y)$