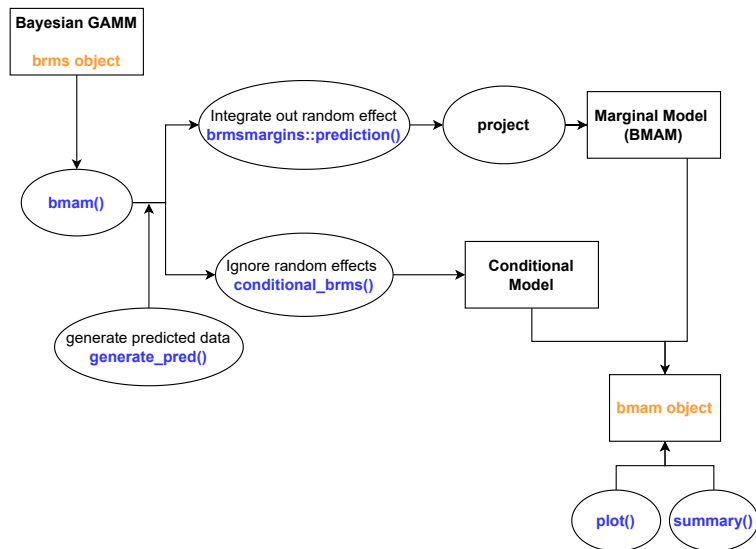


## R functions: BMAM

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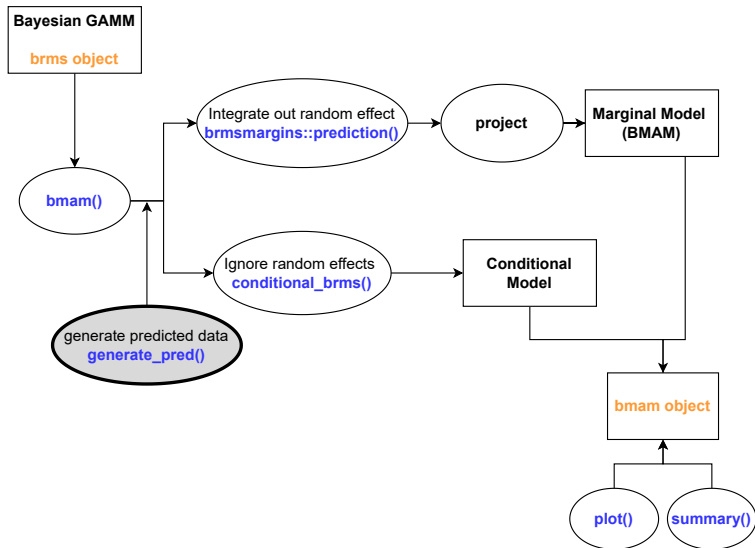
# Diagram



## bmam()

```
bmam <- function(object, preddat, length = 100,
  summarize = TRUE, posterior = TRUE,
  backtrans = c("response", "linear", "identity",
    "invlogit", "exp", "square", "inverse"),
  centered = FALSE, k = 100, ...) {
  ...
}
```

- **object** A fitted brms model object
- **preddat** A data frame containing covariates at which predictions are required
- **length** The number of observations in the generated preddat
- **summarize** Whether or not to calculate summaries of the posterior predictions
- **posterior** Whether or not to save and return the posterior samples
- **backtrans** The type of back transformation to be applied. default: response (use the response scale)
- **centered** Whether or not return centered smooths
- **k** The number of random draws in Monte Carlo method for integrating out the random effects



## generate\_pred()

```
## bmam()
```

```
if (missingArg(preddat)) preddat <- generate_pred(object, length)
```

```
generate_pred <- function(object, length = 100){
```

```
  mf <- model.frame(object) # data in object
```

```
  ## smooth term
```

```
  smterm <- brmsterms(object$formula)$dpars$mu$sm # smooth term
```

```
  stopifnot(!is.null(smterm)) # check
```

```
  smvariable <- lapply(smterm[[2]][-1], function(term.) term. [[2]]) # variable
```

```
  sm_pred <- lapply(smvariable, function(var){
```

```
    x <- mf[[var]]
```

```
    x <- x[which(x!=0)] # remove 0
```

```
    x.max <- max(x)
```

```
    x.min <- min(x)
```

```
    seq(x.min, x.max, length = length)
```

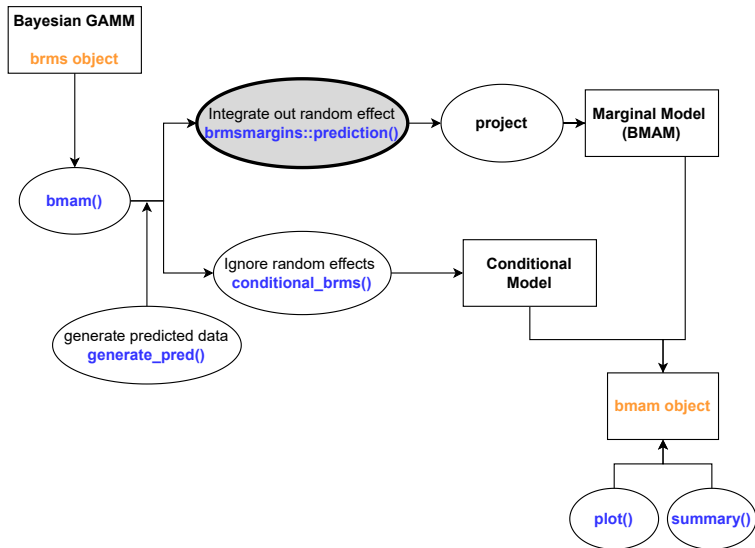
```
  })
```

```
  names(sm_pred) <- smvariable
```

```
  sm_pred <- do.call("cbind.data.frame", sm_pred)
```

```
  ## fix effect
```

```
  ...
```



## bmam() Marginal Model

### Integrate out random effect (brmsmargins::prediction)

Equation 4 in Hedeker's paper

$$\hat{\pi}_{ij}^{pa} = \int_{\theta} g^{-1} \left( \mathbf{x}'_{ij} \hat{\beta}^{ss} + \mathbf{z}'_{ij} \hat{\boldsymbol{\tau}} \theta_i \right) dF(\theta_i)$$

For the  $h^{th}$  draw from posterior distribution,  $h = 1, 2, \dots, H$  ( $H$  is the number of sampling, for example,  $4 \times 1000$ )

- Calculate  $\mathbf{x}_{ij}^{\hat{\beta}^{ss,h}}$ , and  $\mathbf{z}_{ij}^{\hat{\boldsymbol{\tau}}^h}$
- Generate  $K$  numbers from  $N(0, I)$ , denoted as  $\theta^k, k = 1, \dots, K$ .
- Calculate  $g^{-1} \left( \mathbf{x}_{ij}^{\hat{\beta}^{ss,h}} + \mathbf{z}_{ij}^{\hat{\boldsymbol{\tau}}^h} \theta_i^k \right), k = 1, \dots, K$
- Average over  $k$ .  $\hat{\pi}_{ij}^{pa,h} = \sum_{k=1}^K g^{-1} \left( \mathbf{x}_{ij}^{\hat{\beta}^{ss,h}} + \mathbf{z}_{ij}^{\hat{\boldsymbol{\tau}}^h} \theta_i^k \right) / K$

## bmam() Marginal Model

### Integrate out random effect (brmsmargins::prediction)

Equation 4 in Hedeker's paper

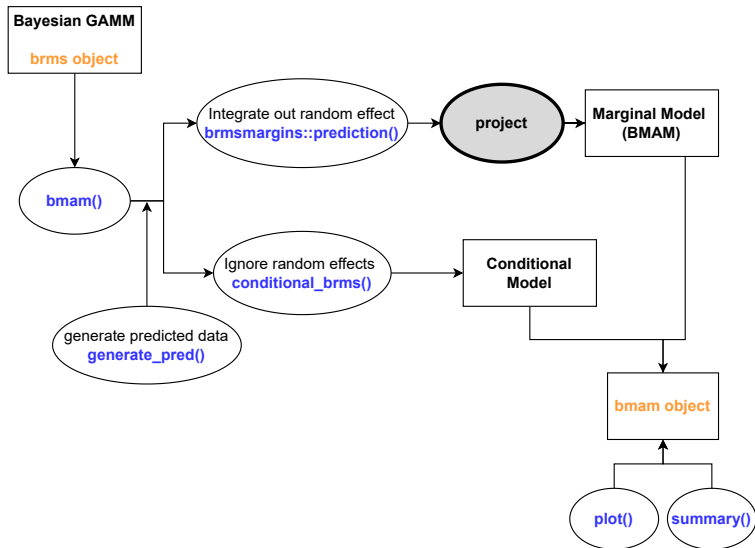
$$\hat{\pi}_{ij}^{pa} = \int_{\theta} g^{-1} \left( \mathbf{x}'_{ij} \hat{\beta}^{ss} + \mathbf{z}'_{ij} \hat{\boldsymbol{\tau}} \theta_i \right) dF(\theta_i)$$

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- Calculate  $\mathbf{x}_{ij}^{\hat{\beta}^{ss,h}}$ , and  $\mathbf{z}_{ij}^{\hat{\boldsymbol{\tau}}^h}$
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- Average over  $k$ .  $\hat{\pi}_{ij}^{pa,h} = \sum_{k=1}^K g^{-1} \left( \mathbf{x}_{ij}^{\hat{\beta}^{ss,h}} + \mathbf{z}_{ij}^{\hat{\boldsymbol{\tau}}^h} \theta_i^k \right) / K$

```
mu <- brmsmargins::prediction(  
  object, data = model.frame(object),  
  summarize = FALSE, posterior = TRUE, effects = "integrateoutRE",  
  backtrans = backtrans, k = k, raw = TRUE)
```





# bmam() Marginal Model

## Projection

$$f^M(\mathbf{X}) = \mathbf{B}^M \boldsymbol{\alpha}^M$$
$$\hat{\boldsymbol{\alpha}}^M = \operatorname{argmin} \left\| \hat{\boldsymbol{\lambda}}^M - \mathbf{B}^M \boldsymbol{\alpha}^M \right\| = \left( \mathbf{B}^{M\top} \mathbf{B}^M \right)^{-1} \mathbf{B}^{M\top} \hat{\boldsymbol{\lambda}}^M.$$

### 1. Design Matrix $\mathbf{B}^M$

```
standata <- make_standata(formula(object), data = model.frame(object))  
## subtract the variables  
if(smooth){  
  data_names <- names(standata) # get the names of data  
  ## Zs: basis function for smooth term (ncol = k-2)  
  Zs_name <- data_names[grep(pattern = "Zs_\\d_\\d", data_names)]  
  Zs <- do.call(cbind, standata[Zs_name])  
  ## set names for Zs  
  Zs_name_list <- mapply(function(i,j)paste(j,seq_len(i),sep="_alpha_"),  
                          lapply(standata[Zs_name],ncol),  
                          Zs_name, SIMPLIFY = FALSE)  
  colnames(Zs) <- as.character(unlist(Zs_name_list))
```

# bmam() Marginal Model

## 1. Design Matrix $B^M$

```
## Xs: basis function for smooth term, without penalty (ncol = 1)
Xs_name <- data_names[grep(pattern = "Xs", data_names)]
Xs <- do.call(cbind, standata[Xs_name])
## set names for Xs
Xs_name_list <- mapply(function(i,j)paste(j,seq_len(i),"alpha",sep="_"),
                        lapply(standata[Xs_name],ncol),
                        Xs_name)
colnames(Xs) <- as.character(unlist(Xs_name_list))

## X: linear term, for example intercept + x1 + x2 + x1:x2
X <- standata$X

## design matrix
B <- cbind(X, Xs, Zs)
}
```

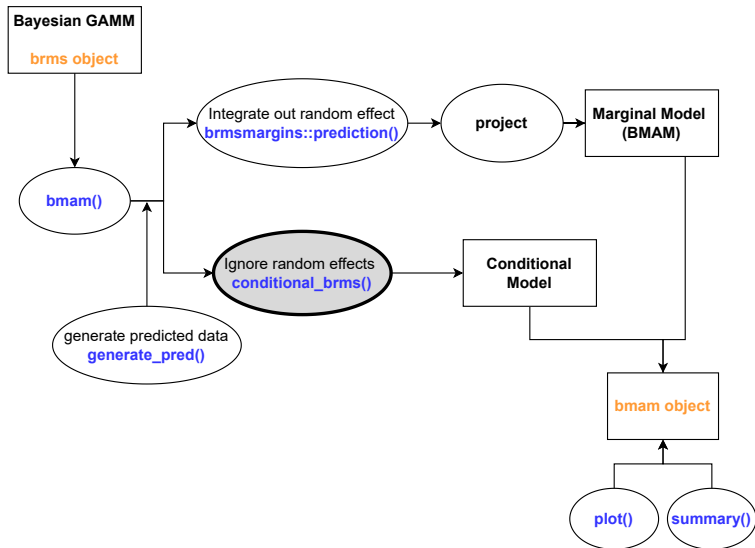
# bmam() Marginal Model

## 2. $\hat{\lambda}^M$

```
y <- links$fun(t(mu$Posterior))
```

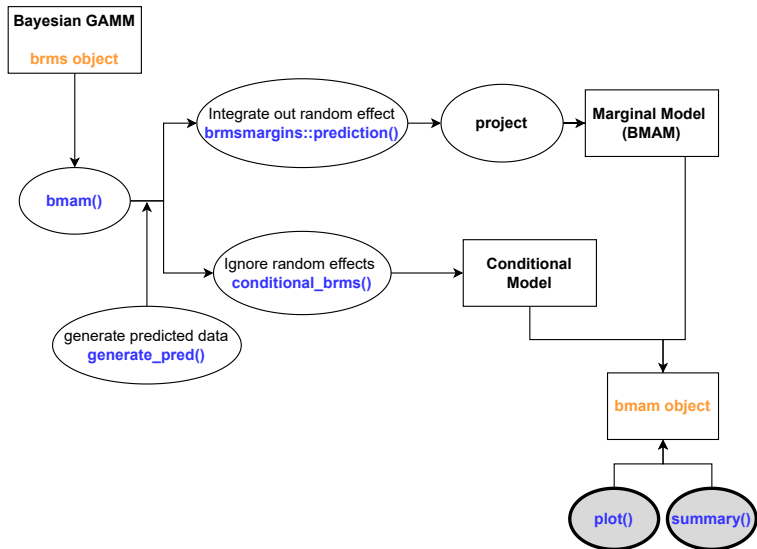
## 3. projection

```
beta <- lmcpp(B, y)  # Cpp file from brmsmargins
                      # beta <- solve( t(B) %*% B ) %*% t(B) %*% y
prep <- prepare_predictions(object, newdata = preddat,
                           check_response = FALSE, re_formula = NA)
## Xs: basis function for smooth term, without penalty (ncol = 1)
pred_Xs <- prep$dparams$mu$sm$fe$Xs
## Zs: basis function for smooth term (ncol = k-2)
pred_Zs <- sapply(prep$dparams$mu$sm$re, function(re.)re.$Zs)
pred_Zs <- do.call(cbind, pred_Zs)
## X: linear term
pred_X <- prep$dparams$mu$fe$X
pred_B <- cbind(pred_X, pred_Xs, pred_Zs)
if(centers) pred_B <- sweep(pred_B, 2, colMeans(pred_B), '-')
Predicted <- pred_B %*% beta
```



## bmam() Conditional Model

```
predict_conditional <- conditional_brms(object, preddat,  
                                         centered = centered, ...)  
  
conditional_brms <- function(object, data, centered = FALSE, ...){  
  yhat <- fitted(  
    object = object, newdata = data,  
    re_formula = NA, scale = "linear",  
    summary=FALSE)  
  if(centered){  
    ones <- matrix(rep(1,ncol(yhat)))  
    H_matrix <- ones %*% solve(t(ones) %*% ones) %*% t(ones)  
    M_matrix <- diag(1,ncol(yhat)) - H_matrix  
    predicted <- M_matrix %*% t(yhat)  
  }else{  
    predicted <- t(yhat)  
  }  
  
  as.data.table(do.call(rbind, apply(predicted, 1, bsummary, ...)))  
}
```



## plot()

```
plot.bmam <- function(object, compared.model,  
                      conditional = TRUE, display = TRUE,  
                      smooth.function){  
  ...  
}
```

- **object** Objects of Class 'bmam'
- **compared.model** Other model (fitted before calling the function) compared with BMAM. Supported models: 1. mam 2. gam 3. brms gam
- **display** Whether or not to display the plots. Default: TRUE
- **conditional** Whether or not to plot the conditional model. Default: TRUE
- **smooth.function** True values of the smooth functions.



## summary()

```
print.bmam <- function(object,...){
  summary(object,...)
  invisible()
}

summary.bmam <- function(object, plot.smooth = FALSE, ...){
  ### 1. Marginal Model #####
  ## smooth term; linear term
  ### 2. Conditional Model #####
  ## smooth term; linear term
  out <- list(BMAM = BMAM, Conditional_Model = Conditional_Model)
  if(plot.smooth){
    gg <- plot(object, ... )
    out$plot <- gg
  }
  invisible(out)
}
```

- **object** Objects of Class 'bmam'
- **plot.smooth** Whether or not to plot bmam