

15. HI across facs data

Fay

2022-08-09

load libraries

```
library(ggplot2)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.2 --
## v tibble 3.1.8      v dplyr 1.0.10
## v tidyr 1.2.1      v stringr 1.4.1
## v readr 2.1.3      v forcats 0.5.2
## v purrr 0.3.5
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(optimx)
```

Import data:

Here, we have the experimental / field data

```
hm <- read.csv("output_data/imputed_mice.csv")

# Selecting facs
Gene_lab <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",
             "IL1RN", "CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",
             "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",
             "TICAM1", "TNF") # "IL.12", "IRG6")

#add a suffix to represent changes in data file
Gene_lab_imp <- paste(Gene_lab, "imp", sep = "_")

facs_wild <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",
             "IL1RN", "CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",
             "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",
             "TICAM1", "TNF") # "IRG6")

facs_wild_imp <- paste(facs_wild, "imp", sep = "_")

Facs_lab <- c("Position", "CD4", "Treg", "Div_Treg", "Treg17", "Th1",
             "Div_Th1", "Th17", "Div_Th17", "CD8", "Act_CD8",
             "Div_Act_CD8", "IFNy_CD4", "IFNy_CD8") #, "Treg_prop",
             # "IL17A_CD4")
```

```
Facs_wild <- c( "Treg", "CD4", "Treg17", "Th1", "Th17", "CD8",
               "Act_CD8", "IFNy_CD4", "IFNy_CD8") #"IL17A_CD4",
```

It is time to apply the package of Alice Balard et al. on our predictions!

Let's see if we indeed have differences across the hybrid index across facs

```
# Selecting the field samples

field <- hm %>%
  dplyr::filter(origin == "Field")

field <- unique(field)

#make a factor out of the melting curves (important for later visualization)
field <- field %>%
  dplyr::mutate(MC.Eimeria = as.factor(MC.Eimeria))

facs <- field %>%
  dplyr::select(all_of(Facs_wild))

#remove rows with only nas
facs <- facs[,colSums(is.na(facs))<nrow(facs)]

#remove columns with only nas
facs <- facs[rowSums(is.na(facs)) != ncol(facs), ]

##select same rows in the first table
field <- field[row.names(facs), ]
```

Install the package

```
##
## * checking for file '/tmp/RtmpdbMChj/remotesea5d12f98911f/alicebalard-parasiteLoad-1b43216/DESCRIPTION' ... OK
## * preparing 'parasiteLoad':
## * checking DESCRIPTION meta-information ... OK
## * checking for LF line-endings in source and make files and shell scripts
## * checking for empty or unneeded directories
## * building 'parasiteLoad_0.1.0.tar.gz'
```

Applying Alice's package on every gene

```
x <- field$CD4

# Define function to be used to test, get the log lik and aic
tryDistrib <- function(x, distrib){
```

```

# deals with fitdistr error:
fit <- tryCatch(MASS::fitdistr(x, distrib), error=function(err) "fit failed")
return(list(fit = fit,
            loglik = tryCatch(fit$loglik, error=function(err) "no loglik computed"),
            AIC = tryCatch(fit$aic, error=function(err) "no aic computed")))
}

findGoodDistr <- function(x, distrib, distrib2){
  l =lapply(distrib, function(i) tryDistrib(x, i))
  names(l) <- distrib
  print(l)
  listDistr <- lapply(distrib2, function(i){
    if (i %in% "t"){
      fitdistrplus::fitdist(x, i, start = list(df =2))
    } else {
      fitdistrplus::fitdist(x,i)
    }
  })
  )
  par(mfrow=c(2,2))
  denscomp(listDistr, legendtext=distrib2)
  cdfcomp(listDistr, legendtext=distrib2)
  qqcomp(listDistr, legendtext=distrib2)
  ppcomp(listDistr, legendtext=distrib2)
  par(mfrow=c(1,1))
}

```

```
tryDistrib(x, "normal")
```

Functions for testing distributions

```

## $fit
##      mean      sd
## 40.2010526 11.1986606
## ( 1.1489583) ( 0.8124362)
##
## $loglik
## [1] -364.2996
##
## $AIC
## NULL

```

```
tryDistrib(x, "binomial")
```

```

## $fit
## [1] "fit failed"
##
## $loglik
## [1] "no loglik computed"
##
## $AIC
## [1] "no aic computed"

```

```
tryDistrib(x, "student")
```

```
## $fit
## [1] "fit failed"
##
## $loglik
## [1] "no loglik computed"
##
## $AIC
## [1] "no aic computed"
```

```
tryDistrib(x, "weibull")
```

```
## $fit
##      shape      scale
## 3.9324346 44.4023805
## ( 0.3090144) ( 1.2244501)
##
## $loglik
## [1] -364.467
##
## $AIC
## NULL
```

```
tryDistrib(x, "weibullshifted")
```

```
## $fit
## [1] "fit failed"
##
## $loglik
## [1] "no loglik computed"
##
## $AIC
## [1] "no aic computed"
```

CD4

```
# remove NA in HI
field <- field %>%
  drop_na(HI)
```

```
field$Sex <- as.factor(field$Sex)
```

```
parasiteLoad::getParamBounds("weibull", data = field, response = "CD4")
```

```
##      L1start      L1LB      L1UB      L2start      L2LB      L2UB
## 40.201052632 0.000000001 68.500000000 40.201052632 0.000000001 68.500000000
## alphaStart      alphaLB      alphaUB myshapeStart      myshapeLB      myshapeUB
## 0.000000000 -5.000000000 5.000000000 1.000000000 0.000000001 5.000000000
```

```
#write a function to test parasite load on a facs cell proportion
```

```
facs_hypothesis <- function(y) {
  parasiteLoad::analyse(data = field,
    response = y,
    model = "normal",
```

```

        group = "Sex")
}

parasite_load_facs <- function(x, y) {
  # x takes the cell without "" and y is the cell with ""
  x <- parasiteLoad::analyse(data = field,
    response = y,
    model = "normal",
    group = "Sex")

  bananaPlot(mod = x$H0,
    data = field,
    response = y,
    group = "Sex") +
    scale_fill_manual(values = c("blue", "red")) +
    scale_color_manual(values = c("blue", "red")) +
    theme_bw()
}

# write another function that combines both

apply_facs <- function(x, y) {

  facs_hypothesis(y)

  parasite_load_facs(x, y)

}

apply_facs(CD4, "CD4")

## [1] "Analysing data for response: CD4"
## [1] "Fit for the response: CD4"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on

```

```

## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.35    1 0.4023428

```

```

## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.29    1 0.448155
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.43    1 0.3525174
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.08    1 0.6971236
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 1.76    1 0.06028844
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.12    1 0.6197217
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 10.29    1 5.721637e-06
## [1] "Testing H2 vs H0"
##      dLL dDF    pvalue
## 1 0.28    3 0.9064051
## [1] "Testing H3 vs H1"
##      dLL dDF    pvalue
## 1 2.06    4 0.3891508
## [1] "Testing H3 vs H2"
##      dLL dDF    pvalue
## 1 12.07    2 5.701451e-06
## [1] "Analysing data for response: CD4"
## [1] "Fit for the response: CD4"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"

```

```

## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

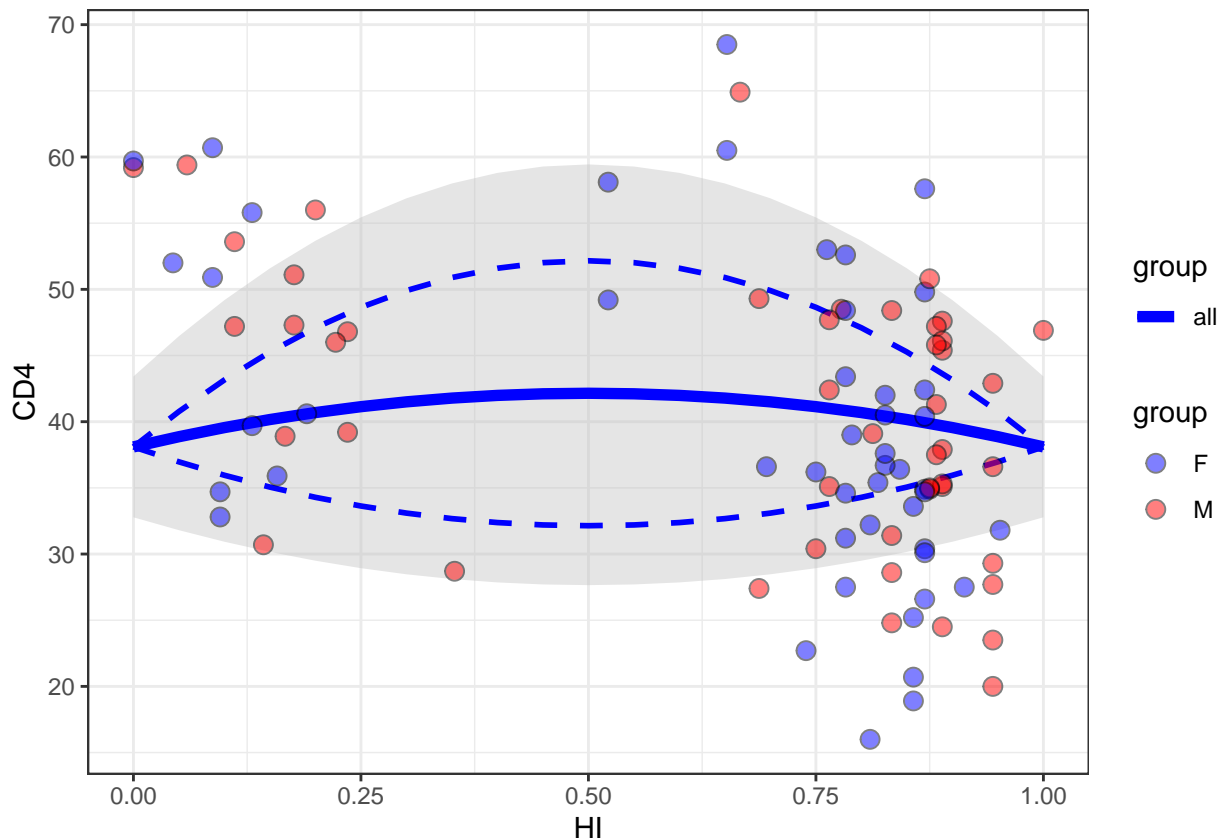
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.35    1 0.4023428
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.29    1 0.448155
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.43    1 0.3525174
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.08    1 0.6971236

```



```
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.76    1 0.06028844
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.12    1 0.6197217
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 10.29    1 5.721637e-06
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 0.28     3 0.9064051
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 2.06     4 0.3891508
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 12.07    2 5.701451e-06

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



Treg

```
apply_fac(Treg, "Treg")
```

```

## [1] "Analysing data for response: Treg"
## [1] "Fit for the response: Treg"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.35    1 0.4059267
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.43    1 0.3510821
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.01    1 0.8741098
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.47    1 0.331375
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 1.07    1 0.1438986
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.96    1 0.16566
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 2.15    1 0.03817179

```

```

## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 14.1   3 3.283602e-06
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 19.02  4 1.099012e-07
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 7.06   2 0.0008546762
## [1] "Analysing data for response: Treg"
## [1] "Fit for the response: Treg"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

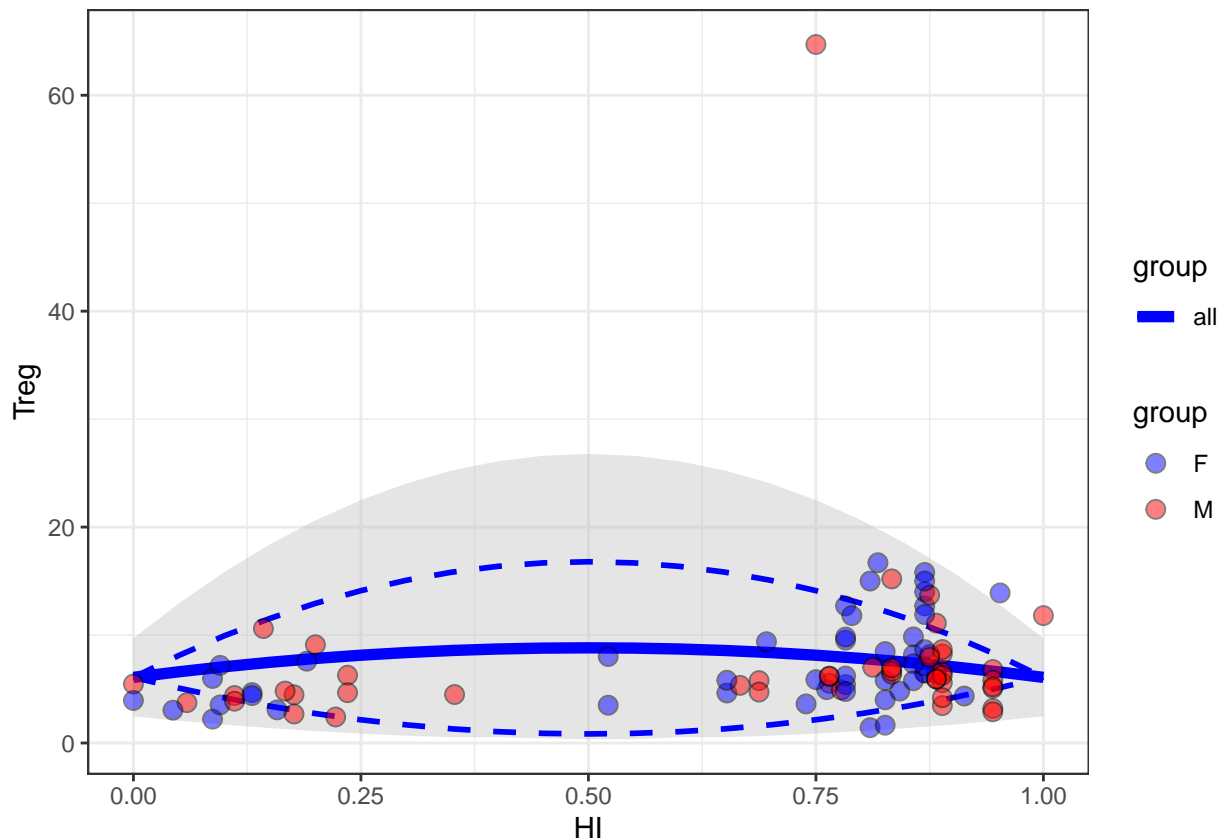
## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.35   1 0.4059267
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.43   1 0.3510821
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.01   1 0.8741098
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.47   1 0.331375

```

```
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.07   1 0.1438986
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.96   1 0.16566
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 2.15   1 0.03817179
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 14.1   3 3.283602e-06
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 19.02  4 1.099012e-07
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 7.06   2 0.0008546762

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



Treg17

```
parasiteLoad::getParamBounds("weibull", data = field, response = "Treg17")
```

```
##      L1start      L1LB      L1UB      L2start      L2LB      L2UB
## 9.002631579 0.000000001 90.900000000 9.002631579 0.000000001 90.900000000
## alphaStart    alphaLB    alphaUB myshapeStart    myshapeLB    myshapeUB
## 0.000000000 -5.000000000 5.000000000 1.000000000 0.000000001 5.000000000
```

#write a function to test parasite load on a facs cell proportion

```
speparam <-      c(L1start = 8,
                  L1LB = 1e-9,
                  L1UB = 89,
                  L2start = 8,
                  L2LB = 1e-9,
                  L2UB = 89,
                  alphaStart = 0, alphaLB = -5, alphaUB = 5,
                  myshapeStart = 1, myshapeLB = 1e-9, myshapeUB = 5)
```

```
parasiteLoad::analyse(data = field,
                      response = "Treg17",
                      model = "normal",
                      group = "Sex")
```

```
## [1] "Analysing data for response: Treg17"
## [1] "Fit for the response: Treg17"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
```

```

## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.16    1 0.5697054
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.15    1 0.582469
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.12    1 0.6213113
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.24    1 0.4904253
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 1.2     1 0.120929
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.11    1 0.636494
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 1.81    1 0.05699535
## [1] "Testing H2 vs H0"
##      dLL dDF    pvalue
## 1 6.35    3 0.005352205
## [1] "Testing H3 vs H1"
##      dLL dDF    pvalue
## 1 10.64   4 0.0002793984

```

```

## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 6.1    2 0.002237467

## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##      L1, alpha, HI), sd = mysd), start = start, method = config$method,
##      optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##      mysd = paramBounds[["mysdLB"]], alpha = paramBounds[["alphaLB"]]),
##      upper = c(L1 = paramBounds[["L1UB"]], mysd = paramBounds[["mysdUB"]],
##      alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      mysd      alpha
## 7.5740269 10.0000000 -0.7263117
##
## Log-likelihood: -356.17
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##      L2, alpha, HI), sd = mysd), start = start, method = config$method,
##      optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##      mysd = paramBounds[["mysdLB"]], L2 = paramBounds[["L2LB"]],
##      alpha = paramBounds[["alphaLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##      mysd = paramBounds[["mysdUB"]], L2 = paramBounds[["L2UB"]],
##      alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      L2      alpha      mysd
## 11.4576037  5.8181620 -0.6359146 10.0000000
##
## Log-likelihood: -354.36
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##      L1, alpha, HI), sd = mysd), start = start, method = config$method,
##      optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##      mysd = paramBounds[["mysdLB"]], alpha = paramBounds[["alphaLB"]]),
##      upper = c(L1 = paramBounds[["L1UB"]], mysd = paramBounds[["mysdUB"]],
##      alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      mysd      alpha
## 6.5854191  6.7935273 -0.7312953
##

```

```

## Log-likelihood: -160.08
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##     L1, alpha, HI), sd = mysd), start = start, method = config$method,
##     optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##     mysd = paramBounds[["mysdLB"]], alpha = paramBounds[["alphaLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], mysd = paramBounds[["mysdUB"]],
##     alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      mysd      alpha
## 7.866301 10.000000 -1.173225
##
## Log-likelihood: -189.75
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##     L2, alpha, HI), sd = mysd), start = start, method = config$method,
##     optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##     mysd = paramBounds[["mysdLB"]], L2 = paramBounds[["L2LB"]],
##     alpha = paramBounds[["alphaLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##     mysd = paramBounds[["mysdUB"]], L2 = paramBounds[["L2UB"]],
##     alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      L2      alpha      mysd
## 10.004169 2.357851 -2.260576 6.000458
##
## Log-likelihood: -154.12
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dnorm(mean = MeanLoad(L1,
##     L2, alpha, HI), sd = mysd), start = start, method = config$method,
##     optimizer = config$optimizer, data = data, lower = c(L1 = paramBounds[["L1LB"]],
##     mysd = paramBounds[["mysdLB"]], L2 = paramBounds[["L2LB"]],
##     alpha = paramBounds[["alphaLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##     mysd = paramBounds[["mysdUB"]], L2 = paramBounds[["L2UB"]],
##     alpha = paramBounds[["alphaUB"]]), control = config$control)
##
## Coefficients:
##      L1      L2      alpha      mysd
## 10.0173748 7.7575792 -0.7687133 10.0000000

```



```

##
## Log-likelihood: -189.6
## Best method: bobyqa
treg17 <- parasiteLoad::analyse(data = field,
                                response = "Treg17",
                                model = "normal",
                                group = "Sex")

## [1] "Analysing data for response: Treg17"
## [1] "Fit for the response: Treg17"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :

```

```

## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, 0, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

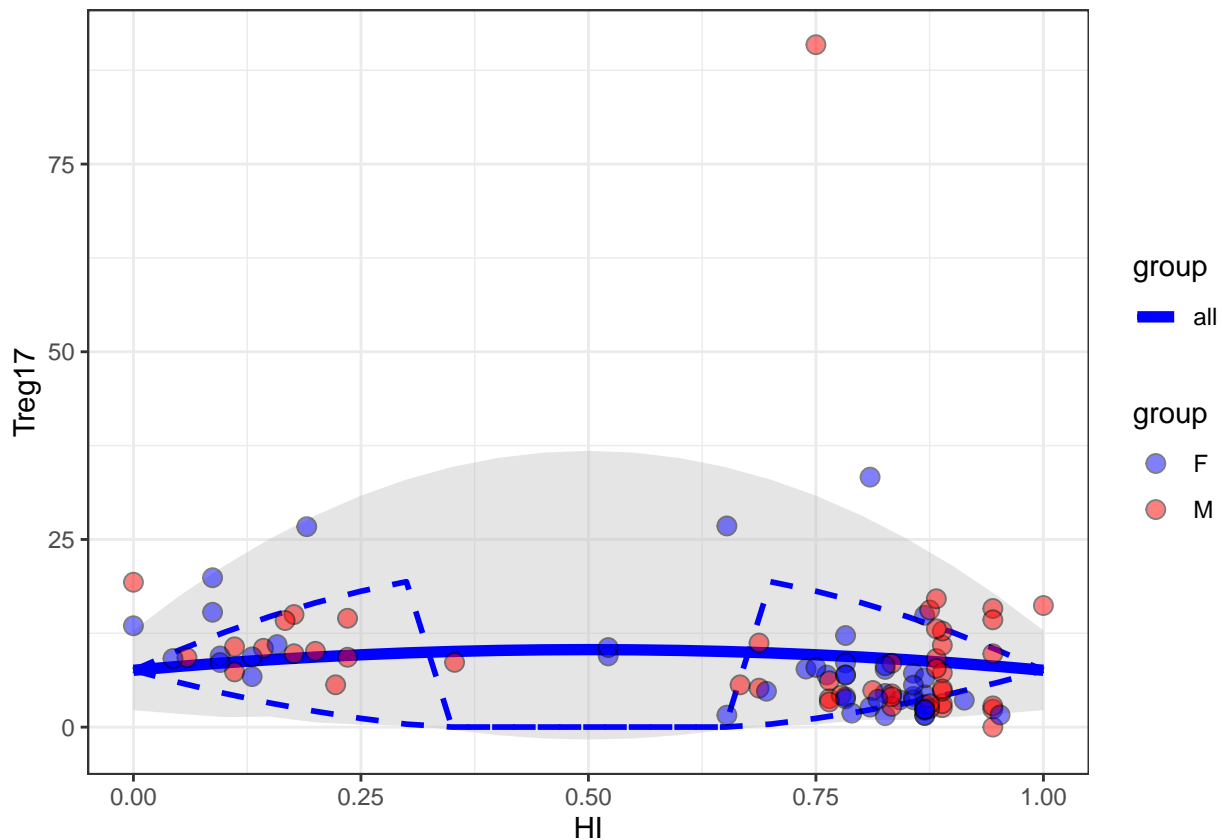
## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.16    1 0.5697054
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.15    1 0.582469
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.12    1 0.6213113
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.24    1 0.4904253
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 1.2     1 0.120929
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.11    1 0.636494
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 1.81    1 0.05699535
## [1] "Testing H2 vs H0"
##      dLL dDF    pvalue
## 1 6.35    3 0.005352205
## [1] "Testing H3 vs H1"
##      dLL dDF    pvalue
## 1 10.64   4 0.0002793984
## [1] "Testing H3 vs H2"
##      dLL dDF    pvalue
## 1 6.1     2 0.002237467

bananaPlot(mod = treg17$H0,
            data = field,
            response = "Treg17",
            group = "Sex") +
  scale_fill_manual(values = c("blue", "red")) +
  scale_color_manual(values = c("blue", "red")) +
  theme_bw()

```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



Th1

```
apply_facs(Th1, "Th1")
```

```
## [1] "Analysing data for response: Th1"
## [1] "Fit for the response: Th1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
```

```

## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.15   1 0.5779705
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.11   1 0.6382398
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1  0    1 0.9655877
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.25   1 0.4815203
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.2    1 0.5235712
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.41   1 0.3657102
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 1.68   1 0.06662083
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 2.59   3 0.1589092
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 3.58   4 0.1273873
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 2.67   2 0.06899189
## [1] "Analysing data for response: Th1"
## [1] "Fit for the response: Th1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"

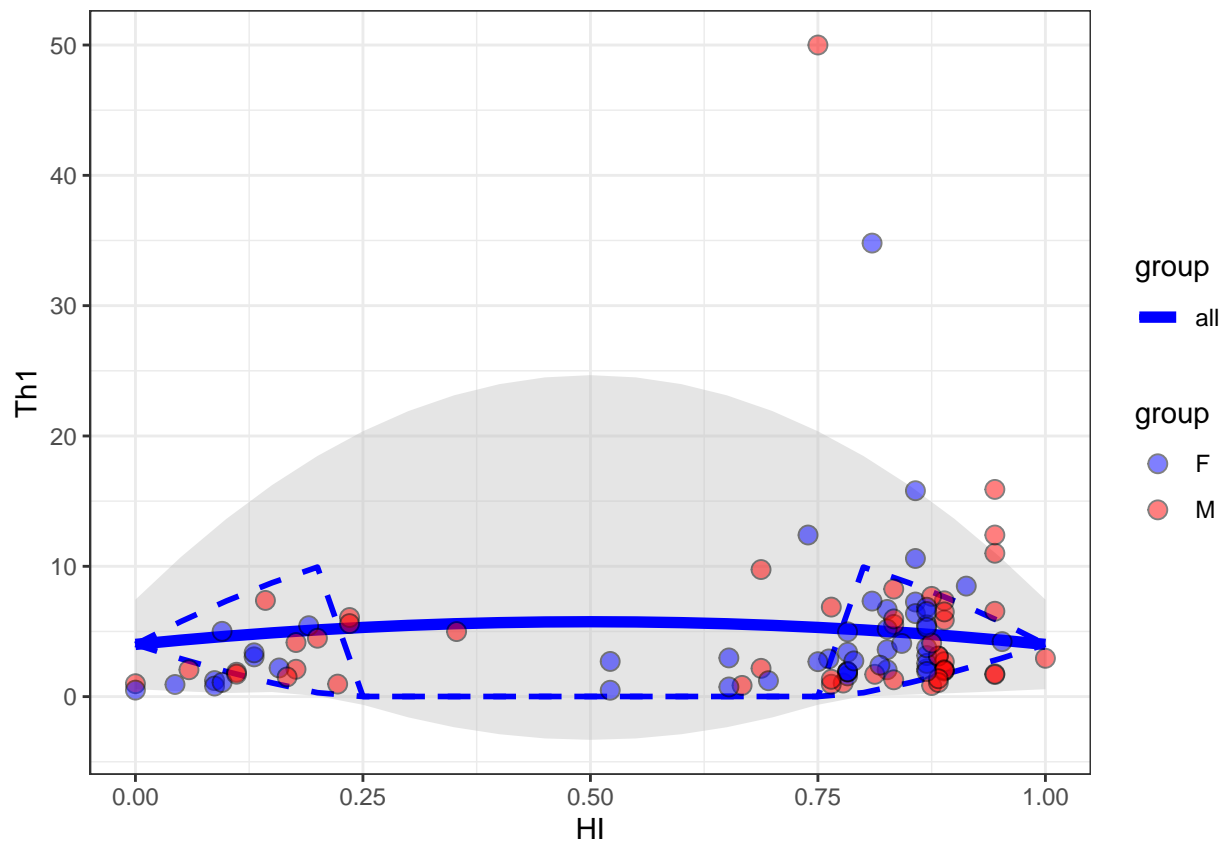
```

```

## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.15   1 0.5779705
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.11   1 0.6382398
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1  0    1 0.9655877
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.25   1 0.4815203
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.2    1 0.5235712
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.41   1 0.3657102
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 1.68   1 0.06662083
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 2.59   3 0.1589092
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 3.58   4 0.1273873
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 2.67   2 0.06899189

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.

```



Th17

```
apply_facets(Th17, "Th17")
```

```
## [1] "Analysing data for response: Th17"
## [1] "Fit for the response: Th17"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
```

```

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.46    1 0.3357295
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.51    1 0.3135027
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.04    1 0.768262
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.45    1 0.345088
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.03    1 0.7956444
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.52    1 0.3096963
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 0.08    1 0.6952432
## [1] "Testing H2 vs H0"
##      dLL dDF    pvalue
## 1 0.16    3 0.9578571
## [1] "Testing H3 vs H1"
##      dLL dDF    pvalue
## 1 0.17    4 0.9863893
## [1] "Testing H3 vs H2"
##      dLL dDF    pvalue
## 1 0.1    2 0.9086336
## [1] "Analysing data for response: Th17"
## [1] "Fit for the response: Th17"

```

```

## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L1, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"

## Warning in bbmle::mle2(response ~ dnorm(mean = MeanLoad(L1, L2, alpha, HI), :
## some parameters are on the boundary: variance-covariance calculations based on
## Hessian may be unreliable

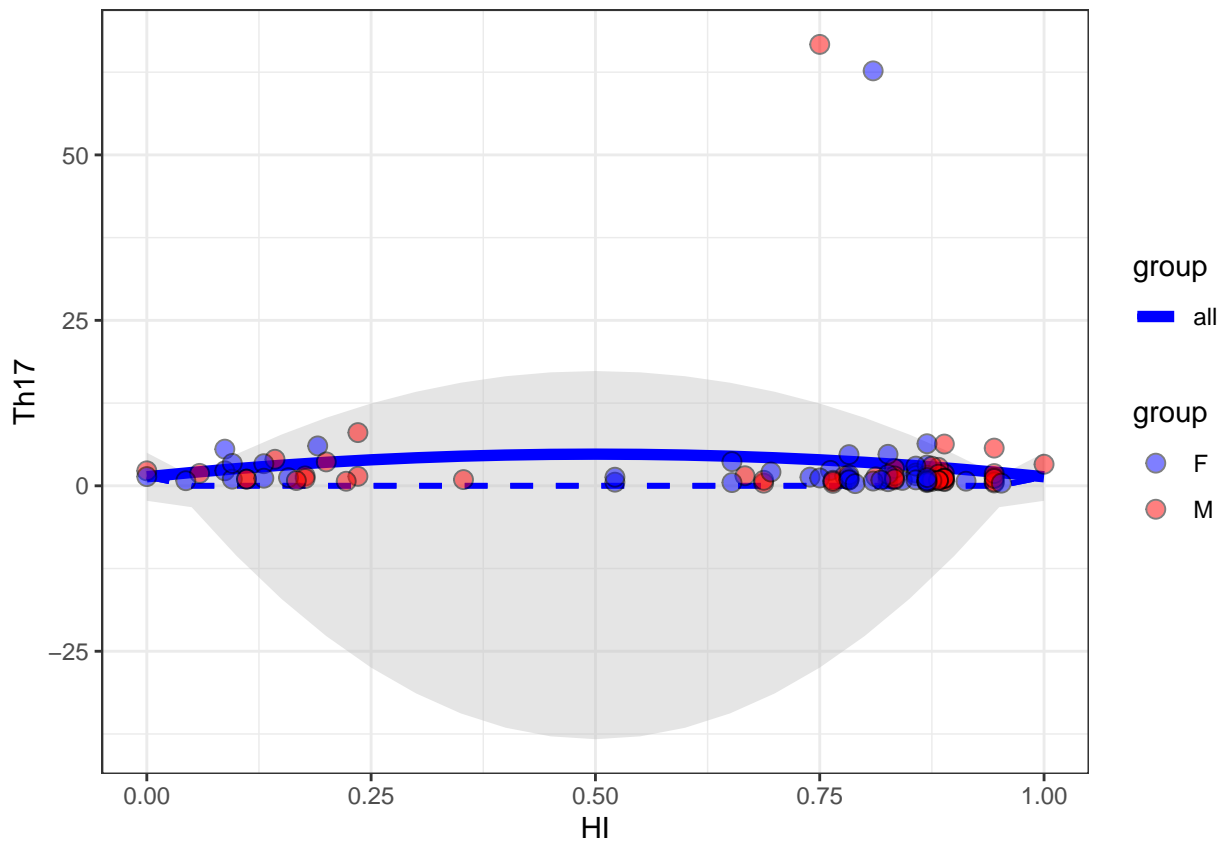
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.46    1 0.3357295
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.51    1 0.3135027
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.04    1 0.768262
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue

```



```
## 1 0.45    1 0.345088
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.03    1 0.7956444
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF    pvalue
## 1 0.52    1 0.3096963
## [1] "Testing H1 vs H0"
##      dLL dDF    pvalue
## 1 0.08    1 0.6952432
## [1] "Testing H2 vs H0"
##      dLL dDF    pvalue
## 1 0.16    3 0.9578571
## [1] "Testing H3 vs H1"
##      dLL dDF    pvalue
## 1 0.17    4 0.9863893
## [1] "Testing H3 vs H2"
##      dLL dDF    pvalue
## 1 0.1    2 0.9086336

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



CD8

```
apply_facs(CD8, "CD8")
```

```
## [1] "Analysing data for response: CD8"
## [1] "Fit for the response: CD8"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1      0      1 0.9282245
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1      0      1 0.948408
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.11      1 0.6464841
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.55      1 0.2954152
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.14      1 0.593814
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.35      1 0.4036176
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 4.38      1 0.003077134
```

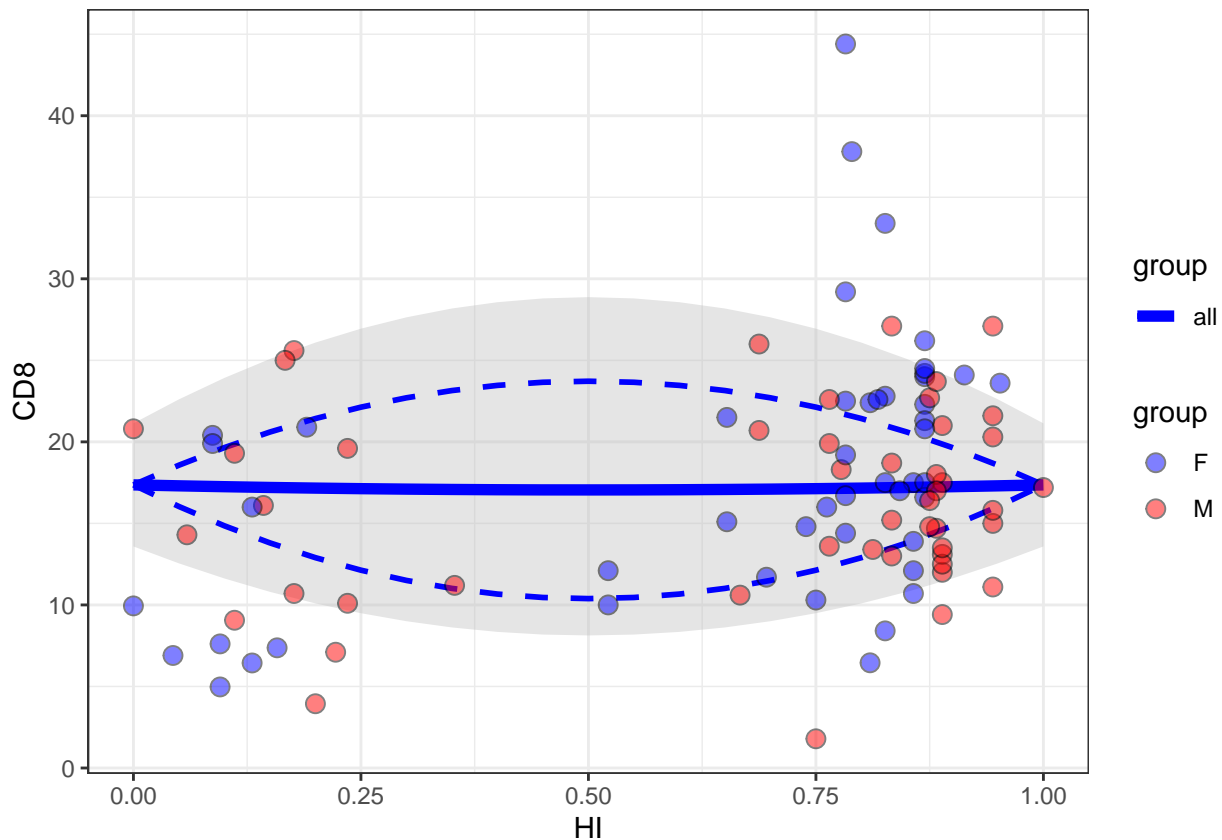
```

## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 3.96   3 0.0477865
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 4.89   4 0.0444183
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 5.31   2 0.004944148
## [1] "Analysing data for response: CD8"
## [1] "Fit for the response: CD8"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1   0   1 0.9282245
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1   0   1 0.948408
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.11   1 0.6464841
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.55   1 0.2954152
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.14   1 0.593814
## [1] "Testing H3 groupB no alpha vs alpha"

```

```
##      dLL dDF      pvalue
## 1 0.35   1 0.4036176
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 4.38   1 0.003077134
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 3.96   3 0.0477865
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 4.89   4 0.0444183
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 5.31   2 0.004944148

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



Act_CD8

```
apply_facets(Act_CD8, "Act_CD8")
```

```
## [1] "Analysing data for response: Act_CD8"
## [1] "Fit for the response: Act_CD8"
## [1] "Fitting for all"
```

```

## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF  pvalue
## 1 0.26   1 0.469064
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF  pvalue
## 1 0.21   1 0.5202331
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF  pvalue
## 1 0.74   1 0.2227827
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF  pvalue
## 1 0.09   1 0.666736
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF  pvalue
## 1 0.23   1 0.4931557
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF  pvalue
## 1  0    1 0.9609715
## [1] "Testing H1 vs H0"
##      dLL dDF  pvalue
## 1 3.6   1 0.007311083
## [1] "Testing H2 vs H0"
##      dLL dDF  pvalue
## 1 2.62   3 0.1554824
## [1] "Testing H3 vs H1"
##      dLL dDF  pvalue
## 1 2.26   4 0.3411303
## [1] "Testing H3 vs H2"

```

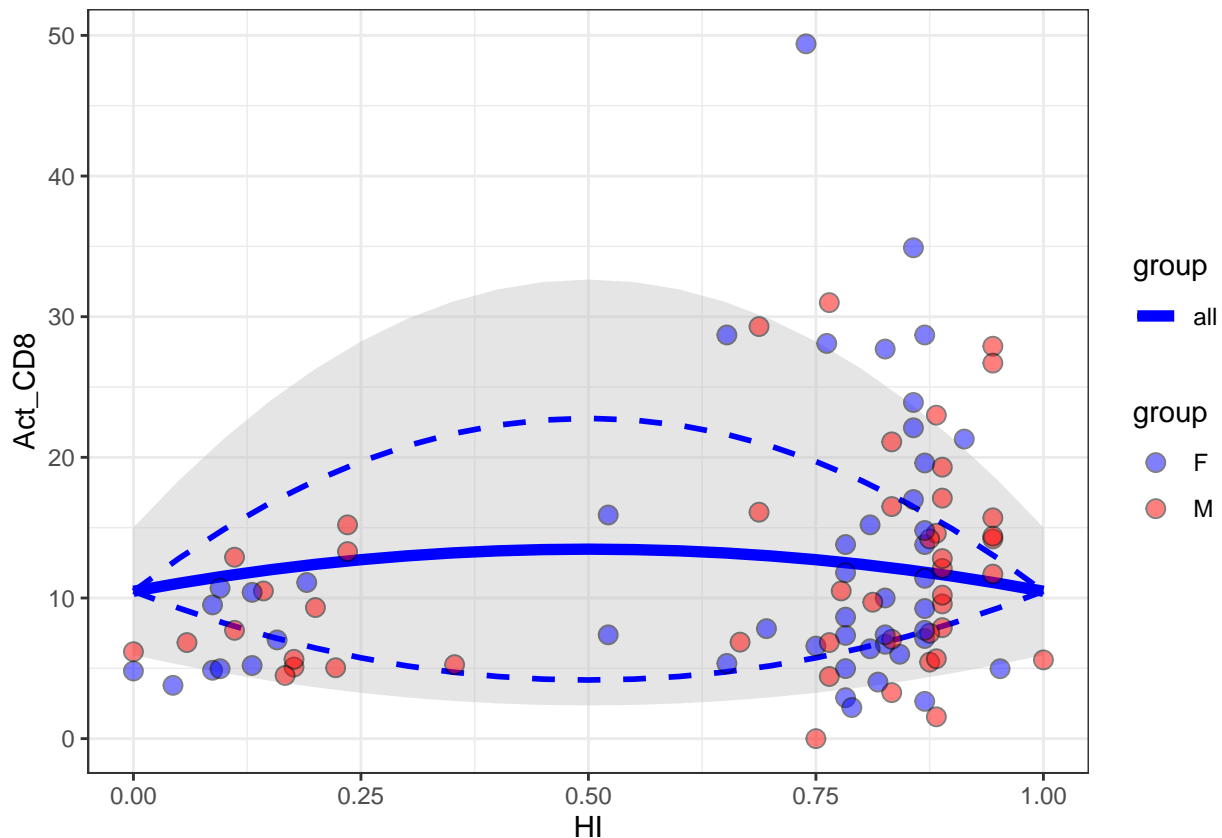
```

##      dLL dDF      pvalue
## 1 3.24    2 0.03929196
## [1] "Analysing data for response: Act_CD8"
## [1] "Fit for the response: Act_CD8"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.26    1 0.469064
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.21    1 0.5202331
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.74    1 0.2227827
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.09    1 0.666736
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.23    1 0.4931557
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1  0      1 0.9609715
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 3.6     1 0.007311083
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue

```

```
## 1 2.62 3 0.1554824
## [1] "Testing H3 vs H1"
## dLL dDF pvalue
## 1 2.26 4 0.3411303
## [1] "Testing H3 vs H2"
## dLL dDF pvalue
## 1 3.24 2 0.03929196

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



IFNy_CD4

```
apply_facets(IFNy_CD4, "IFNy_CD4")
```

```
## [1] "Analysing data for response: IFNy_CD4"
## [1] "Fit for the response: IFNy_CD4"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
```

```

## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.33   1 0.1034662
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.9    1 0.05134493
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.1    1 0.6569514
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.99   1 0.1589698
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.34   1 0.4102441
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.03   1 0.1503508
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 1.3    1 0.1073324
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 5.76   3 0.009203481
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 5.66   4 0.02311103
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 1.2    2 0.3016324
## [1] "Analysing data for response: IFNy_CD4"
## [1] "Fit for the response: IFNy_CD4"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"

```

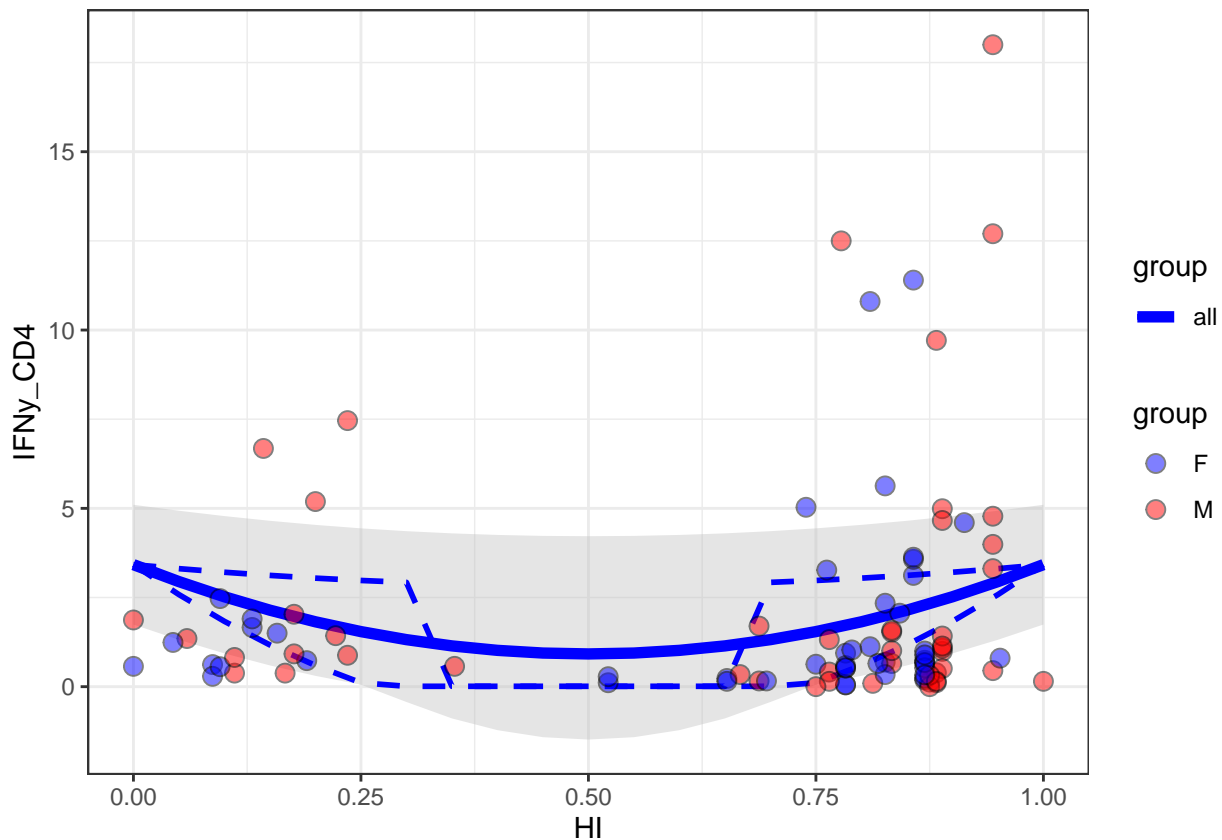


```

## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.33   1 0.1034662
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.9    1 0.05134493
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.1    1 0.6569514
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.99   1 0.1589698
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.34   1 0.4102441
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 1.03   1 0.1503508
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 1.3    1 0.1073324
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 5.76   3 0.009203481
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 5.66   4 0.02311103
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 1.2    2 0.3016324

```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



IFNy_CD8

```
apply_facs(IFNy_CD8, "IFNy_CD8")
```

```
## [1] "Analysing data for response: IFNy_CD8"
## [1] "Fit for the response: IFNy_CD8"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
```

```

## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 2.55   1 0.02395587
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 2.16   1 0.037683
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 3.85   1 0.0055213
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.15   1 0.5791645
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.47   1 0.3300561
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.86   1 0.1904154
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 8.92   1 2.393654e-05
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 1.52   3 0.3865656
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 0.37   4 0.9463027
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 7.78   2 0.0004192104
## [1] "Analysing data for response: IFNy_CD8"
## [1] "Fit for the response: IFNy_CD8"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupA : F"
## [1] "Fitting model basic without alpha"

```

```

## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Fitting for groupB : M"
## [1] "Fitting model basic without alpha"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 2.55   1 0.02395587
## [1] "Testing H1 no alpha vs alpha"
##      dLL dDF      pvalue
## 1 2.16   1 0.037683
## [1] "Testing H2 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 3.85   1 0.0055213
## [1] "Testing H2 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.15   1 0.5791645
## [1] "Testing H3 groupA no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.47   1 0.3300561
## [1] "Testing H3 groupB no alpha vs alpha"
##      dLL dDF      pvalue
## 1 0.86   1 0.1904154
## [1] "Testing H1 vs H0"
##      dLL dDF      pvalue
## 1 8.92   1 2.393654e-05
## [1] "Testing H2 vs H0"
##      dLL dDF      pvalue
## 1 1.52   3 0.3865656
## [1] "Testing H3 vs H1"
##      dLL dDF      pvalue
## 1 0.37   4 0.9463027
## [1] "Testing H3 vs H2"
##      dLL dDF      pvalue
## 1 7.78   2 0.0004192104

## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.

```

