

Variable names in dominance plots

```
library("metagam")

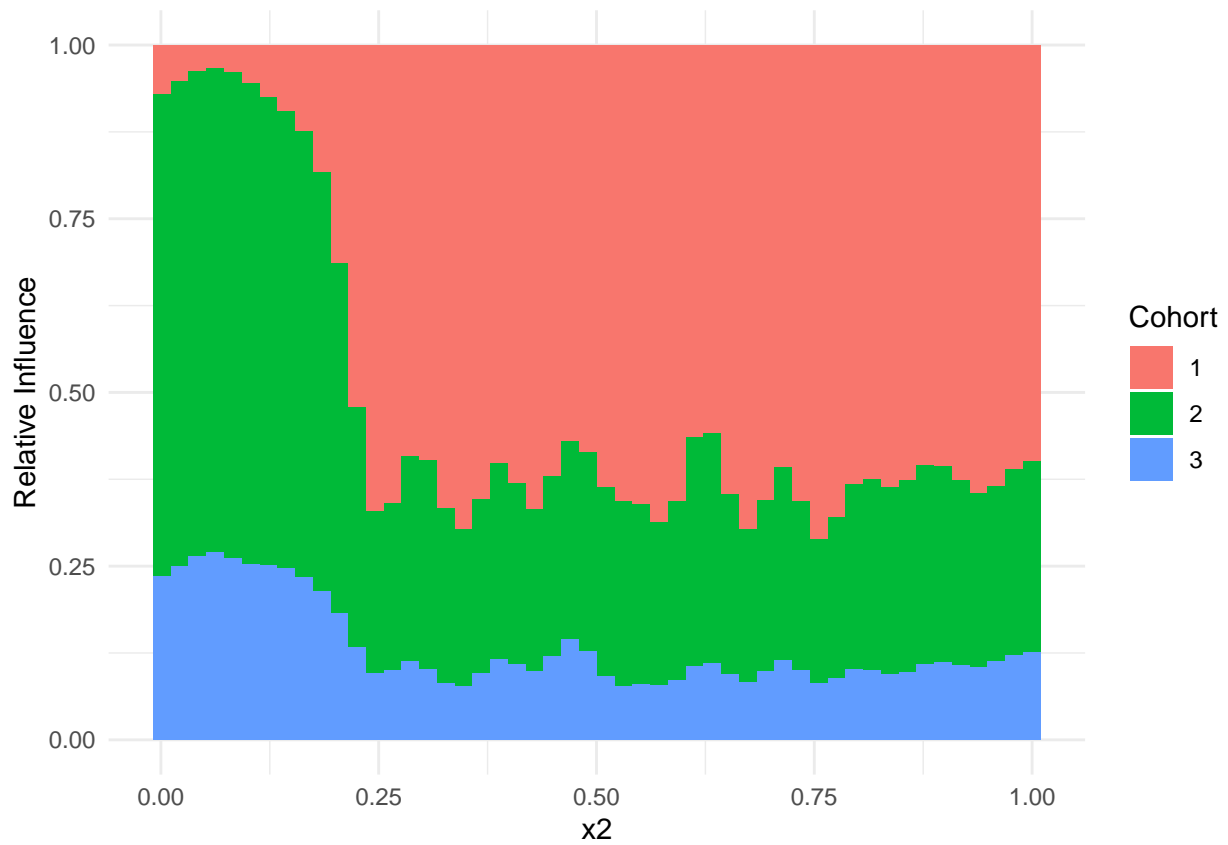
## simulate datasets, with noise level increasing with number,
## so dataset 1 has least noise and dataset 3 has most
set.seed(123)
num.datasets <- 3
datasets <- lapply(
  seq_len(num.datasets),
  function(x) mgcv::gamSim(scale = x, verbose = FALSE))

# Then delete all rows of dataset 1 for which x<0.2
df <- datasets[[1]]
df[df$x2<0.2,] <- NA
datasets[[1]] <- df

## fit a generalized additive model to each dataset separately
models <- lapply(datasets, function(dat){
  ## Full fit using mgcv
  gamfit <- mgcv::gam(y ~ s(x0, bs = "cr") + s(x1, bs = "cr") + s(x2, bs = "cr"), data = dat)
  ## Extract the necessary components for performing a meta-analysis
  ## This removes all subject-specific data
  strip_rawdata(gamfit)
})
```

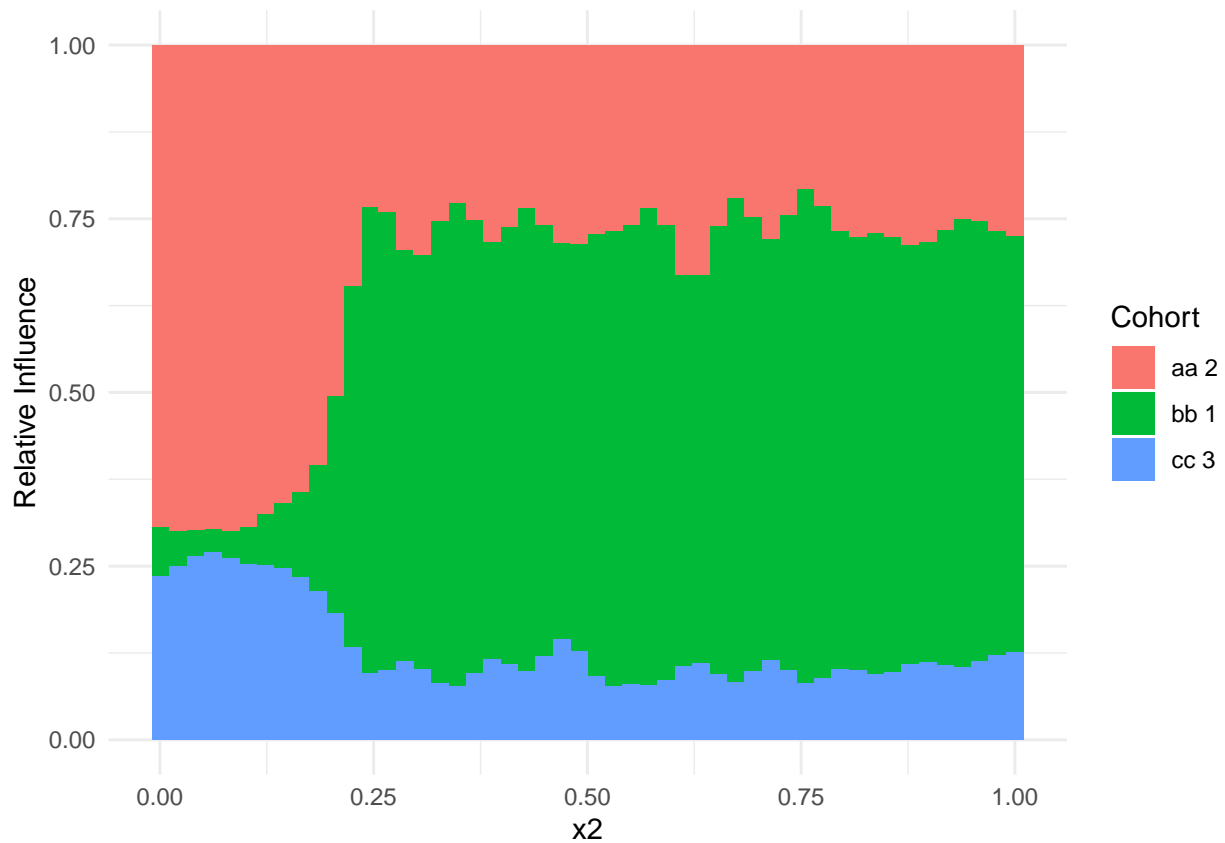
Running without specifying names. Looks correct.

```
meta_analysis <- metagam(models, grid_size = 50, terms = "s(x2)")
plot_dominance(meta_analysis)
```



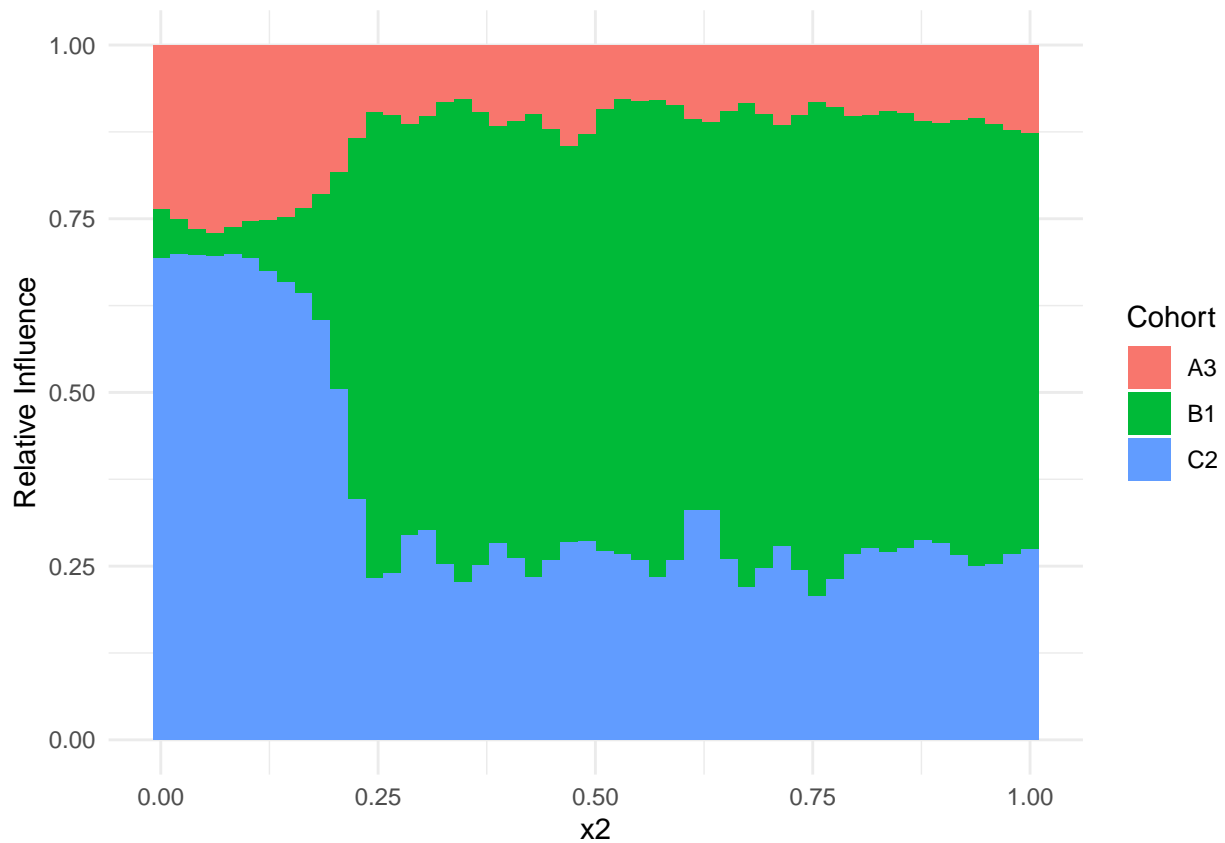
Set the names.

```
names(models) <- c("bb 1", "aa 2", "cc 3")
meta_analysis <- metagam(models, grid_size = 50, terms = "s(x2)")
plot_dominance(meta_analysis)
```



Change names in the returned object.

```
names(models) <- NULL
meta_analysis <- metagam(models, grid_size = 50, terms = "s(x2)")
names(meta_analysis$cohort_estimates) <- c("B1", "C2", "A3")
plot_dominance(meta_analysis)
```



Set labels manually. Still looks correct.

```
names(models) <- NULL
meta_analysis <- metagam(models, grid_size = 50, terms = "s(x2)")
plot_dominance(meta_analysis) +
  ggplot2::scale_fill_discrete(labels = c("Data 1", "Data 2", "Data 3"))
```

