5.Gene_expression_analysis

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 genes
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 = "_")

Genes_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")

Genes_wild_imp <- paste(Genes_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 genes

```
# 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))

genes_mouse <- field %>%
  dplyr::select(all_of(Genes_wild_imp))


genes <- genes_mouse  %>%
  rename_with(~str_remove(., '_imp'))


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

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


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

#remove the non imputed genes from the field
field <- field %>%
  dplyr::select(-c(all_of(Genes_wild), all_of(Genes_wild_imp)))

#add the columns of genes with the removed suffix
field <- cbind(field, genes)
```

Install the package

```
##
## * checking for file '/tmp/RtmpiMFSkO/remotesdce027c504ebd/alicebalard-parasiteLoad-1b43216/DESCRIPTI
## * 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$IDO1



# 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")))
}



findGoodDist <- function(x, distribs, distribs2){
  l =lapply(distribs, function(i) tryDistrib(x, i))
  names(l) <- distribs
  print(l)
  listDistr <- lapply(distribs2, 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=distribs2)
  cdfcomp(listDistr, legendtext=distribs2)
  qqcomp(listDistr, legendtext=distribs2)
  ppcomp(listDistr, legendtext=distribs2)
  par(mfrow=c(1,1))
}
```

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

Functions for testing distributions

```
## $fit
##       mean          sd
##   14.9738149    4.2770476
##  ( 0.2333321) ( 0.1649907)
##
## $loglik
## [1] -965.0597
##
## $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")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced

## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## $fit
##      shape        scale
##    3.6238040   16.5831772
##  ( 0.1440917) ( 0.2652173)
##
## $loglik
## [1] -970.569
##
## $AIC
## NULL
```

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

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

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

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

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

```
##      L1start         L1LB         L1UB      L2start         L2LB         L2UB
## 20.324385989  0.000000001 29.607514874 20.324385989  0.000000001 29.607514874
##   alphaStart      alphaLB      alphaUB myshapeStart    myshapeLB    myshapeUB
##  0.000000000 -5.000000000  5.000000000  1.000000000  0.000000001  5.000000000
```

```
IFNy <- parasiteLoad::analyse(data = field,
                        response = "IFNy",
                        model = "weibull",
                        group = "Sex")
```

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

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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"
## [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 0.66   1 0.2517858
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.29   1 0.4474705
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.02   1 0.832149
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF     pvalue
## 1 1.85   1 0.05473712
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9831096
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF   pvalue
## 1 1.18   1 0.124967
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.56   1 0.2883876
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 2.11   3 0.2387539
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 3.61   4 0.1243628
## [1] "Testing H3 vs H2"
##    dLL dDF   pvalue
## 1 2.07   2 0.126495
```

```
parasiteLoad::analyse(data = field,
                      response = "IFNy",
                      model = "weibull",
                      group = "Sex")
```

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

```
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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"
## [1] "Did converge"
## [1] "Fitting model basic with alpha"
## [1] "Did converge"
```

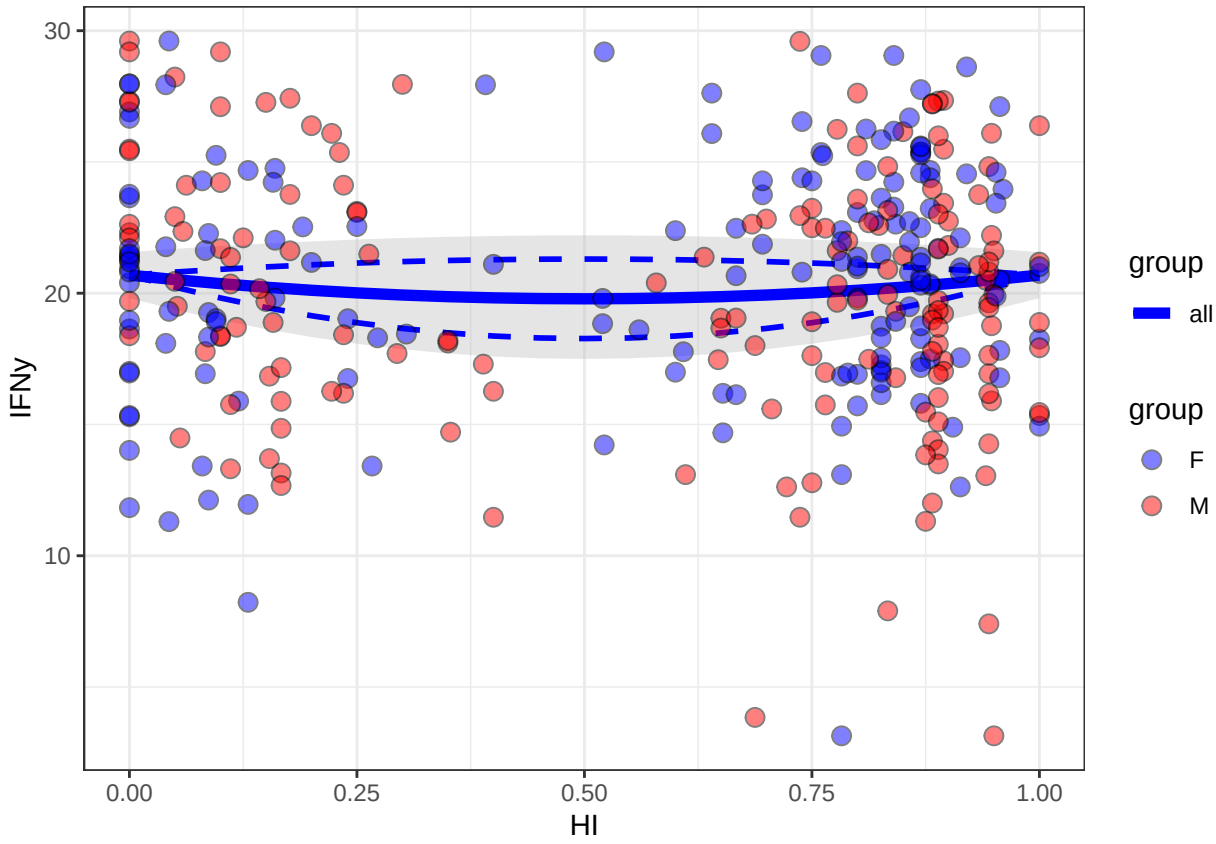
```
## [1] "Fitting model advanced without alpha"
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
## [1] "Did converge"
## [1] "Testing H0 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.66   1 0.2517858
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.29   1 0.4474705
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.02   1 0.832149
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF     pvalue
## 1 1.85   1 0.05473712
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9831096
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF   pvalue
## 1 1.18   1 0.124967
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.56   1 0.2883876
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 2.11   3 0.2387539
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 3.61   4 0.1243628
## [1] "Testing H3 vs H2"
##    dLL dDF   pvalue
## 1 2.07   2 0.126495
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.69024871  0.08730446  5.00000000
##
## Log-likelihood: -988.65
## Best method: L-BFGS-B
##
## $H1
```

```
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.96025558 20.26437679  0.06185067  5.00000000
##
## Log-likelihood: -988.09
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 20.3516954 -0.0227467  5.0000000
##
## Log-likelihood: -484.19
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##        L1     alpha   myshape
## 20.992353  0.223117  4.746739
##
## Log-likelihood: -502.35
## Best method: bobyqa
```

```
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1           L2        alpha      myshape
## 20.217709299 20.617126188 -0.002474524  5.000000000
##
## Log-likelihood: -484.11
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 21.8866269 19.9939560  0.1845004  4.8063868
##
## Log-likelihood: -500.37
## Best method: bobyqa
```

```
bananaPlot(mod = IFNy$H0,
             data = field,
             response = "IFNy",
             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.
```




```
CXCR3 <- parasiteLoad::analyse(data = field,
                          response = "CXCR3",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: CXCR3"
## [1] "Fit for the response: CXCR3"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : some parameters are on the boundary: variance-covariance
## calculations based on Hessian may be unreliable
```

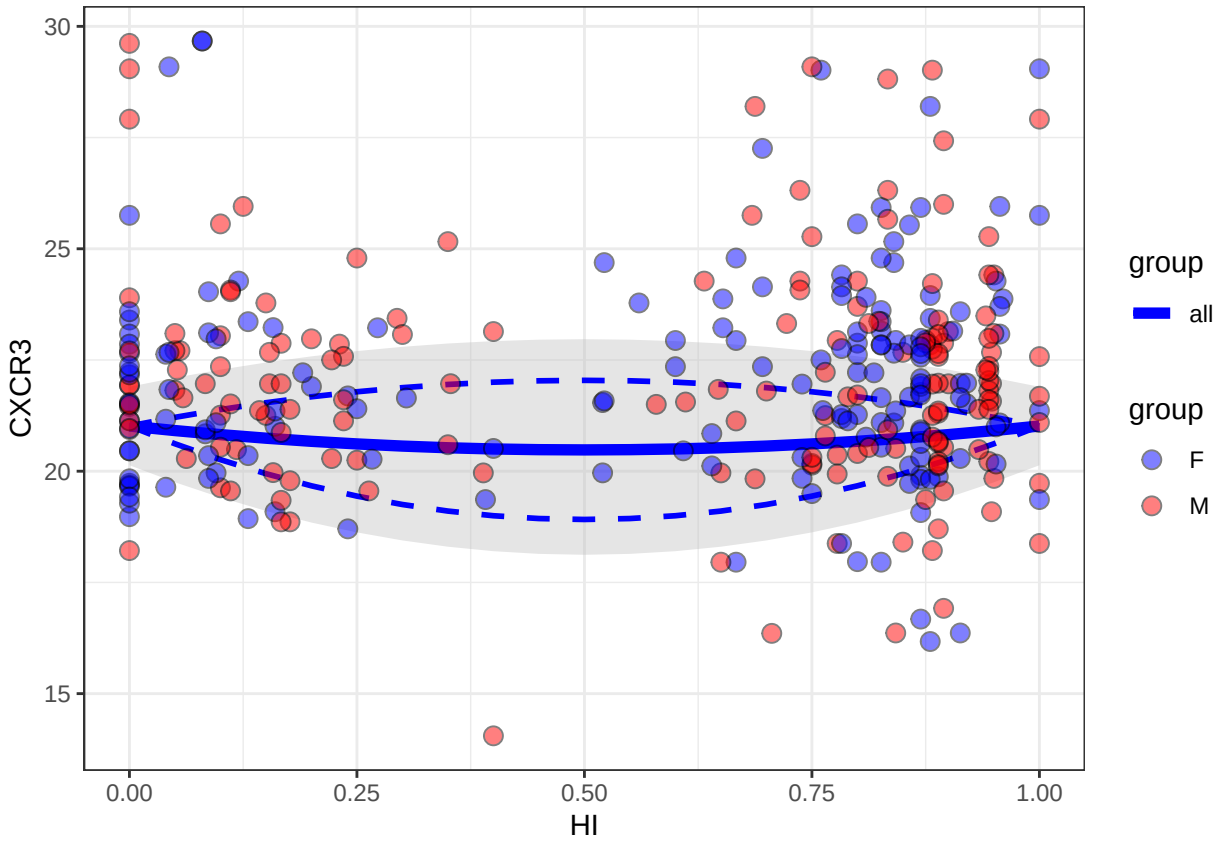
```
## [1] "Did converge"
## [1] "Fitting model advanced with alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.22   1 0.5055693
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.26   1 0.4742228
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.04   1 0.7746347
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.22   1 0.5111876
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.09   1 0.6644541
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.2   1 0.5225651
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.04   1 0.7693663
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.04   3 0.9944332
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.12   4 0.9933796
## [1] "Testing H3 vs H2"
##    dLL dDF   pvalue
## 1 0.12   2 0.883247
```

```
bananaPlot(mod = CXCR3$H0,
             data = field,
             response = "CXCR3",
             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.
```




```
IL.6 <- parasiteLoad::analyse(data = field,
                          response = "IL.6",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: IL.6"
## [1] "Fit for the response: IL.6"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.02   1 0.8393193
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.03   1 0.8089688
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.05   1 0.741014
## [1] "Testing H2 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9518636
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.03   1 0.8017708
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9699687
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.03   1 0.8106281
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.05   3 0.9929598
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.21   4 0.9812223
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.19   2 0.8261012
```

```
##All
print(IL.6)
```

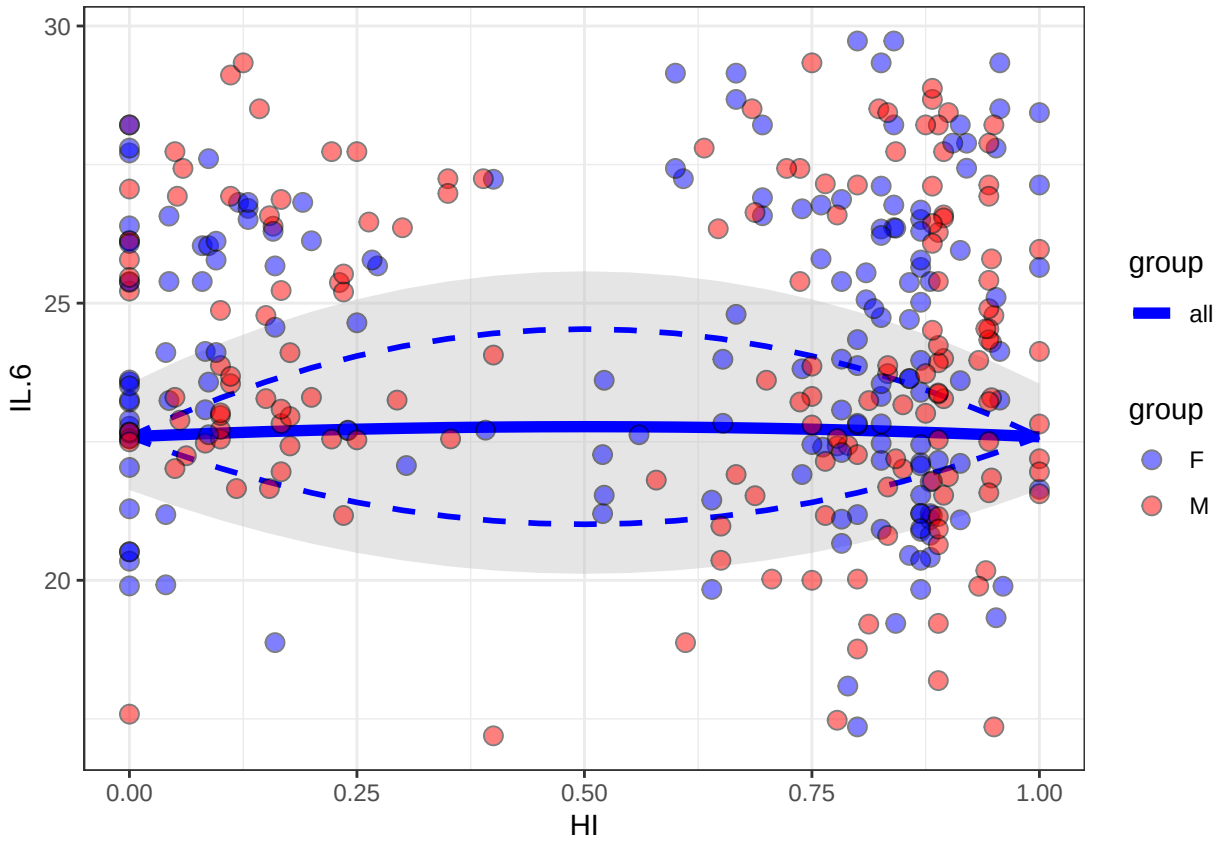
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 22.58999695 -0.01607126  5.00000000
##
## Log-likelihood: -911.25
## Best method: bobyqa
##
## $H1
##
```

```
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 22.66785259 22.50068352 -0.01951112  5.00000000
##
## Log-likelihood: -911.22
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 22.52100877 -0.03584427  5.00000000
##
## Log-likelihood: -453.96
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1        alpha      myshape
## 22.677100619  0.007009489  5.000000000
##
## Log-likelihood: -457.25
## Best method: bobyqa
##
```

```
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 22.43641291 22.65082900 -0.02847721  5.00000000
##
## Log-likelihood: -453.94
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1           L2        alpha      myshape
## 22.989357479 22.420914894  0.004403685  5.000000000
##
## Log-likelihood: -457.08
## Best method: bobyqa
```

```
bananaPlot(mod = IL.6$H0,
             data = field,
             response = "IL.6",
             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.
```




```
IL.10 <- parasiteLoad::analyse(data = field,
                         response = "IL.10",
                         model = "weibull",
                         group = "Sex")
```

```
## [1] "Analysing data for response: IL.10"
## [1] "Fit for the response: IL.10"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.23   1 0.5010902
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.14   1 0.6005157
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.02   1 0.8624423
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF  pvalue
## 1 0.33   1 0.41589
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9987065
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.32   1 0.4259674
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.22   1 0.5066345
## [1] "Testing H2 vs H0"
##    dLL dDF   pvalue
## 1 0.19   3 0.946087
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.26   4 0.9723588
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.29   2 0.7477948
```

```
##All
print(IL.10)
```

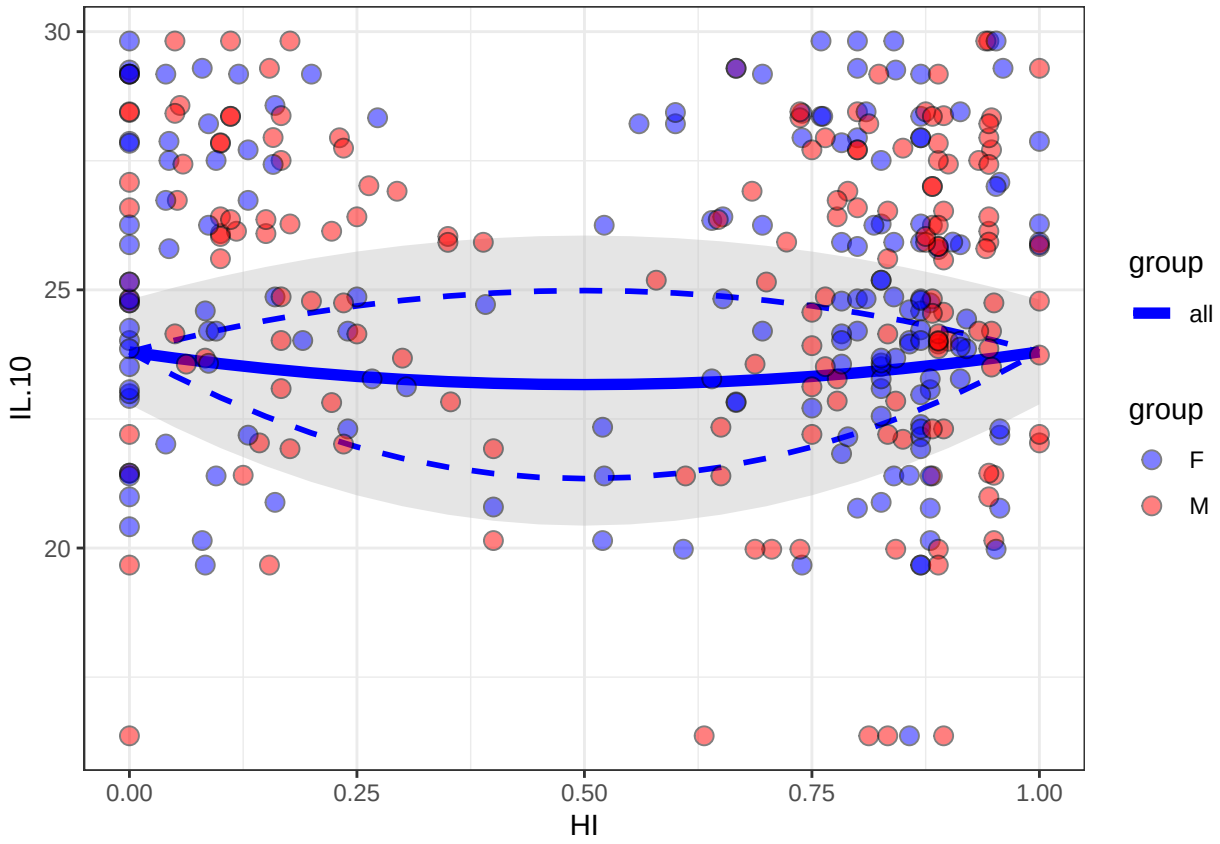
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 23.79755825  0.05316292  5.00000000
##
## Log-likelihood: -925.38
## Best method: bobyqa
##
## $H1
##
```

```
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 24.01675937 23.52780528  0.04254845  5.00000000
##
## Log-likelihood: -925.16
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 23.51206803  0.01830796  5.00000000
##
## Log-likelihood: -460.18
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 24.13262497  0.09640101  5.00000000
##
## Log-likelihood: -465.02
## Best method: bobyqa
##
```

```
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1           L2        alpha      myshape
## 2.367822e+01 2.321003e+01 1.886213e-04 5.000000e+00
##
## Log-likelihood: -460.08
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 24.49745982 23.84504233  0.09484606  5.00000000
##
## Log-likelihood: -464.82
## Best method: bobyqa
```

```
bananaPlot(mod = IL.10$H0,
             data = field,
             response = "IL.10",
             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.
```




```
IL.13 <- parasiteLoad::analyse(data = field,
                          response = "IL.13",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: IL.13"
## [1] "Fit for the response: IL.13"
## [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 0.18   1 0.5521365
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.06   1 0.7217253
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.06   1 0.7366577
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.11   1 0.6325055
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.02   1 0.8244486
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.07   1 0.7181146
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.92   1 0.1759323
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 1.79   3 0.3117642
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 2.12   4 0.3756039
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 1.25   2 0.2875489
```

```
##All
print(IL.13)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 16.50843208  0.07029571  3.14190401
```

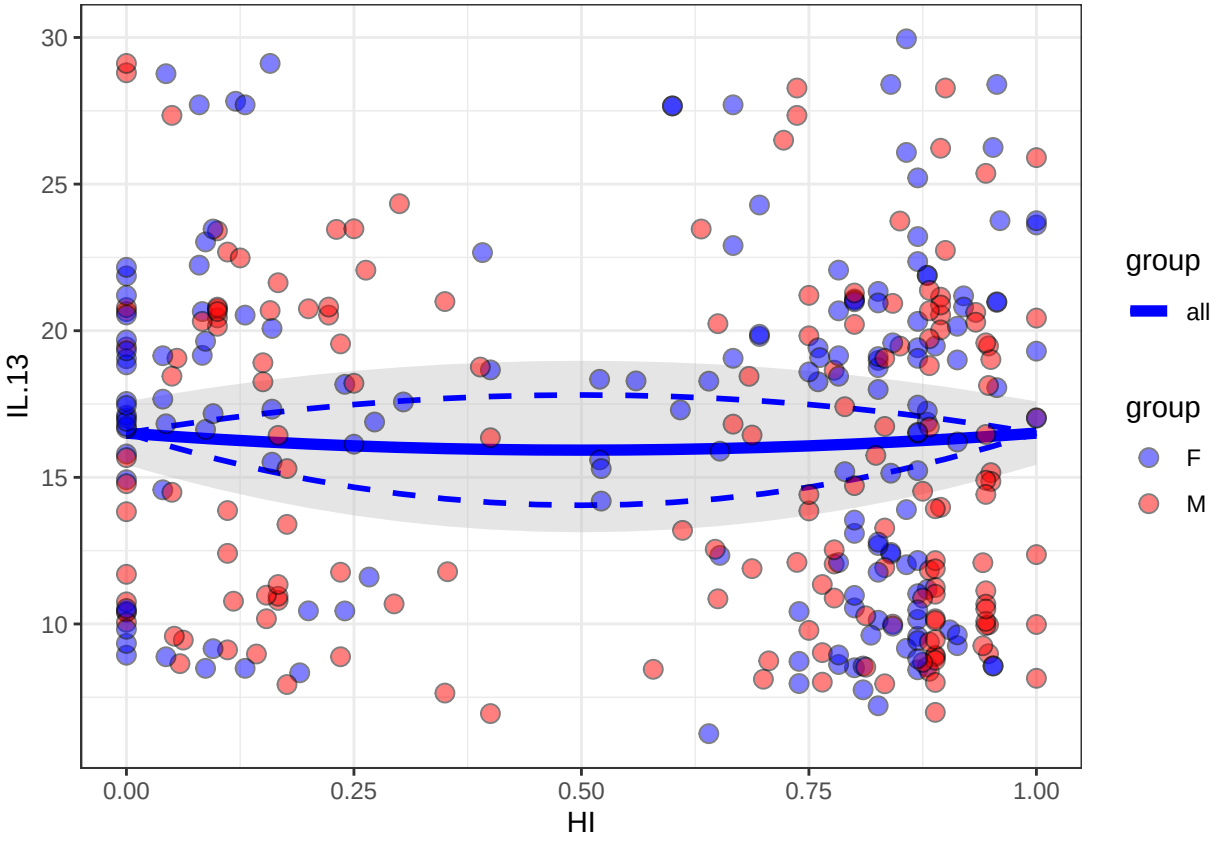
```
##
## Log-likelihood: -1051.24
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 17.02446741 15.93571446  0.04321609  3.14726570
##
## Log-likelihood: -1050.33
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 17.03260540  0.05303081  3.27638465
##
## Log-likelihood: -524.74
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
```

```
##          L1       alpha     myshape
## 15.97223965  0.08515253  3.04268815
##
## Log-likelihood: -524.72
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 17.24881953 16.74900563  0.03625393  3.27694381
##
## Log-likelihood: -524.64
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 16.88175484 15.17136945  0.06525595  3.05982504
##
## Log-likelihood: -523.57
## Best method: bobyqa
```

```
bananaPlot(mod = IL.13$H0,
             data = field,
             response = "IL.13",
             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.
```




```
IL1RN <- parasiteLoad::analyse(data = field,
                          response = "IL1RN",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: IL1RN"
## [1] "Fit for the response: IL1RN"
## [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 0.56   1 0.2901087
## [1] "Testing H1 no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.5   1 0.3169167
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.34   1 0.4130223
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.23   1 0.4951568
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.22   1 0.5086703
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.25   1 0.4762912
## [1] "Testing H1 vs H0"
##   dLL dDF    pvalue
## 1   0   1 0.9246391
## [1] "Testing H2 vs H0"
##   dLL dDF    pvalue
## 1   2   3 0.2624357
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 2.08   4 0.3849876
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.09   2 0.9155911
```

```
##All
print(IL1RN)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
```

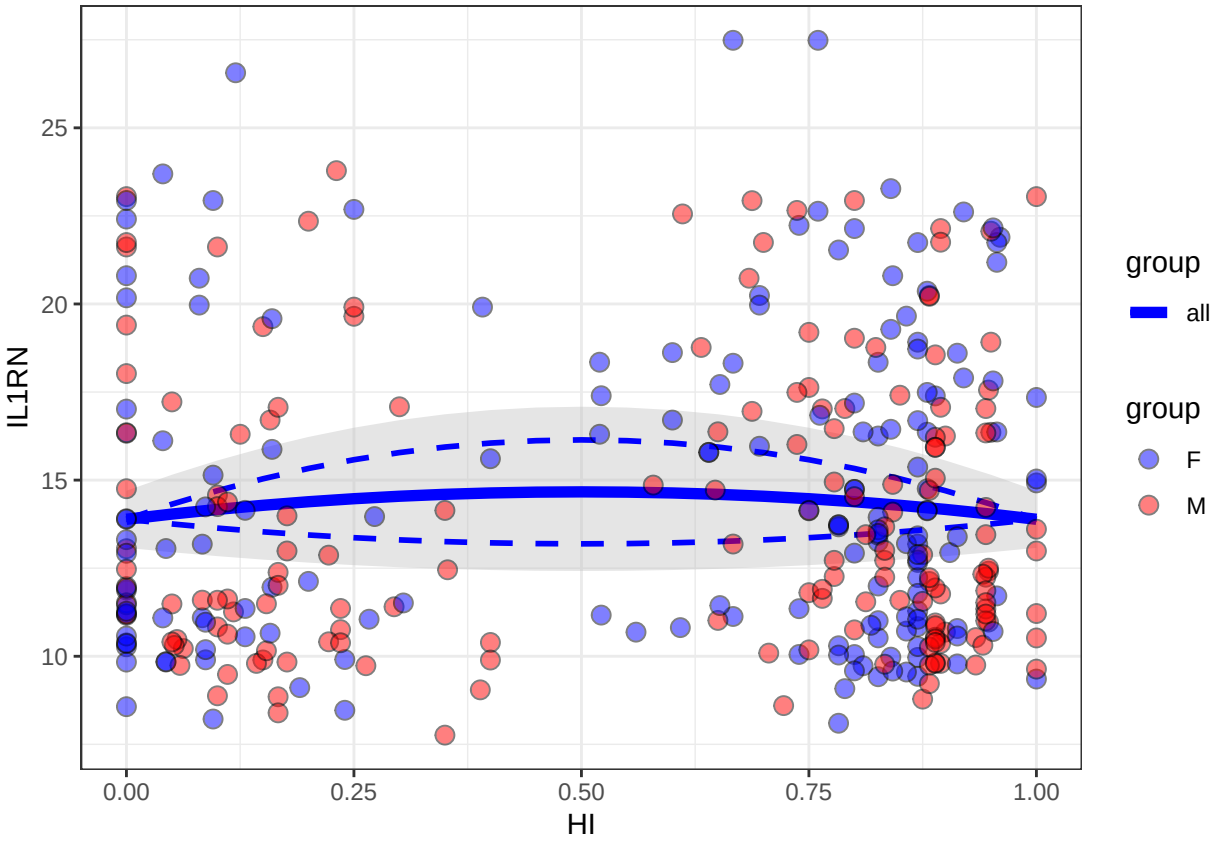
```
## Coefficients:
##         L1      alpha    myshape
## 13.8884526 -0.1120665  3.5362050
##
## Log-likelihood: -960.62
## Best method: L-BFGS-B
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 13.8627496 13.9212988 -0.1093738  3.5356807
##
## Log-likelihood: -960.62
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 14.1847982 -0.1267833  3.4743759
##
## Log-likelihood: -486.06
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
```

```
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 13.59582919 -0.09714878  3.65174801
##
## Log-likelihood: -472.56
## Best method: L-BFGS-B
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 14.0607245 14.3794851 -0.1077201  3.4719635
##
## Log-likelihood: -486
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 13.6947842 13.4953217 -0.1030035  3.6541427
##
## Log-likelihood: -472.53
## Best method: bobyqa
```

```
bananaPlot(mod = IL1RN$H0,
             data = field,
             response = "IL1RN",
             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.
```




```
CXCR3 <- parasiteLoad::analyse(data = field,
                        response = "CXCR3",
                        model = "weibull",
                        group = "Sex")
```

```
## [1] "Analysing data for response: CXCR3"
## [1] "Fit for the response: CXCR3"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.22   1 0.5055693
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.26   1 0.4742228
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.04   1 0.7746347
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.22   1 0.5111876
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.09   1 0.6644541
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.2   1 0.5225651
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.04   1 0.7693663
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.04   3 0.9944332
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.12   4 0.9933796
## [1] "Testing H3 vs H2"
##    dLL dDF   pvalue
## 1 0.12   2 0.883247
```

```
##All
print(CXCR3)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
```

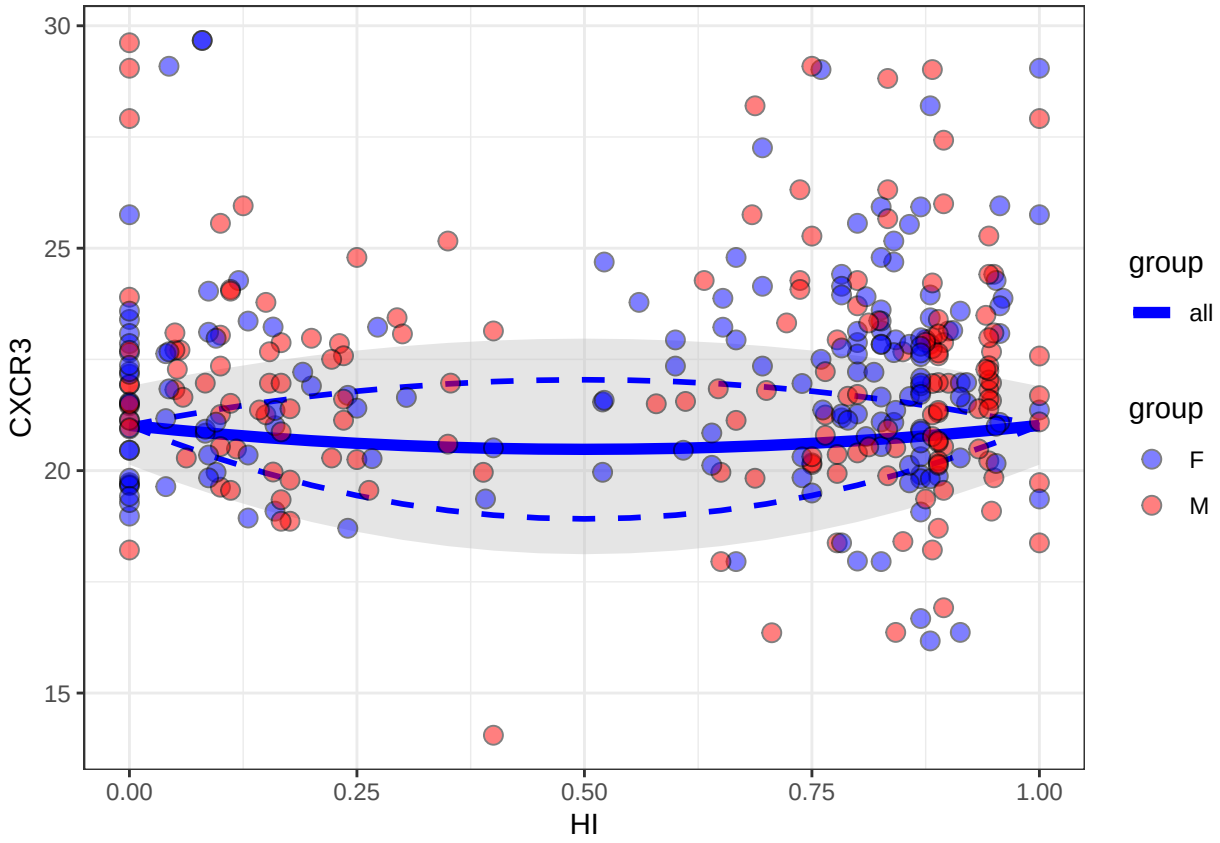
```
##          L1       alpha     myshape
## 21.01580067  0.05112701  5.00000000
##
## Log-likelihood: -882.06
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 20.9304045 21.1230062  0.0563175  5.0000000
##
## Log-likelihood: -882.01
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.89937579  0.03101896  5.00000000
##
## Log-likelihood: -438.54
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
```

```
##
## Coefficients:
##          L1       alpha     myshape
## 21.13472692  0.07153824  5.00000000
##
## Log-likelihood: -443.48
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.72128575 21.18914701  0.04952108  5.00000000
##
## Log-likelihood: -438.42
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 21.17856231 21.09202894  0.07029018  5.00000000
##
## Log-likelihood: -443.47
## Best method: bobyqa
```

```
bananaPlot(mod = CXCR3$H0,
             data = field,
             response = "CXCR3",
             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.
```




```
CASP1 <- parasiteLoad::analyse(data = field,
                          response = "CASP1",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: CASP1"
## [1] "Fit for the response: CASP1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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   1 0.9737535
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.02   1 0.8314078
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.13   1 0.6089647
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.19   1 0.5408948
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.01   1 0.8638685
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.19   1 0.5324426
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.52   1 0.3058981
## [1] "Testing H2 vs H0"
##   dLL dDF    pvalue
## 1 0.4   3 0.8489512
## [1] "Testing H3 vs H1"
##   dLL dDF    pvalue
## 1 0.5   4 0.9085279
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.63   2 0.5340604
```

```
##All
print(CASP1)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1        alpha      myshape
## 21.209529655  0.002511567  5.000000000
```

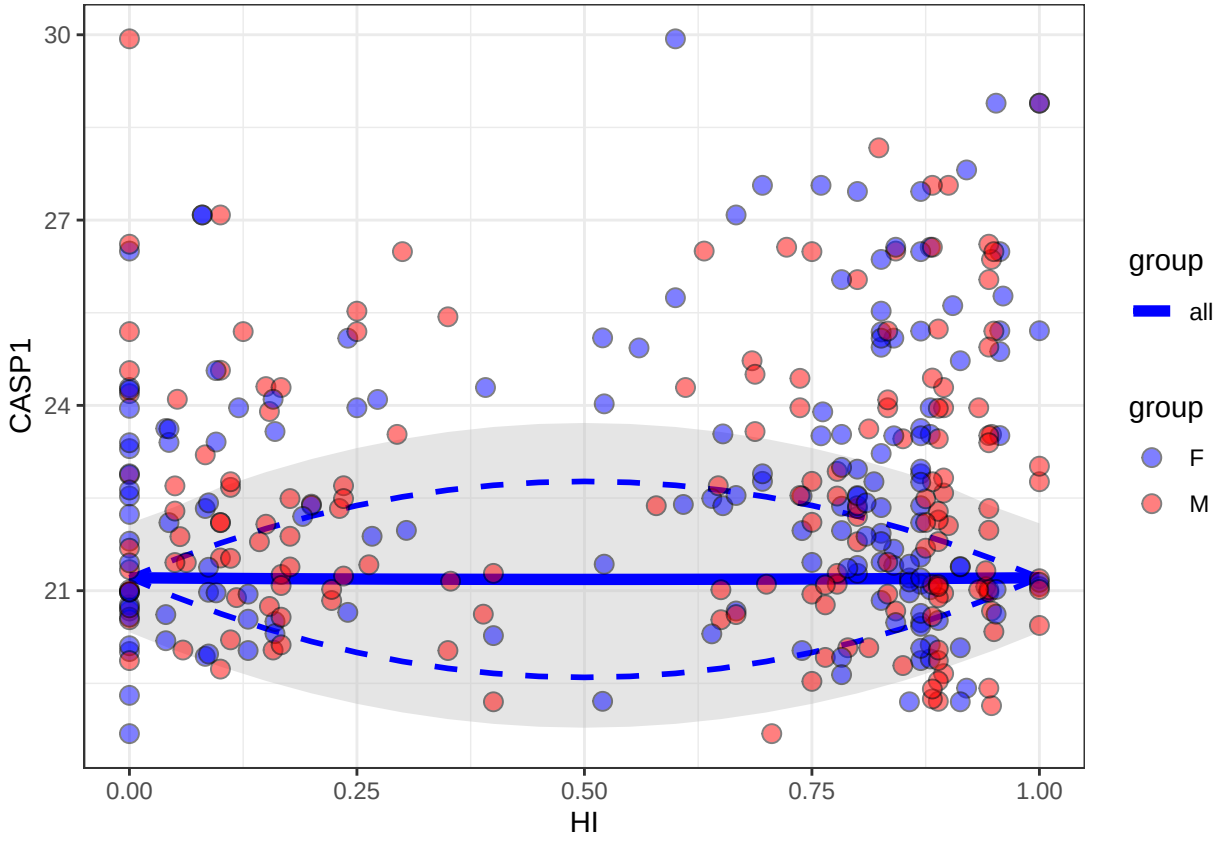
```
##
## Log-likelihood: -881.53
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 20.8849146 21.5596163  0.0163553  5.0000000
##
## Log-likelihood: -881.01
## Best method: L-BFGS-B
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 21.02511902 -0.05449916  5.00000000
##
## Log-likelihood: -440.37
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
```

```
##          L1       alpha     myshape
## 21.43162135  0.06709017  5.00000000
##
## Log-likelihood: -440.76
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.59367199 21.63330732 -0.01876619  5.00000000
##
## Log-likelihood: -439.78
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 21.29831475 21.53853178  0.06840526  5.00000000
##
## Log-likelihood: -440.73
## Best method: bobyqa
```

```
bananaPlot(mod = CASP1$H0,
             data = field,
             response = "CASP1",
             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.
```




```
CXCL9 <- parasiteLoad::analyse(data = field,
                          response = "CXCL9",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: CXCL9"
## [1] "Fit for the response: CXCL9"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.01   1 0.8808258
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.05   1 0.7405773
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.32   1 0.4218952
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.67   1 0.2483961
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.14   1 0.6016775
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.69   1 0.2389278
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.67   1 0.2472652
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 1.01   3 0.5684693
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.96   4 0.7493469
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.62   2 0.5363909
```

```
##All
print(CXCL9)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.03715603  0.01178308  5.00000000
##
## Log-likelihood: -908.94
```

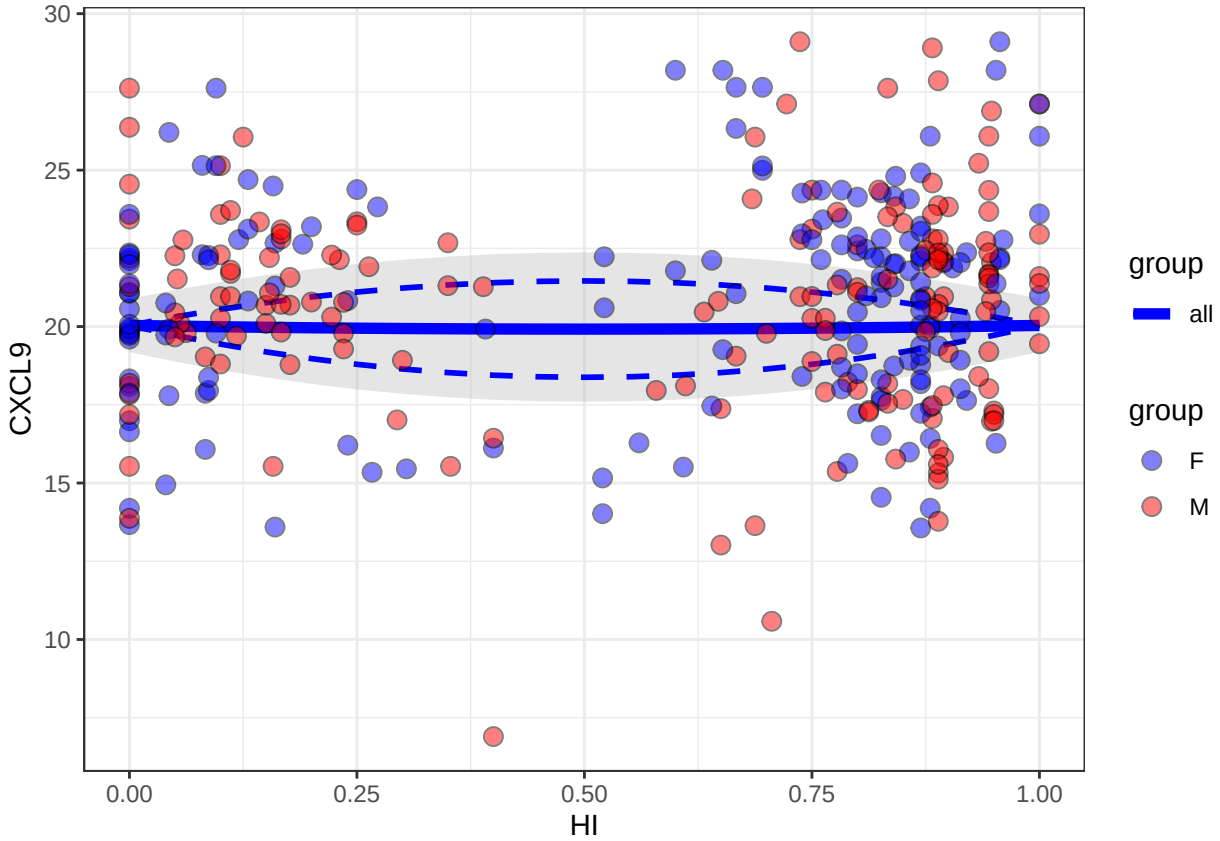
```
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##        L1        L2     alpha   myshape
## 19.685362 20.403686  0.026173  5.000000
##
## Log-likelihood: -908.27
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 19.64030450 -0.08658131  5.00000000
##
## Log-likelihood: -452.67
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 20.5498491  0.1331794  5.0000000
```

```
##
## Log-likelihood: -455.26
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 19.25409331 20.14158750 -0.05770046  5.00000000
##
## Log-likelihood: -452.16
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 20.3135368 20.7375346  0.1355425  5.0000000
##
## Log-likelihood: -455.15
## Best method: bobyqa
```

```
bananaPlot(mod = CXCL9$H0,
             data = field,
             response = "CXCL9",
             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.
```




```
IDO1 <- parasiteLoad::analyse(data = field,
                          response = "IDO1",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: IDO1"
## [1] "Fit for the response: IDO1"
## [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 0.01   1 0.9108008
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.01   1 0.9046158
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.14   1 0.5902886
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.17   1 0.5655159
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.06   1 0.7207048
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.12   1 0.6289754
## [1] "Testing H1 vs H0"
##   dLL dDF   pvalue
## 1   0   1 0.964358
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 1.37   3 0.4330405
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 1.57   4 0.5359263
## [1] "Testing H3 vs H2"
##   dLL dDF   pvalue
## 1 0.2   2 0.822106
```

```
##All
print(IDO1)
```

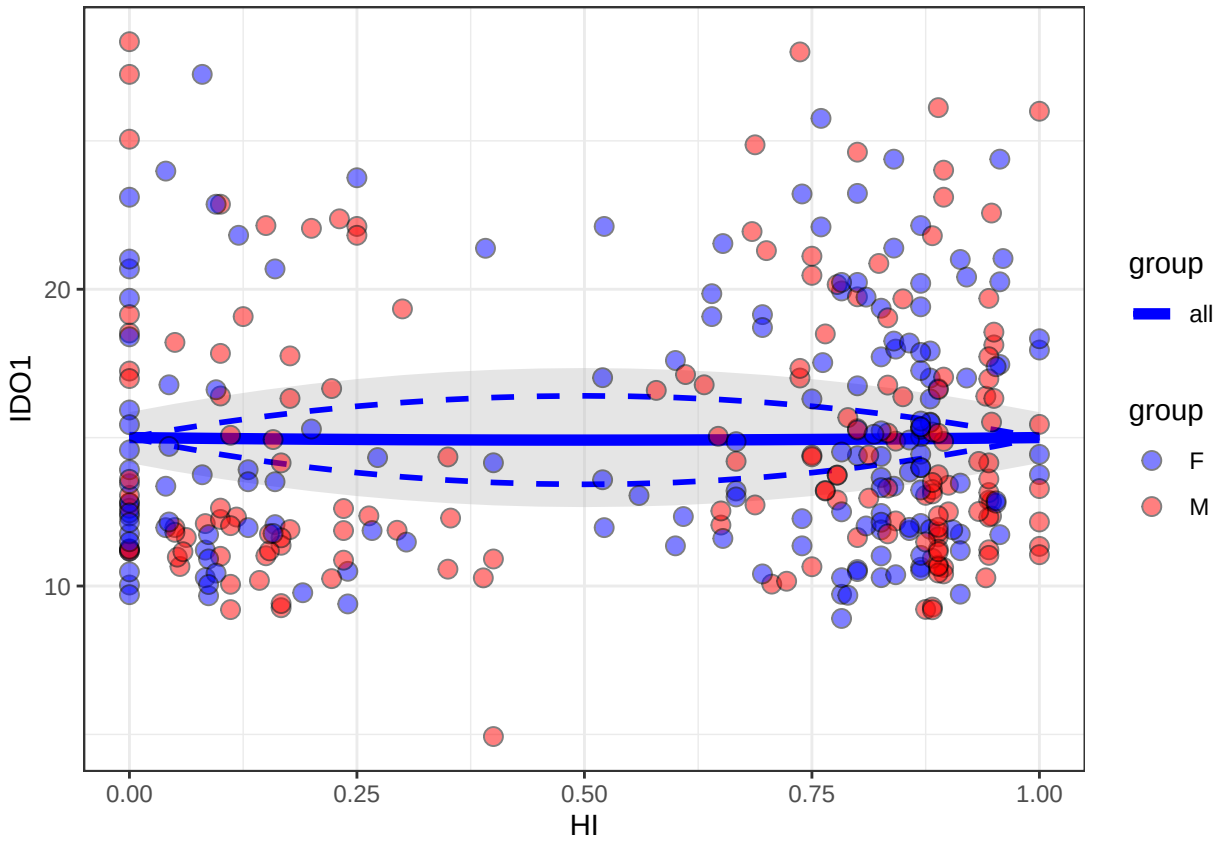
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
```

```
## 15.00264988  0.01139145  3.63005592
##
## Log-likelihood: -967.56
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 14.98987464 15.01905741  0.01262131  3.62969203
##
## Log-likelihood: -967.56
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 14.85602738 -0.07599562  3.86814620
##
## Log-likelihood: -475.47
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
```

```
## Coefficients:
##          L1       alpha     myshape
## 15.11552180  0.08467351  3.44741951
##
## Log-likelihood: -490.72
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 14.70119786 15.09822004 -0.05310727  3.86207765
##
## Log-likelihood: -475.37
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 15.31770178 14.89970904  0.07278724  3.45230103
##
## Log-likelihood: -490.63
## Best method: bobyqa
```

```
bananaPlot(mod = IDO1$H0,
             data = field,
             response = "IDO1",
             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.
```




```
IRGM1 <- parasiteLoad::analyse(data = field,
                          response = "IRGM1",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: IRGM1"
## [1] "Fit for the response: IRGM1"
## [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 0.25   1 0.4828264
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.25   1 0.4790555
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.27   1 0.4615785
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.01   1 0.9073188
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.51   1 0.3113833
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9406887
## [1] "Testing H1 vs H0"
##   dLL dDF    pvalue
## 1   0   1 0.9210063
## [1] "Testing H2 vs H0"
##    dLL dDF      pvalue
## 1 6.39   3 0.005150543
## [1] "Testing H3 vs H1"
##    dLL dDF      pvalue
## 1 7.71   4 0.003916921
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 1.32   2 0.2660179
```

```
##All
print(IRGM1)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
```

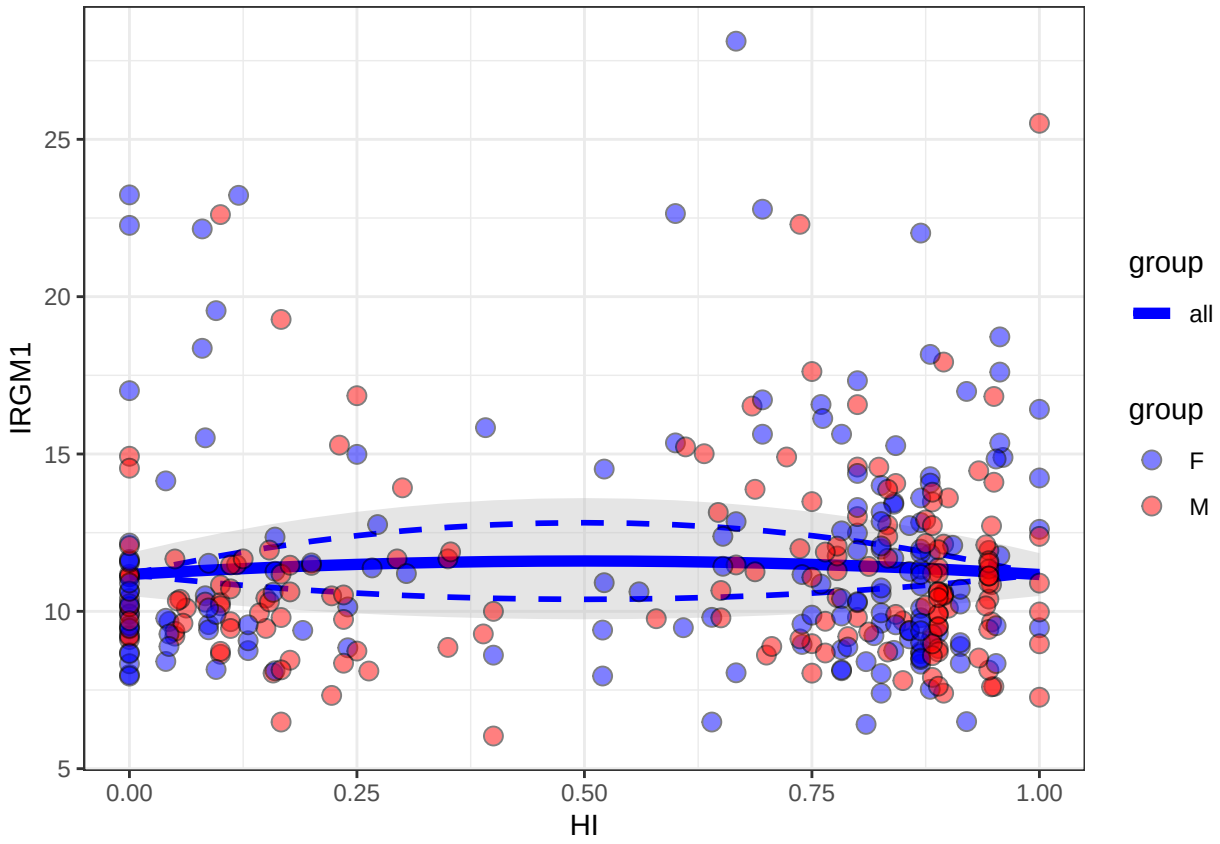
```
##
## Coefficients:
##          L1       alpha     myshape
## 11.17017483 -0.07675286  3.29231849
##
## Log-likelihood: -892.09
## Best method: L-BFGS-B
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 11.19517027 11.14297819 -0.07887767  3.29287057
##
## Log-likelihood: -892.08
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 11.3809696 -0.1190043  3.0978950
##
## Log-likelihood: -460.24
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
```

```
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 11.08940618  0.01678416  3.64359536
##
## Log-likelihood: -425.46
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 11.6954367 10.9134859 -0.1754937  3.1186321
##
## Log-likelihood: -459.79
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 10.57034646 11.44148976  0.01068023  3.66474971
##
## Log-likelihood: -424.58
## Best method: bobyqa
```

```
bananaPlot(mod = IRGM1$H0,
             data = field,
             response = "IRGM1",
             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.
```




```
MPO <- parasiteLoad::analyse(data = field,
                             response = "MPO",
                             model = "weibull",
                             group = "Sex")
```

```
## [1] "Analysing data for response: MPO"
## [1] "Fit for the response: MPO"
## [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 0.28   1 0.4506038
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.05   1 0.7426079
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.22   1 0.5097674
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.09   1 0.6787043
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9497328
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.06   1 0.7205988
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 1.27   1 0.1111564
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.42   3 0.8384331
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 1.18   4 0.6698744
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 2.03   2 0.1318847
```

```
##All
print(MP0)
```

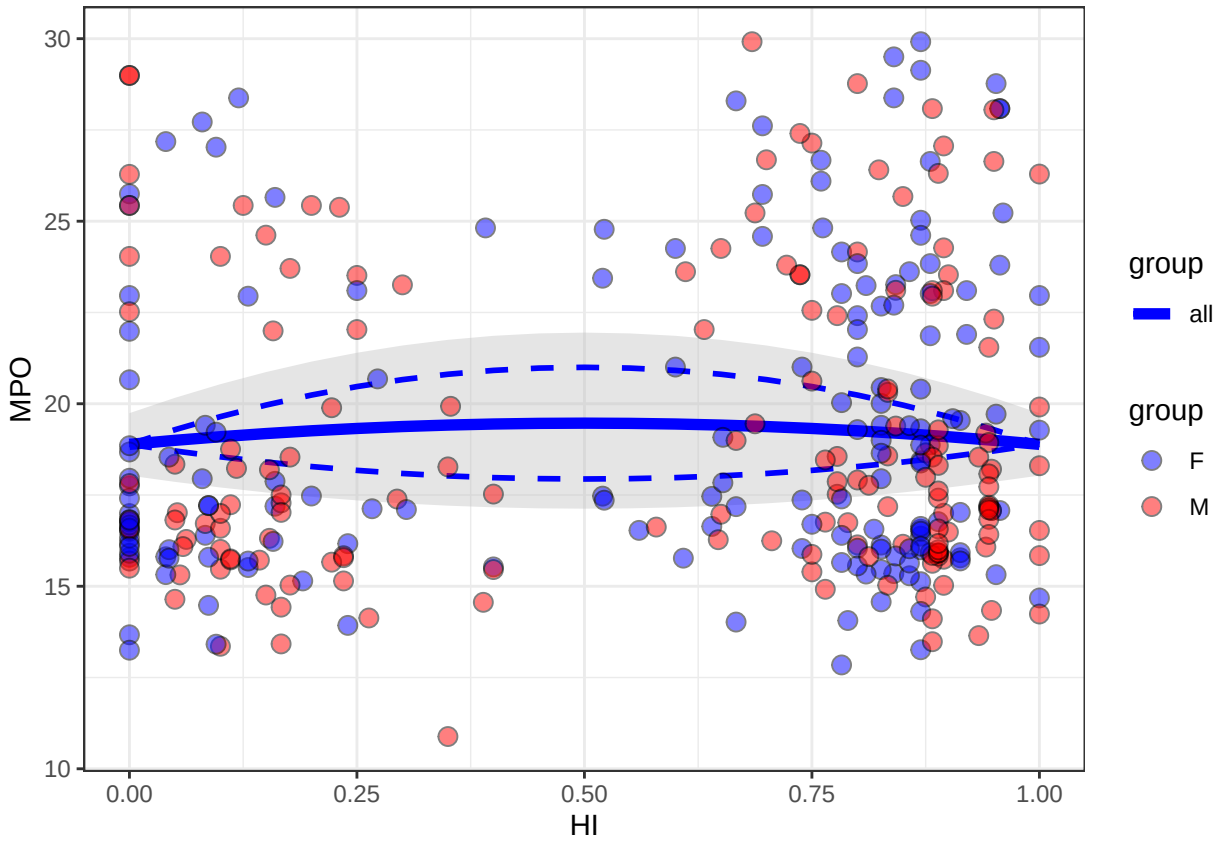
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
```

```
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 18.88682832 -0.06152658  4.73863762
##
## Log-likelihood: -966.78
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 18.45418558 19.46250711 -0.02710868  4.75321830
##
## Log-likelihood: -965.51
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 19.00516123 -0.07925123  4.74245535
##
## Log-likelihood: -484.03
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
```

```
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 18.76083530 -0.04579065  4.74712904
##
## Log-likelihood: -482.32
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1           L2        alpha      myshape
## 18.276755907 20.102222390 -0.007553099  4.796631202
##
## Log-likelihood: -482.03
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 18.67473735 18.86181091 -0.04039904  4.74654510
##
## Log-likelihood: -482.3
## Best method: bobyqa
```

```
bananaPlot(mod = MPO$HO,
             data = field,
             response = "MPO",
             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.
```




```
MUC2 <- parasiteLoad::analyse(data = field,
                          response = "MUC2",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: MUC2"
## [1] "Fit for the response: MUC2"
## [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 0.52   1 0.3057463
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.41   1 0.3670518
## [1] "Testing H2 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.1   1 0.6547489
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.56   1 0.287872
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.07   1 0.7138228
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.49   1 0.3213355
## [1] "Testing H1 vs H0"
##    dLL dDF   pvalue
## 1 0.12   1 0.623392
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.91   3 0.6119527
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.98   4 0.7413755
## [1] "Testing H3 vs H2"
##   dLL dDF    pvalue
## 1 0.2   2 0.8200142
```

```
##All
print(MUC2)
```

```
## $H0
##
```

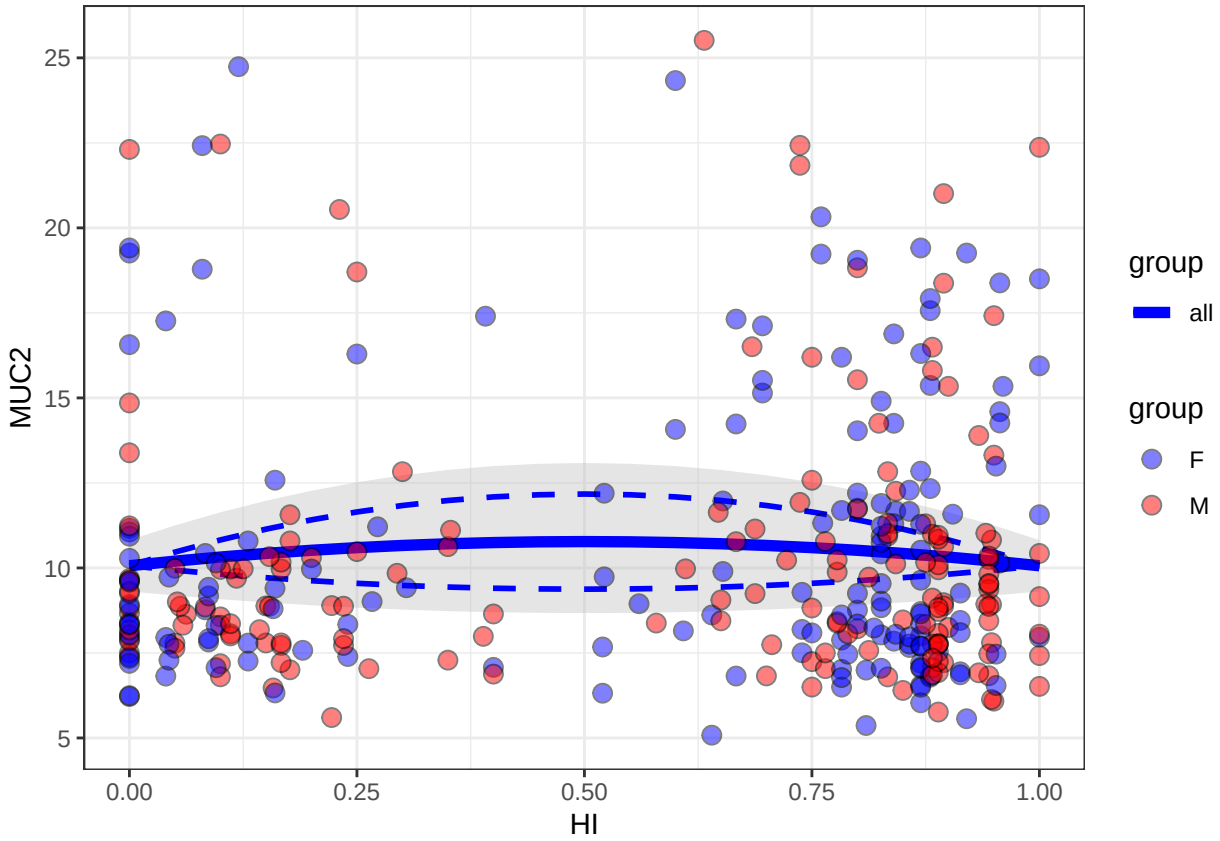
```
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 10.0645924 -0.1410886  2.7147814
##
## Log-likelihood: -924.26
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
##  9.9323423 10.2167620 -0.1263492  2.7135673
##
## Log-likelihood: -924.14
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 10.43249397 -0.08628109  2.70433445
##
## Log-likelihood: -467.28
## Best method: bobyqa
##
```

```
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
##  9.6742862 -0.2088907  2.7354638
##
## Log-likelihood: -456.07
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 10.35304248 10.54201510 -0.07356332  2.70263258
##
## Log-likelihood: -467.26
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
##  9.4382374  9.8947008 -0.1946406  2.7364057
```

```
##
## Log-likelihood: -455.9
## Best method: L-BFGS-B
```

```
bananaPlot(mod = MUC2$H0,
             data = field,
             response = "MUC2",
             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.
```




```
MUC5AC <- parasiteLoad::analyse(data = field,
                        response = "MUC5AC",
                        model = "weibull",
                        group = "Sex")
```

```
## [1] "Analysing data for response: MUC5AC"
## [1] "Fit for the response: MUC5AC"
## [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 0.49   1 0.3242363
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.16   1 0.5731564
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.16   1 0.5753486
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.36   1 0.3938868
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1   0   1 0.9685347
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.29   1 0.4482543
## [1] "Testing H1 vs H0"
##    dLL dDF     pvalue
## 1 1.85   1 0.05458726
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.46   3 0.8215748
## [1] "Testing H3 vs H1"
##   dLL dDF    pvalue
## 1 0.7   4 0.8434708
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 2.09   2 0.1235107
```

```
##All
print(MUC5AC)
```

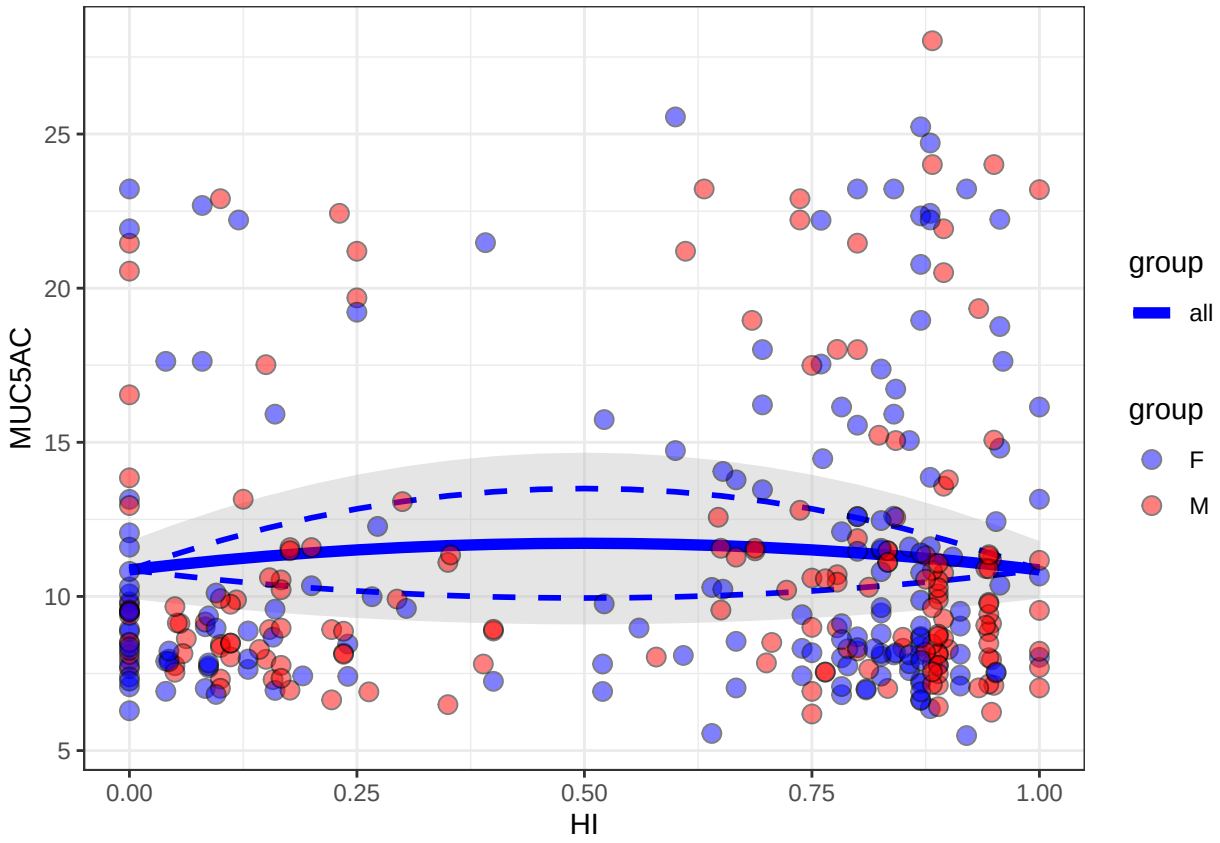
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 10.8620013 -0.1589915  2.4693767
##
## Log-likelihood: -979.39
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 10.26779042 11.59977368 -0.08936617  2.48414143
##
## Log-likelihood: -977.54
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##        L1     alpha   myshape
```

```
## 11.074019 -0.132203  2.425930
##
## Log-likelihood: -493.98
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 10.6463386 -0.1874133  2.5174540
##
## Log-likelihood: -484.95
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##           L1           L2        alpha      myshape
## 10.339856834 12.259360151  0.009137354  2.447691595
##
## Log-likelihood: -492.33
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
```

```
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 10.2012548 11.0668466 -0.1643341  2.5266863
##
## Log-likelihood: -484.51
## Best method: bobyqa
```

```
bananaPlot(mod = MUC5AC$HO,
             data = field,
             response = "MUC5AC",
             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.
```




```
MYD88 <- parasiteLoad::analyse(data = field,
                          response = "MYD88",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: MYD88"
## [1] "Fit for the response: MYD88"
```

```
## [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 0.84   1 0.1954896
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.34   1 0.4083067
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 1.16   1 0.1278721
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.03   1 0.794752
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.4   1 0.3697472
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.02   1 0.8281283
## [1] "Testing H1 vs H0"
##    dLL dDF     pvalue
## 1 2.15   1 0.03795947
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 1.97   3 0.2685514
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 1.81   4 0.4594119
```

```
## [1] "Testing H3 vs H2"
##   dLL dDF    pvalue
## 1   2   2 0.1356903
```

```
##All
print(MYD88)
```

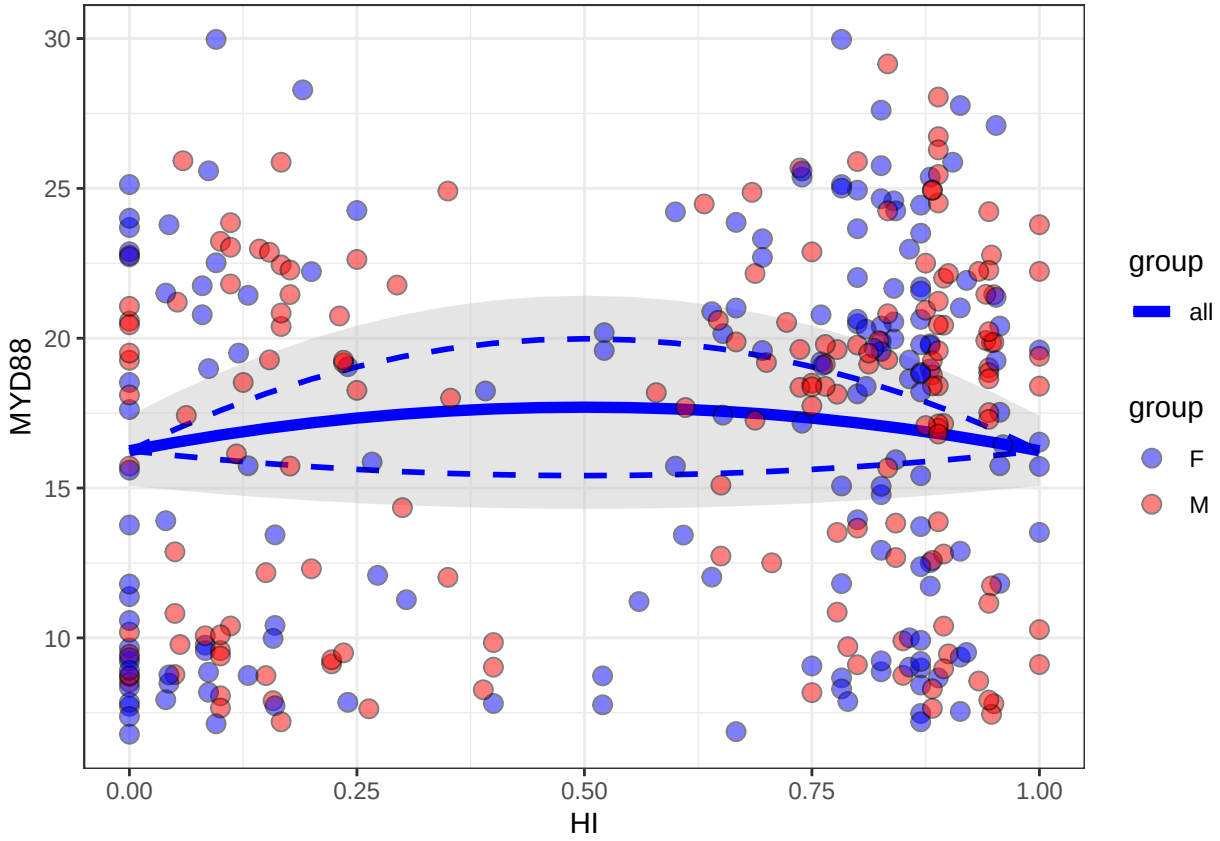
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 16.2449748 -0.1789631  3.2253666
##
## Log-likelihood: -1065.49
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##        L1        L2     alpha   myshape
## 15.517292 17.167621 -0.113392  3.231067
##
## Log-likelihood: -1063.34
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
```

```
##
## Coefficients:
##        L1     alpha   myshape
## 15.512727 -0.325497  2.998869
##
## Log-likelihood: -537.85
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 16.97673995 -0.04590207  3.50886831
##
## Log-likelihood: -525.68
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 15.0069656 16.5977118 -0.2007167  2.9965888
##
## Log-likelihood: -537.03
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
```

```
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 16.06810587 17.67269230 -0.03752719  3.52570849
##
## Log-likelihood: -524.5
## Best method: bobyqa
```

```
bananaPlot(mod = MYD88$H0,
             data = field,
             response = "MYD88",
             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.
```




```
NCR1 <- parasiteLoad::analyse(data = field,
                         response = "NCR1",
                         model = "weibull",
```

```
                          group = "Sex")
```

```
## [1] "Analysing data for response: NCR1"
## [1] "Fit for the response: NCR1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.61   1 0.2684288
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.61   1 0.2705437
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.44   1 0.3504842
## [1] "Testing H2 groupB no alpha vs alpha"
##   dLL dDF   pvalue
## 1 0.2   1 0.529421
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.5   1 0.3186621
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.19   1 0.5359293
## [1] "Testing H1 vs H0"
##   dLL dDF    pvalue
## 1   0   1 0.9321356
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.08   3 0.9840896
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.15   4 0.9894042
## [1] "Testing H3 vs H2"
```

```
##    dLL dDF   pvalue
## 1 0.08   2 0.925101
```

```
##All
print(NCR1)
```

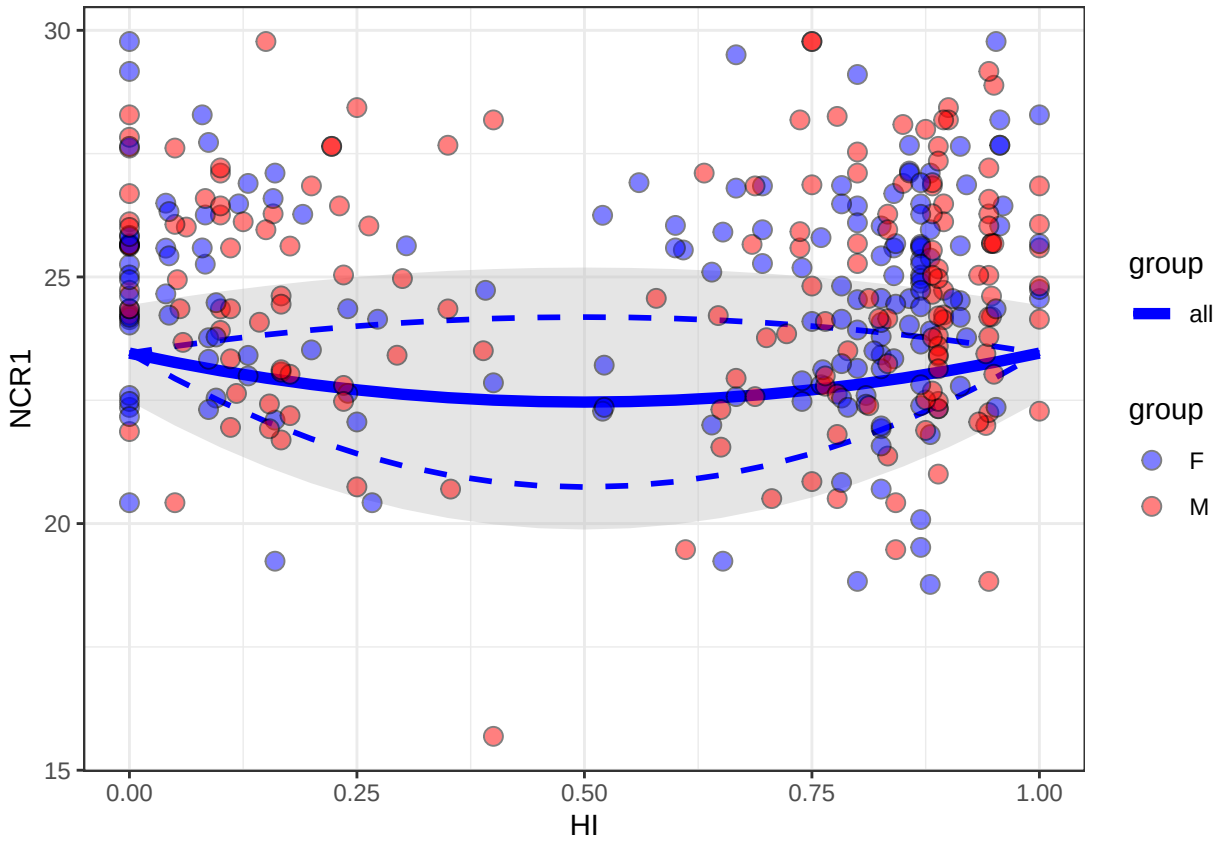
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 23.45565309  0.08461379  5.00000000
##
## Log-likelihood: -901.71
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 23.42698792 23.48902918  0.08586507  5.00000000
##
## Log-likelihood: -901.71
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
```

```
## Coefficients:
##          L1       alpha     myshape
## 23.42834867  0.09654131  5.00000000
##
## Log-likelihood: -447.5
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 23.4720228  0.0712557  5.0000000
##
## Log-likelihood: -454.13
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 23.2822075 23.6564823  0.1087355  5.0000000
##
## Log-likelihood: -447.44
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
```

```
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 23.57272862 23.38949167  0.07033244  5.00000000
##
## Log-likelihood: -454.12
## Best method: bobyqa
```

```
bananaPlot(mod = NCR1$H0,
             data = field,
             response = "NCR1",
             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.
```




```
PRF1 <- parasiteLoad::analyse(data = field,
                          response = "PRF1",
                          model = "weibull",
                          group = "Sex")
```

```
## [1] "Analysing data for response: PRF1"
## [1] "Fit for the response: PRF1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"

## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.21   1 0.5197419
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.08   1 0.6892661
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.18   1 0.5434798
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.04   1 0.7798337
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.06   1 0.7186597
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.04   1 0.7837832
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.74   1 0.2248806
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.04   3 0.9936139
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 0.08   4 0.9972789
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.77   2 0.4631052
```

```
##All
print(PRF1)
```

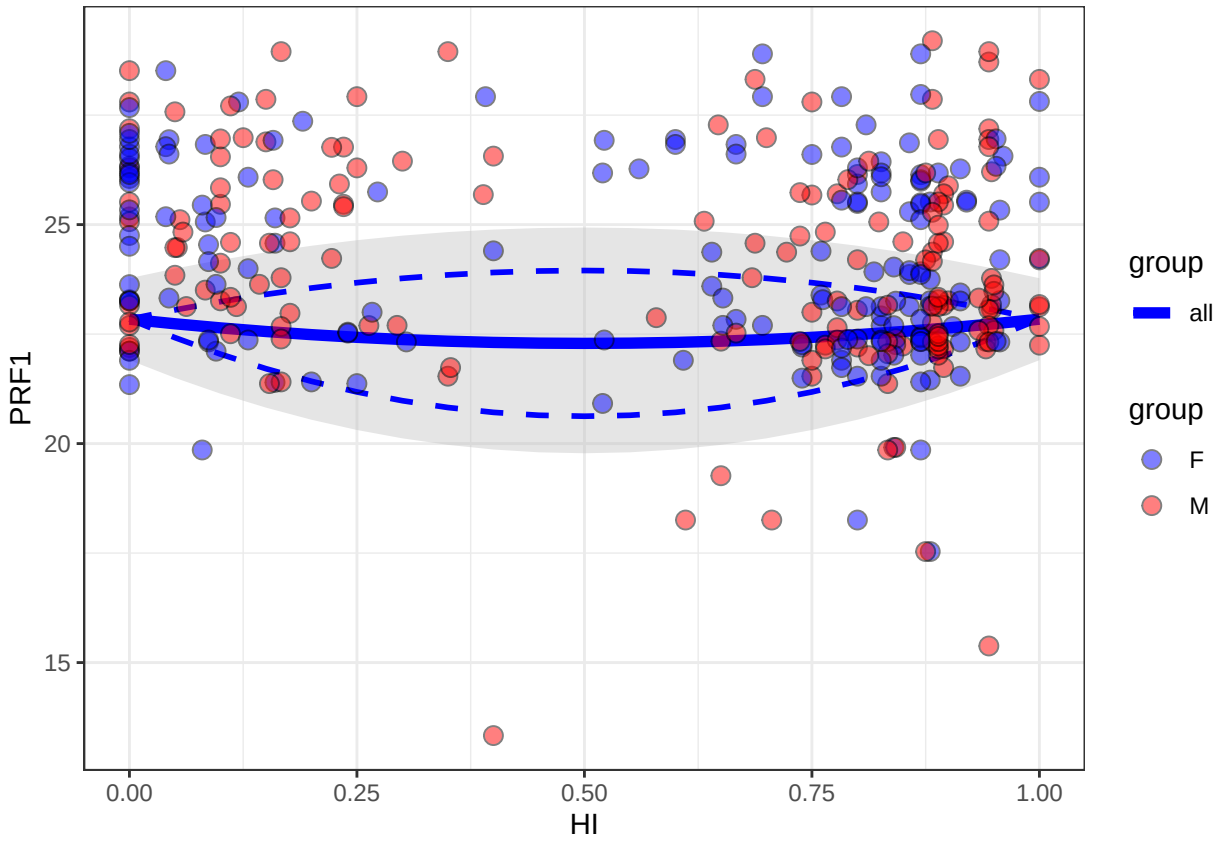
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 22.84079185  0.04837661  5.00000000
##
## Log-likelihood: -898.52
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 23.23025299 22.37680428  0.03098564  5.00000000
##
## Log-likelihood: -897.78
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
```

```
## 22.96223877  0.06104387  5.00000000
##
## Log-likelihood: -446.46
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 22.69765211  0.03171756  5.00000000
##
## Log-likelihood: -452.01
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 23.19047045 22.57642097  0.03912663  5.00000000
##
## Log-likelihood: -446.29
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
```

```
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 23.30272378 22.23436072  0.03143155  5.00000000
##
## Log-likelihood: -451.42
## Best method: bobyqa
```

```
bananaPlot(mod = PRF1$H0,
             data = field,
             response = "PRF1",
             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.
```




```
RETNLB <- parasiteLoad::analyse(data = field,
                         response = "RETNLB",
                         model = "weibull",
                         group = "Sex")
```

```
## [1] "Analysing data for response: RETNLB"
## [1] "Fit for the response: RETNLB"
```

```
## [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 0.9   1 0.1787273
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.59   1 0.2791009
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.25   1 0.4808199
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 1.09   1 0.1406946
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.03   1 0.8109798
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF   pvalue
## 1 1.1   1 0.138904
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.43   1 0.3517452
## [1] "Testing H2 vs H0"
##    dLL dDF     pvalue
## 1 5.33   3 0.01370442
## [1] "Testing H3 vs H1"
##    dLL dDF     pvalue
## 1 5.79   4 0.02076584
```

```
## [1] "Testing H3 vs H2"
##    dLL dDF   pvalue
## 1 0.89   2 0.409547
```

```
##All
print(RETNLB)
```

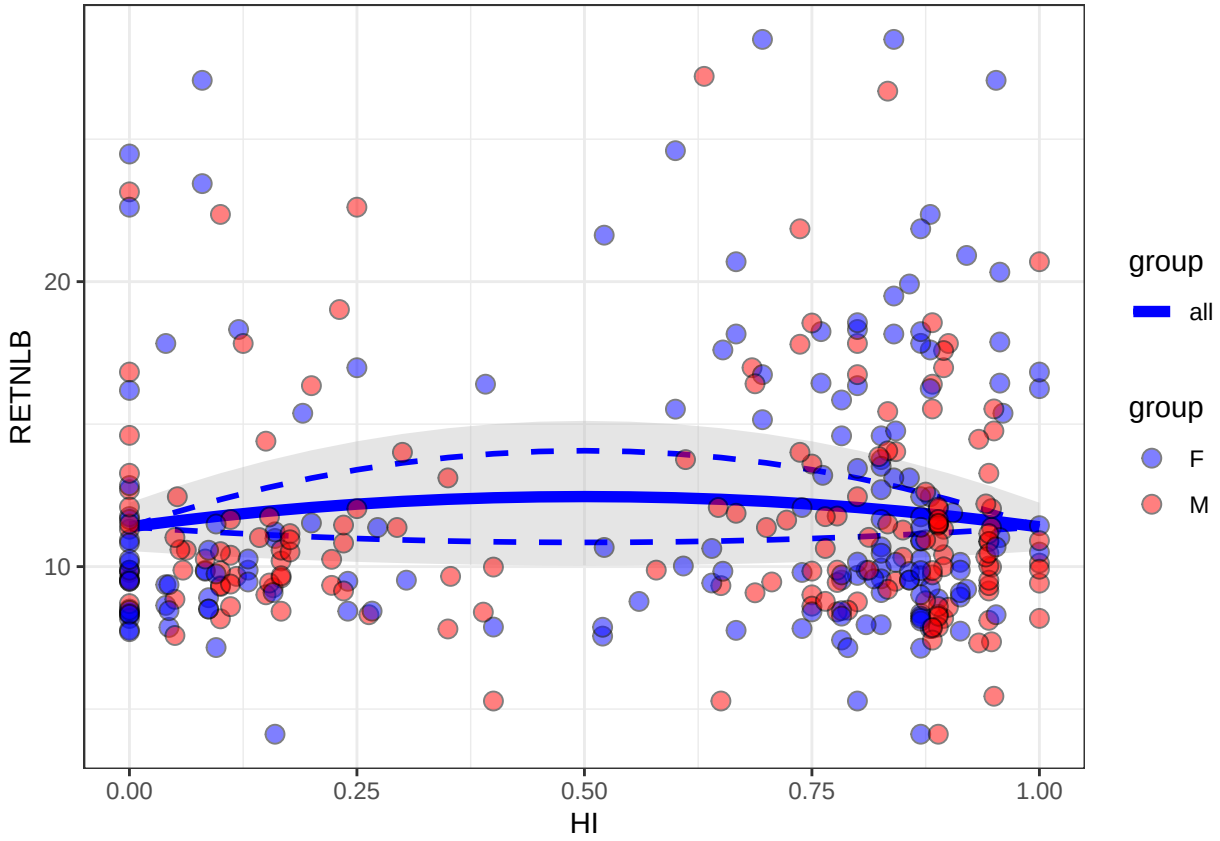
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 11.3947383 -0.1865405  2.7922466
##
## Log-likelihood: -962.16
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 11.1321373 11.7332364 -0.1526044  2.7930403
##
## Log-likelihood: -961.73
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
```

```
##
## Coefficients:
##         L1      alpha    myshape
## 11.8523231 -0.1443193  2.6223194
##
## Log-likelihood: -494.85
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 10.8461275 -0.2702412  3.0775108
##
## Log-likelihood: -461.97
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 11.30938946 12.69408248 -0.04991117  2.62809510
##
## Log-likelihood: -493.97
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
```

```
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 10.9046706 10.7850353 -0.2750895  3.0782814
##
## Log-likelihood: -461.96
## Best method: bobyqa
```

```
bananaPlot(mod = RETNLB$H0,
             data = field,
             response = "RETNLB",
             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.
```




```
SOCS1 <- parasiteLoad::analyse(data = field,
                         response = "SOCS1",
                         model = "weibull",
```

```
                          group = "Sex")
```

```
## [1] "Analysing data for response: SOCS1"
## [1] "Fit for the response: SOCS1"
## [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 0.08   1 0.6968521
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.07   1 0.7032541
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.42   1 0.360933
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.29   1 0.4466131
## [1] "Testing H3 groupA no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.2   1 0.5233439
## [1] "Testing H3 groupB no alpha vs alpha"
##   dLL dDF    pvalue
## 1 0.3   1 0.4411229
## [1] "Testing H1 vs H0"
##   dLL dDF    pvalue
## 1   0   1 0.9997406
## [1] "Testing H2 vs H0"
##    dLL dDF     pvalue
```

```
## 1 3.99   3 0.04652887
## [1] "Testing H3 vs H1"
##    dLL dDF     pvalue
## 1 5.38   4 0.02942989
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 1.39   2 0.2487879
```

```
##All
print(SOCS1)
```

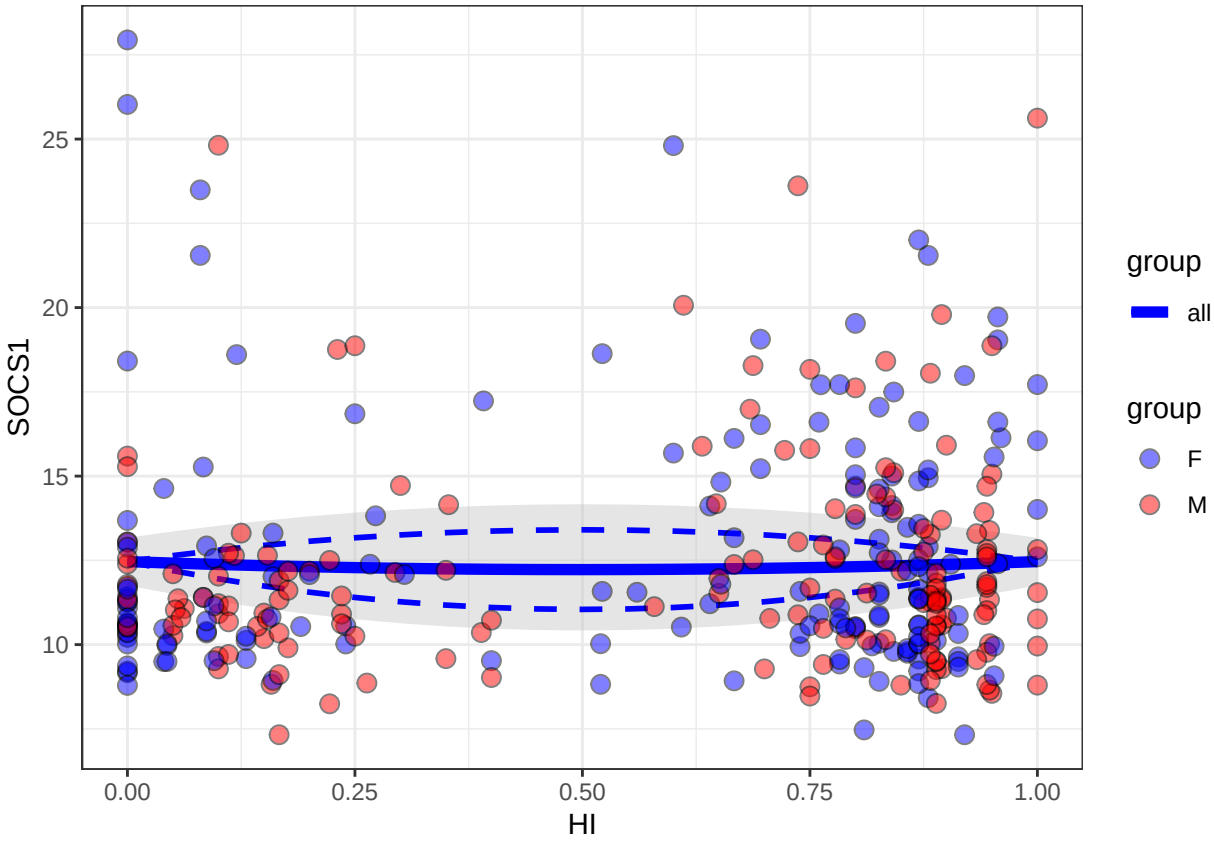
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 12.46259971  0.03805308  3.55748321
##
## Log-likelihood: -896.9
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 12.46251973 12.46269580  0.03806105  3.55747912
##
## Log-likelihood: -896.9
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
```

```
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 13.0228727  0.1240535  3.4356182
##
## Log-likelihood: -458.09
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 11.7576820 -0.1077952  3.7678240
##
## Log-likelihood: -434.82
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 13.27475574 12.67956710  0.09230638  3.45523184
##
## Log-likelihood: -457.85
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
```

```
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 11.1632706 12.1873202 -0.1082272  3.7933302
##
## Log-likelihood: -433.66
## Best method: bobyqa
```

```
bananaPlot(mod = SOCS1$H0,
             data = field,
             response = "SOCS1",
             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.
```



```
TICAM1 <- parasiteLoad::analyse(data = field,
                        response = "TICAM1",
                        model = "weibull",
                        group = "Sex")
```

```
## [1] "Analysing data for response: TICAM1"
## [1] "Fit for the response: TICAM1"
## [1] "Fitting for all"
## [1] "Fitting model basic without alpha"
```

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.02   1 0.8588164
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.03   1 0.8171199
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.52   1 0.3060157
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.93   1 0.1714787
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.22   1 0.5056968
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.88   1 0.1840509
## [1] "Testing H1 vs H0"
##    dLL dDF   pvalue
## 1 0.06   1 0.737448
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 1.49   3 0.3937815
```

```
## [1] "Testing H3 vs H1"
##   dLL dDF    pvalue
## 1 2.4   4 0.3090792
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.96   2 0.3828012
```

```
##All
print(TICAM1)
```

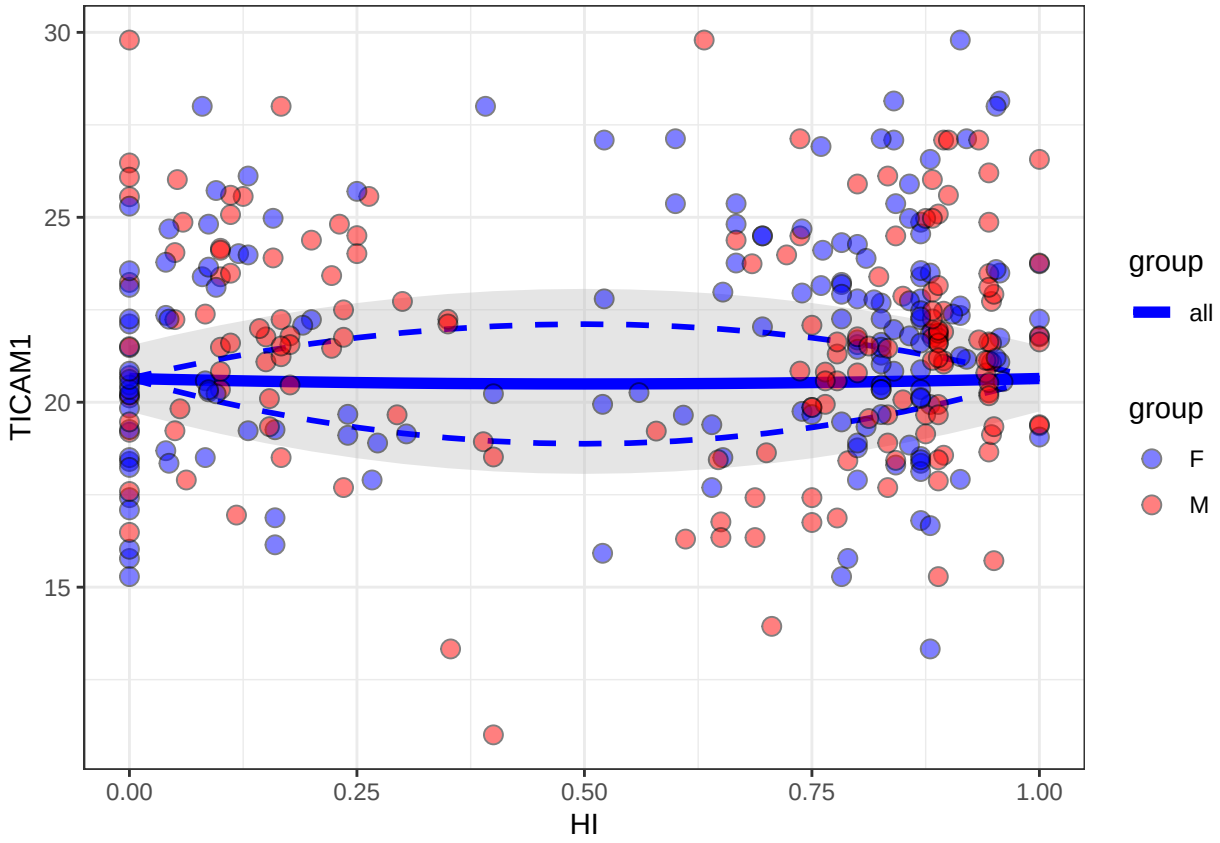
```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.64171054  0.01426967  5.00000000
##
## Log-likelihood: -901.88
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.53982148 20.75369228  0.01875113  5.00000000
##
## Log-likelihood: -901.83
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
```

```
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 20.0896385 -0.1178428  5.0000000
##
## Log-likelihood: -449.44
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1      alpha    myshape
## 21.2451772  0.1543419  5.0000000
##
## Log-likelihood: -450.95
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 19.67850186 20.69393176 -0.07828164  5.00000000
##
## Log-likelihood: -448.82
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
```

```
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##         L1         L2      alpha    myshape
## 21.6600518 20.9055174  0.1512905  5.0000000
##
## Log-likelihood: -450.61
## Best method: bobyqa
```

```
bananaPlot(mod = TICAM1$H0,
             data = field,
             response = "TICAM1",
             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.
```



```
TNF <- parasiteLoad::analyse(data = field,
                         response = "TNF",
                         model = "weibull",
                         group = "Sex")
```

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

```
## Warning in bbmle::mle2(response ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 ~ dweibull(shape = myshape, scale =
## MeanLoad(L1, : 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 0.05   1 0.7411005
## [1] "Testing H1 no alpha vs alpha"
##    dLL dDF   pvalue
## 1 0.04   1 0.781124
## [1] "Testing H2 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.07   1 0.7184082
## [1] "Testing H2 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.36   1 0.3939985
## [1] "Testing H3 groupA no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.01   1 0.8883941
## [1] "Testing H3 groupB no alpha vs alpha"
##    dLL dDF    pvalue
## 1 0.31   1 0.4330952
## [1] "Testing H1 vs H0"
##    dLL dDF    pvalue
## 1 0.03   1 0.8158423
## [1] "Testing H2 vs H0"
##    dLL dDF    pvalue
## 1 0.39   3 0.8550257
```

```
## [1] "Testing H3 vs H1"
##    dLL dDF    pvalue
## 1 1.09   4 0.7034955
## [1] "Testing H3 vs H2"
##    dLL dDF    pvalue
## 1 0.73   2 0.4835663
```

```
##All
print(TNF)
```

```
## $H0
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.86796883  0.02509584  5.00000000
##
## Log-likelihood: -894.53
## Best method: bobyqa
##
## $H1
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.93711560 20.78648789  0.02157473  5.00000000
##
## Log-likelihood: -894.51
## Best method: bobyqa
##
## $H2
## $H2$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
```

```
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 20.60072284 -0.03886658  5.00000000
##
## Log-likelihood: -441.98
## Best method: bobyqa
##
## $H2$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L1, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], alpha = paramBounds[["alphaLB"]],
##         myshape = paramBounds[["myshapeLB"]]), upper = c(L1 = paramBounds[["L1UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1       alpha     myshape
## 21.14988038  0.09140306  5.00000000
##
## Log-likelihood: -452.16
## Best method: bobyqa
##
##
## $H3
## $H3$groupA
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 20.37729319 20.95442949 -0.01586029  5.00000000
##
## Log-likelihood: -441.8
## Best method: bobyqa
##
## $H3$groupB
##
## Call:
## bbmle::mle2(minuslogl = response ~ dweibull(shape = myshape,
```

```
##     scale = MeanLoad(L1, L2, alpha, HI)/gamma(1 + (1/myshape))),
##     start = start, method = config$method, optimizer = config$optimizer,
##     data = data, lower = c(L1 = paramBounds[["L1LB"]], L2 = paramBounds[["L2LB"]],
##         alpha = paramBounds[["alphaLB"]], myshape = paramBounds[["myshapeLB"]]),
##     upper = c(L1 = paramBounds[["L1UB"]], L2 = paramBounds[["L2UB"]],
##         alpha = paramBounds[["alphaUB"]], myshape = paramBounds[["myshapeUB"]]),
##     control = config$control)
##
## Coefficients:
##          L1          L2       alpha     myshape
## 21.65658064 20.71070024  0.08526609  5.00000000
##
## Log-likelihood: -451.62
## Best method: L-BFGS-B
```

```
bananaPlot(mod = TNF$H0,
             data = field,
             response = "TNF",
             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.
```