

Octopamine mediates mating interactions in the house cricket (*Acheta domesticus*)

```
library(dplyr)
library(tidyverse)
library(fields)
library(plotly)
library(broom)

crk_mate <- read.csv("~/Desktop/Cricket experiments/cricketdatathis.csv")
glimpse(crk_mate)
attach(crk_mate)
```

Generalized Linear models

For our collected variables we run a series of generalized linear models to visualize results

```
model_init <- glm(init ~ massdiff + bitediff + glanddiff, data = crk_mate)

model_latency2 <- glm(latency2 ~ bitediff * glanddiff, data = crk_mate)
summary(model_latency2)
```

```
##
## Call:
## glm(formula = latency2 ~ bitediff * glanddiff, data = crk_mate)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4079.9  -1091.2      1.1    917.8   5265.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    9942.19    298.25  33.336 < 2e-16 ***
## bitediff        809.40    2282.90   0.355  0.72391
## glanddiff       86.78     175.50   0.494  0.62242
## bitediff:glanddiff -4475.89    1505.50  -2.973  0.00395 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 3221266)
##
##      Null deviance: 292161034  on 79  degrees of freedom
## Residual deviance: 244816180  on 76  degrees of freedom
## (79 observations deleted due to missingness)
## AIC: 1431.7
##
## Number of Fisher Scoring iterations: 2
```

```
model_matetime2 <-glm(matetime2 ~ massdiff + bitediff * glanddiff, data = crk_mate)
summary(model_matetime2)
```

```
##
## Call:
## glm(formula = matetime2 ~ massdiff + bitediff * glanddiff, data = crk_mate)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -167.88   -29.40   -11.58    49.06   144.67
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      28.74      30.50   0.942  0.35439
## massdiff        -732.29     210.75  -3.475  0.00174 **
## bitediff         136.48     173.34   0.787  0.43794
## glanddiff        -16.98      12.86  -1.320  0.19794
## bitediff:glanddiff  23.20     113.76   0.204  0.83991
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 6152.159)
##
##      Null deviance: 270560  on 31  degrees of freedom
## Residual deviance: 166108  on 27  degrees of freedom
## (127 observations deleted due to missingness)
## AIC: 376.56
##
## Number of Fisher Scoring iterations: 2
```

Logistic Regression Models

Confidence intervals of bite force difference on accessory gland difference on cricket mating outcomes.

```
logit_mated <- glm(mated ~ bitediff + glanddiff, data = crk_mate, family = binomial(link = "logit"))
summary(logit_mated)
```

```
##
## Call:
## glm(formula = mated ~ bitediff + glanddiff, family = binomial(link = "logit"),
##      data = crk_mate)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.6531  -0.4980  -0.3666   2.4974
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.3047      0.4752  -4.85 1.24e-06 ***
## bitediff       5.5047      2.7384   2.01  0.0444 *
## glanddiff     -0.4474      0.1998  -2.24  0.0251 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

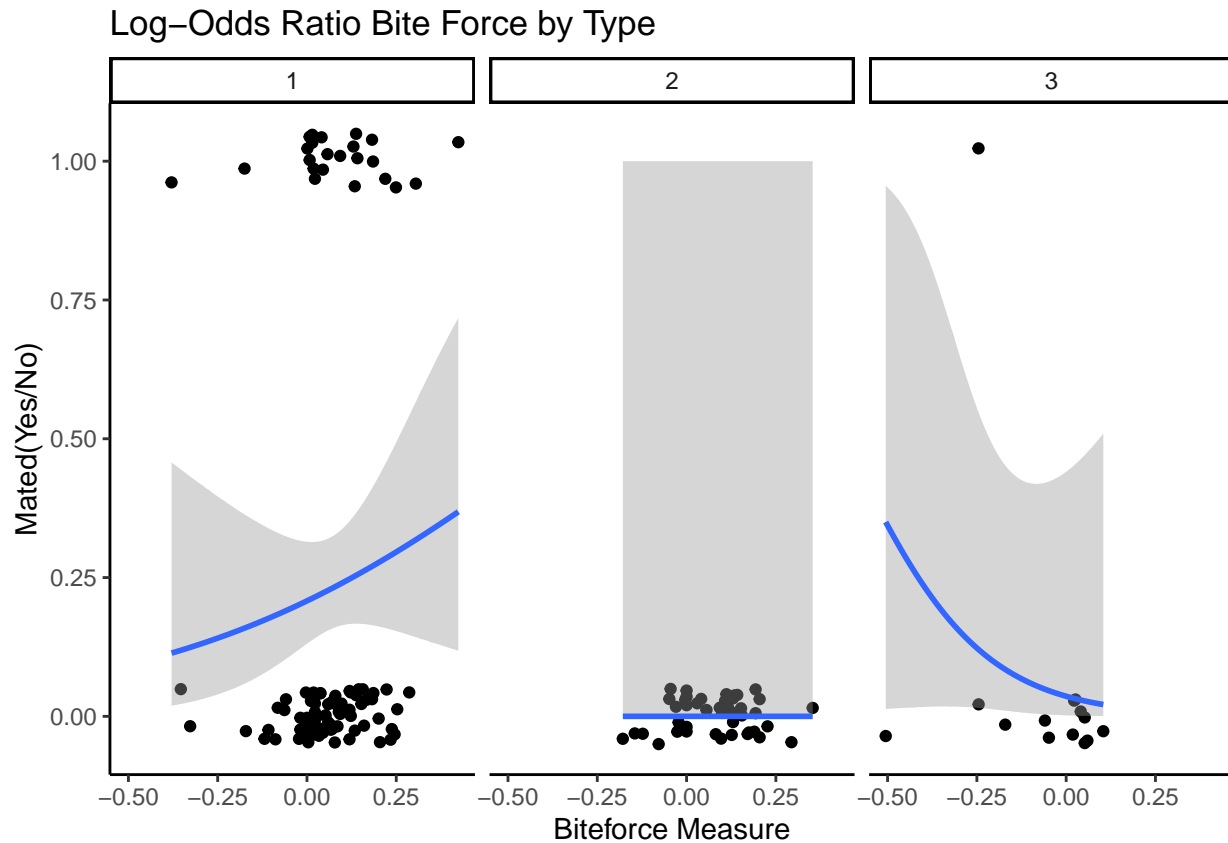
```
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 87.646 on 90 degrees of freedom
## Residual deviance: 79.815 on 88 degrees of freedom
## (68 observations deleted due to missingness)
## AIC: 85.815
##
## Number of Fisher Scoring iterations: 4
tidy(logit_mated, exponentiate = TRUE, conf.int = TRUE)

## # A tibble: 3 x 7
##   term          estimate std.error statistic    p.value conf.low conf.high
##   <chr>          <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)    0.0998    0.475    -4.85 0.00000124  0.0353    0.233
## 2 bitediff      246.        2.74     2.01 0.0444      1.32  73710.
## 3 glanddiff      0.639    0.200    -2.24 0.0251      0.423    0.937

plotsubsets <- ggplot(data = crk_mate, aes(y = mated, x = bitediff, group = type)) +
  geom_jitter(width = 0, height = 0.05) +
  xlab("Biteforce Measure") +
  ylab("Mated(Yes/No)") +
  ggtitle("Log-Odds Ratio Bite Force by Type")

plotsubsets + geom_smooth(method = 'glm',
  method.args = list(binomial(link = 'logit')),
  se = TRUE) + facet_wrap(~type) + theme_classic()

## `geom_smooth()` using formula = 'y ~ x'
```



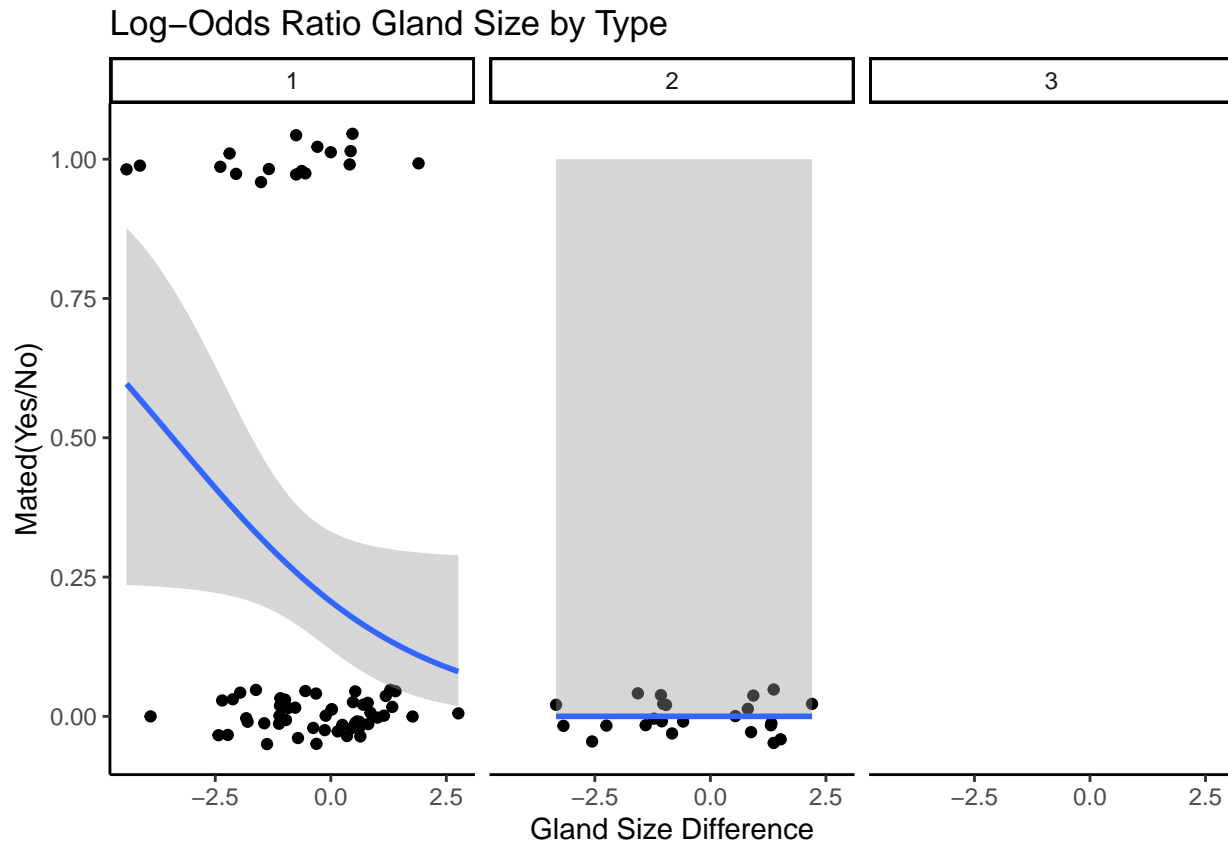
```
plotsubsets0 <- ggplot(data = crk_mate, aes(y = mated, x = glanddiff, group = type)) +
  geom_jitter(width = 0, height = 0.05) +
  xlab("Gland Size Difference") +
  ylab("Mated(Yes/No)") +
  ggtitle("Log-Odds Ratio Gland Size by Type")
```

```
plotsubsets0 + geom_smooth(method = 'glm',
  method.args = list(binomial(link = 'logit')),
  se = TRUE) + facet_wrap(~type) + theme_classic()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 68 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 68 rows containing missing values (`geom_point()`).
```



Surface renderings

```
##fix them use the scale parameter
trials.fitness <- Tps(cbind(bitediff,thoraxdiff),matetime)
summary(trials.fitness)
```

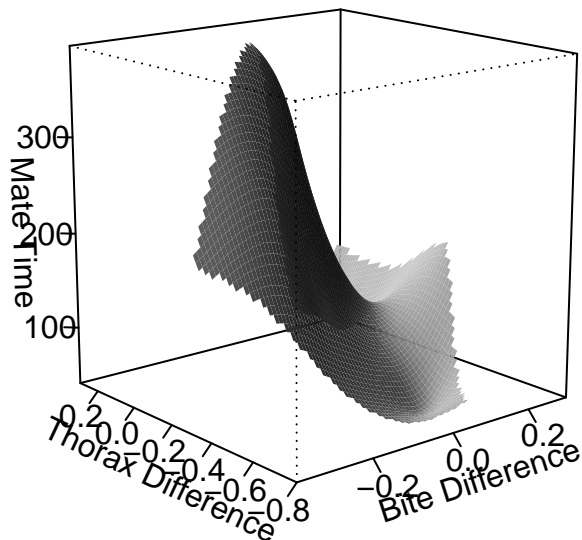
```
## CALL:
## Tps(x = cbind(bitediff, thoraxdiff), Y = matetime)
##
## Number of Observations:          25
## Number of unique points:         25
## Number of parameters in the null space 3
## Parameters for fixed spatial drift 3
## Effective degrees of freedom:      11
## Residual degrees of freedom:       14
## MLE tau                           80.02
## GCV tau                           88.44
## MLE sigma                         3491000
## Scale passed for covariance (sigma) <NA>
## Scale passed for nugget (tau^2)    <NA>
## Smoothing parameter lambda        0.001834
##
## Residual Summary:
##      min    1st Q   median    3rd Q     max
## -142.60  -51.69   11.29   33.95   211.30
```

```
##
## Covariance Model: Rad.cov
## Names of non-default covariance arguments:
##     p
##
## DETAILS ON SMOOTHING PARAMETER:
## Method used:   GCV      Cost: 1
##   lambda      trA      GCV   GCV.one GCV.model   tauHat
## 1.834e-03 1.100e+01 1.396e+04 1.396e+04      NA 8.844e+01
##
## Summary of all estimates found for lambda
##           lambda      trA      GCV tauHat -lnLike Prof converge
## GCV          0.001834 10.996 13963  88.44      136.4      10
## GCV.model      NA      NA      NA      NA      NA      NA
## GCV.one        0.001834 10.996 13963  88.44      NA      10
## RMSE           NA      NA      NA      NA      NA      NA
## pure error      NA      NA      NA      NA      NA      NA
## REML           0.048355  4.289 15463 113.18      136.0      1
```

```
data.output <- predictSurface(trials.fitness)
```

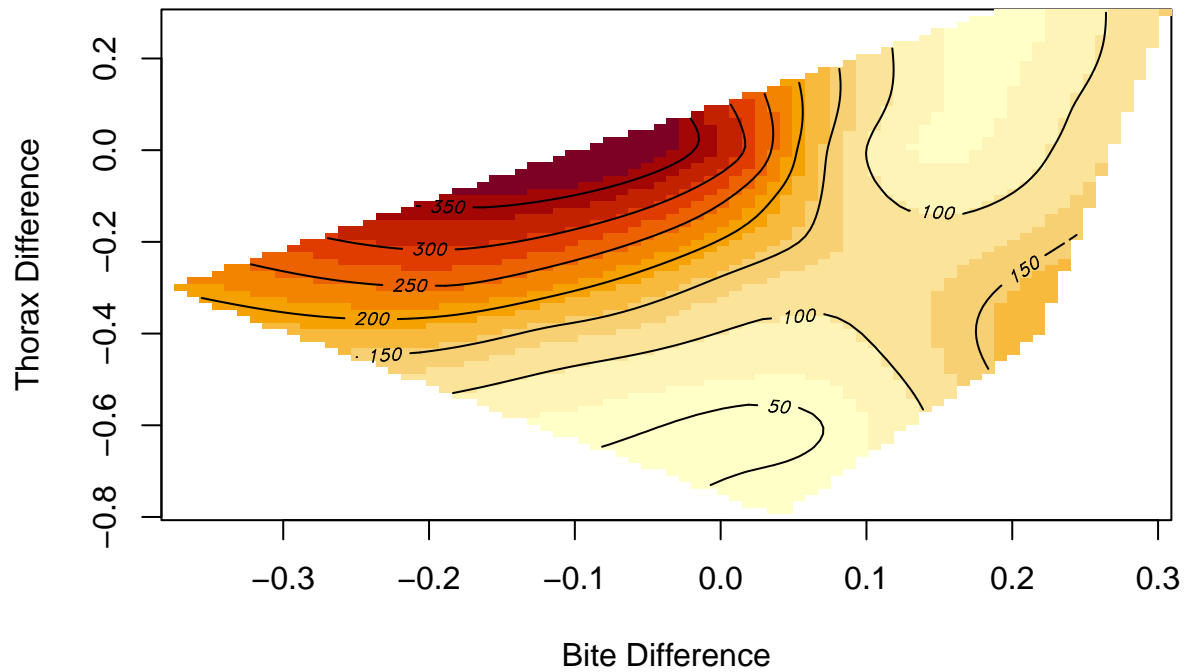
```
persp(data.output,col="lightgrey",border=NA,shade=0.75,theta=320,phi=15,d=5,axes=T,ticktype="detailed",
```

Mating time Differences based on biteforce and thorax width

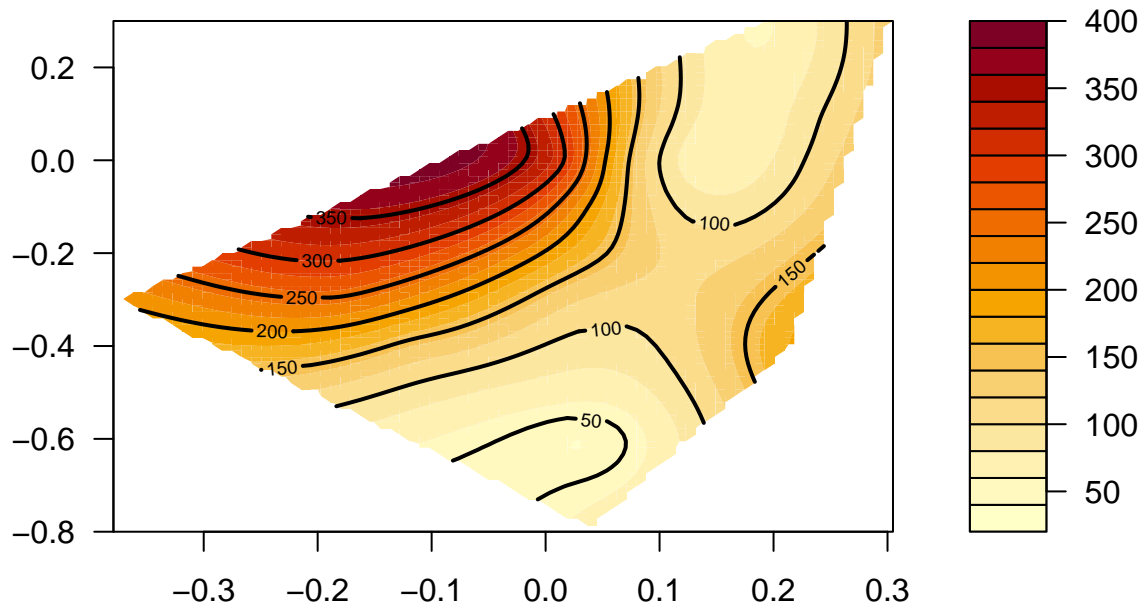


```
image(data.output, xlab="Bite Difference",ylab="Thorax Difference", main="Mating time Differences vs bi
contour(data.output, col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```

Mating time Differences vs biteforce and thorax width



```
filled.contour(data.output, plot.axes = {
  axis(1)
  axis(2)
  contour(data.output, add = TRUE, lwd = 2)
})
```



```
trials.fitness <- Tps(cbind(bitediff, thoraxdiff), matetime)
summary(trials.fitness)
```

CALL:

```

## Tps(x = cbind(bitediff, thoraxdiff), Y = matetime)
##
## Number of Observations:          25
## Number of unique points:         25
## Number of parameters in the null space 3
## Parameters for fixed spatial drift 3
## Effective degrees of freedom:     11
## Residual degrees of freedom:      14
## MLE tau                           80.02
## GCV tau                           88.44
## MLE sigma                         3491000
## Scale passed for covariance (sigma) <NA>
## Scale passed for nugget (tau^2)   <NA>
## Smoothing parameter lambda       0.001834
##
## Residual Summary:
##   min   1st Q  median   3rd Q    max
## -142.60 -51.69  11.29  33.95  211.30
##
## Covariance Model: Rad.cov
##   Names of non-default covariance arguments:
##       p
##
## DETAILS ON SMOOTHING PARAMETER:
## Method used:   GCV   Cost: 1
##   lambda      trA      GCV   GCV.one GCV.model   tauHat
## 1.834e-03 1.100e+01 1.396e+04 1.396e+04      NA 8.844e+01
##
## Summary of all estimates found for lambda
##           lambda      trA      GCV tauHat -lnLike Prof converge
## GCV           0.001834 10.996 13963  88.44      136.4      10
## GCV.model           NA      NA      NA      NA      NA      NA
## GCV.one           0.001834 10.996 13963  88.44      NA      10
## RMSE              NA      NA      NA      NA      NA      NA
## pure error         NA      NA      NA      NA      NA      NA
## REML              0.048355  4.289 15463 113.18      136.0      1

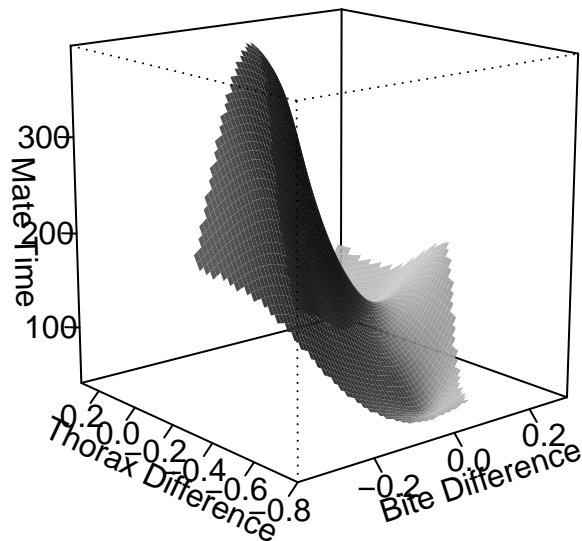
```

```

data.output.g <- predictSurface(trials.fitness)
persp(data.output.g,col="lightgrey",border=NA,shade=0.75,theta=320,phi=15,d=5,axes=T,ticktype="detailed")

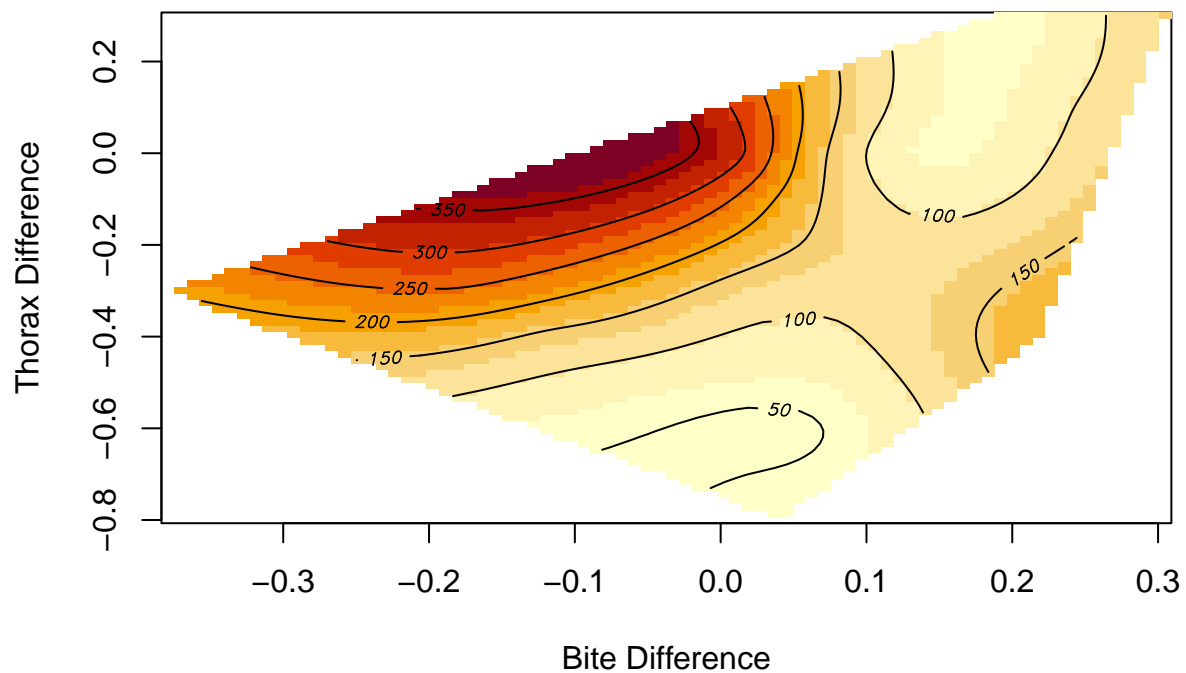
```


Mating time Differences based on biteforce and thorax width

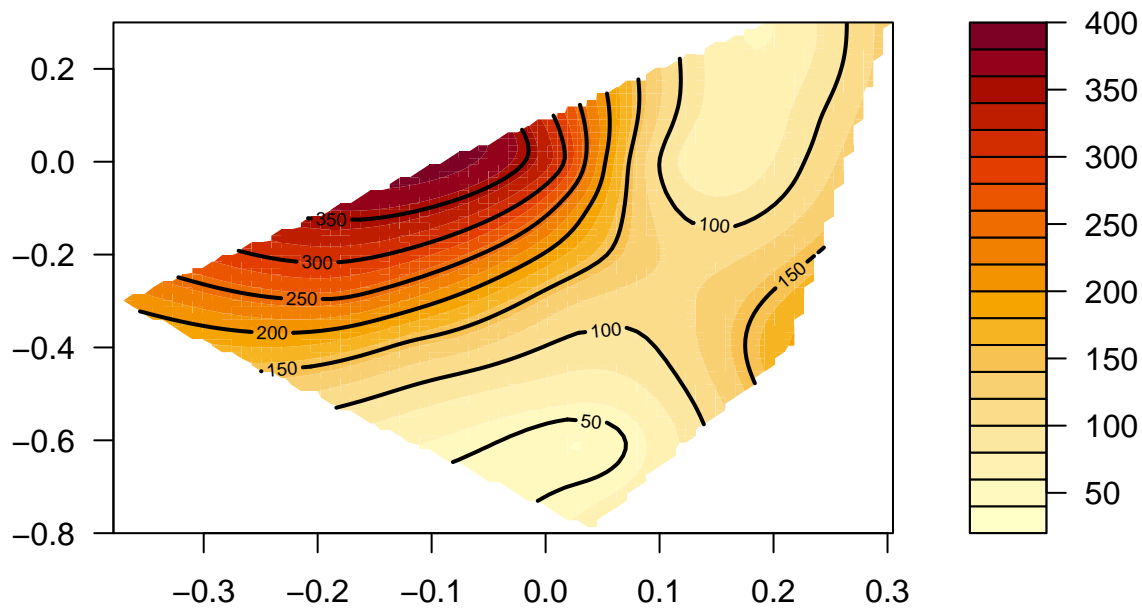


```
image(data.output.g, xlab="Bite Difference", ylab="Thorax Difference", main="Mating time Differences vs l  
contour(data.output.g, col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```

Mating time Differences vs biteforce and thorax width



```
filled.contour(data.output.g, plot.axes = {  
  axis(1)  
  axis(2)  
  contour(data.output.g, add = TRUE, lwd = 2)  
}  
)
```



```
##second pairing
```

```
trials.fitness11 <- Tps(cbind(bitediff,thoraxdiff),matetime2)
```

```
## Warning:
```

```
## Grid searches over lambda (nugget and sill variances) with minima at the endpoints:
```

```
## (GCV) Generalized Cross-Validation
```

```
## minimum at right endpoint lambda = 144.1948 (eff. df= 3.000991 )
```

```
summary(trials.fitness11)
```

```
## CALL:
```

```
## Tps(x = cbind(bitediff, thoraxdiff), Y = matetime2)
```

```
##
```

```
## Number of Observations: 37
```

```
## Number of unique points: 36
```

```
## Number of parameters in the null space 3
```

```
## Parameters for fixed spatial drift 3
```

```
## Effective degrees of freedom: 3
```

```
## Residual degrees of freedom: 34
```

```
## MLE tau 80.18
```

```
## GCV tau 83.77
```

```
## Pure error tau 26.87
```

```
## MLE sigma 44.59
```

```
## Scale passed for covariance (sigma) <NA>
```

```
## Scale passed for nugget (tau^2) <NA>
```

```
## Smoothing parameter lambda 144.2
```

```
##
```

```
## Residual Summary:
```

```
## min 1st Q median 3rd Q max
```

```
## -132.000 -64.870 2.575 64.730 160.700
```

```
##
```

```
## Covariance Model: Rad.cov
```

```
## Names of non-default covariance arguments:
```

```
## p
```

```
##
```

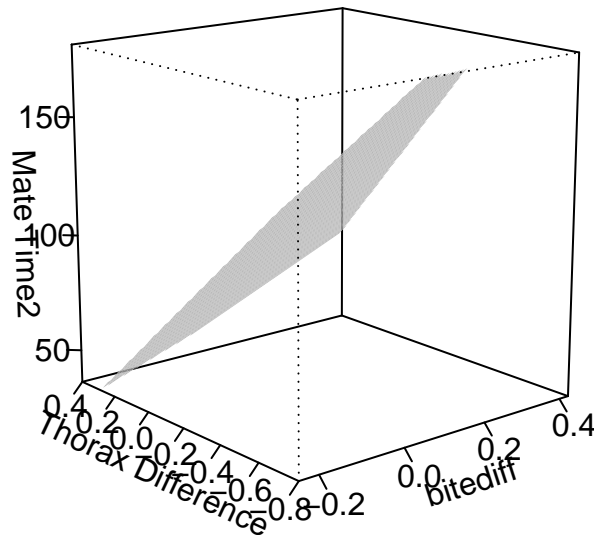
```
## DETAILS ON SMOOTHING PARAMETER:
```

```
## Method used: GCV Cost: 1
## lambda trA GCV GCV.one GCV.model tauHat
## 144.195 3.001 8723.418 7637.218 8586.127 83.772
##
## Summary of all estimates found for lambda
## lambda trA GCV tauHat -lnLike Prof converge
## GCV 1.442e+02 3.001 8723 83.77 193.4 NA
## GCV.model 3.113e-06 34.200 5148 20.00 NA NA
## GCV.one 5.312e-06 33.577 4954 21.41 NA 14
## RMSE NA NA NA NA NA NA
## pure error 1.310e-05 32.245 73293 26.87 206.7 NA
## REML 1.442e+02 3.001 8723 83.77 193.4 NA
```

```
data.output11 <- predictSurface(trials.fitness11)
```

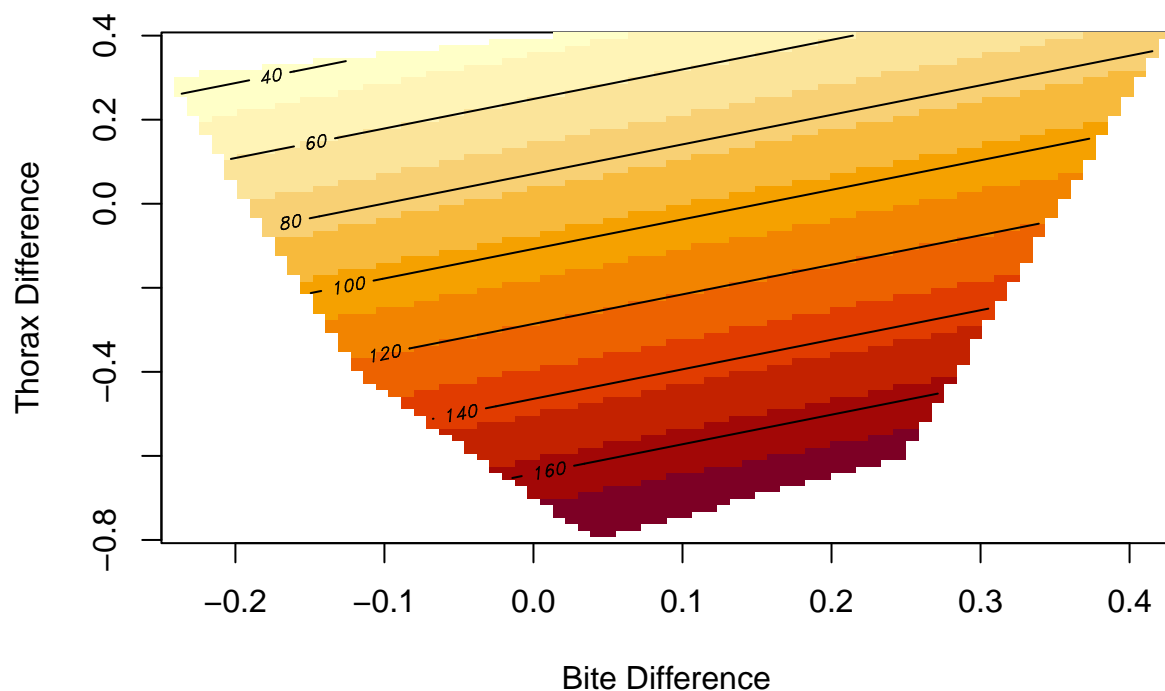
```
persp(data.output11,col="lightgrey",border=NA,shade=0.75,theta=320,phi=15,d=5,axes=T,ticktype="detailed")
```

Mating time Differences of 2nd pairing based on biteforce and thorax v

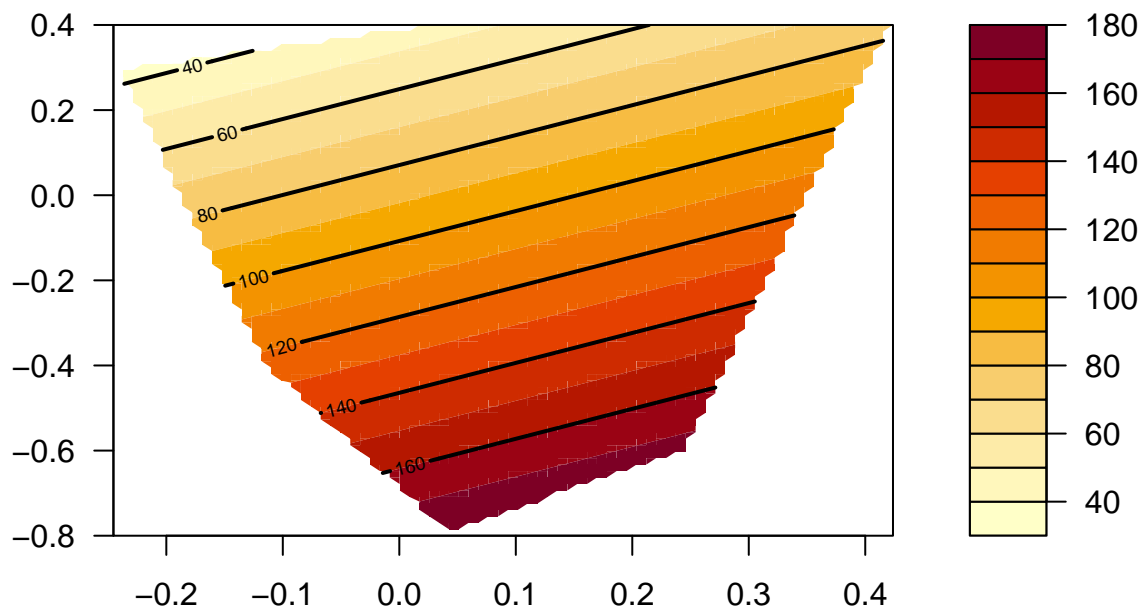


```
image(data.output11, xlab="Bite Difference",ylab="Thorax Difference", main="Mating time Differences of 1",
contour(data.output11, col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```

Mating time Differences of 2nd pairing vs biteforce and thorax width



```
filled.contour(data.output11, plot.axes = {
  axis(1)
  axis(2)
  contour(data.output11, add = TRUE, lwd = 2)
})
```



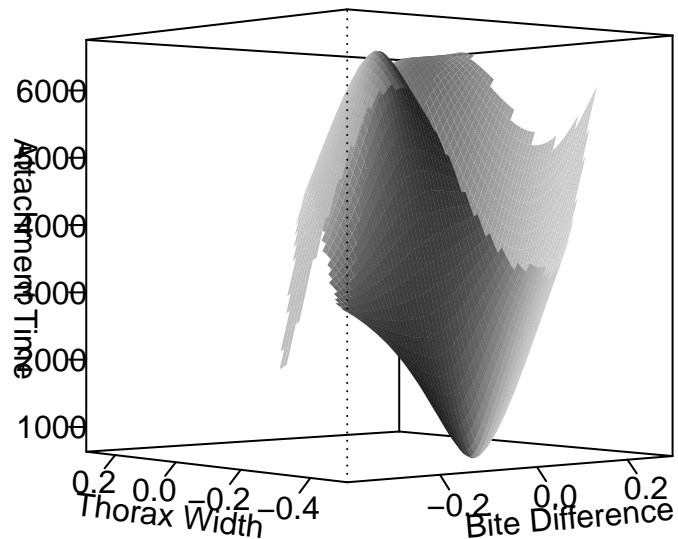
```
#first pairing
trials.fitness0 <- Tps(cbind(bitediff, thoraxdiff), attachtime)
summary(trials.fitness0)
```

```
## CALL:
## Tps(x = cbind(bitediff, thoraxdiff), Y = attachtime)
##
## Number of Observations:          11
## Number of unique points:         11
## Number of parameters in the null space 3
## Parameters for fixed spatial drift 3
## Effective degrees of freedom:      8.4
## Residual degrees of freedom:       2.6
## MLE tau                           919.4
## GCV tau                           1109
## MLE sigma                         1.655e+09
## Scale passed for covariance (sigma) <NA>
## Scale passed for nugget (tau^2)    <NA>
## Smoothing parameter lambda        0.0005106
##
## Residual Summary:
##      min      1st Q      median      3rd Q      max
## -1126.0000 -185.7000  -0.9822   314.7000   753.4000
##
## Covariance Model: Rad.cov
## Names of non-default covariance arguments:
##      p
##
## DETAILS ON SMOOTHING PARAMETER:
## Method used:  GCV      Cost: 1
##      lambda      trA      GCV      GCV.one GCV.model      tauHat
## 5.106e-04 8.447e+00 5.295e+06 5.295e+06      NA 1.109e+03
##
## Summary of all estimates found for lambda
##      lambda      trA      GCV tauHat -lnLike Prof converge
## GCV      5.106e-04 8.447 5295370 1109      74.38      19
## GCV.model      NA      NA      NA      NA      NA      NA
## GCV.one      5.106e-04 8.447 5295370 1109      NA      19
## RMSE      NA      NA      NA      NA      NA      NA
## pure error      NA      NA      NA      NA      NA      NA
## REML      4.856e+01 3.001 8778486 2527      74.03      NA

data.output0 <- predictSurface(trials.fitness0)

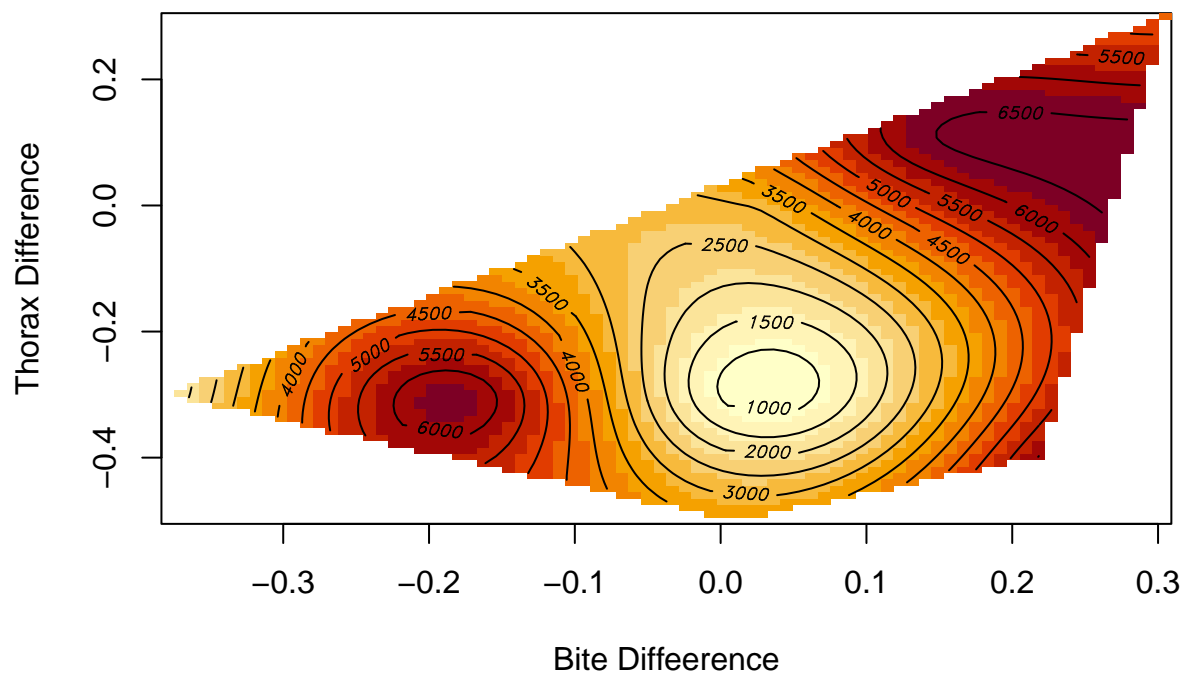
persp(data.output0,col="lightgrey",border=NA,shade=0.75,theta=320,phi=360,d=5,axes=T,ticktype="detailed")
```

Attachment time Differences based on Bite Force and Thorax Width

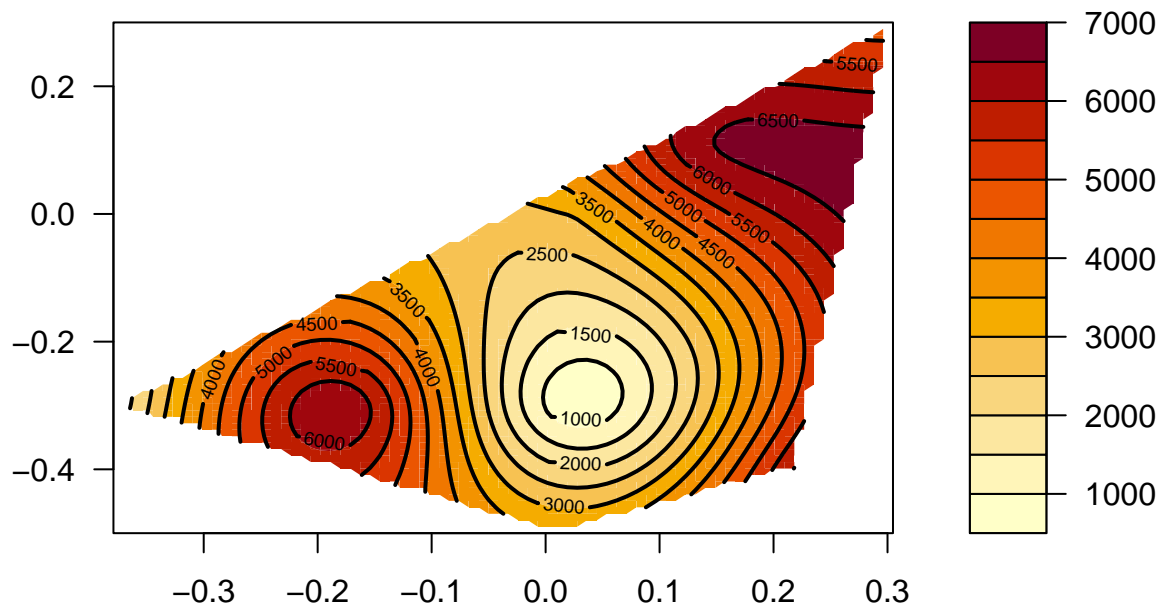


```
image(data.output0, xlab="Bite Difference", ylab="Thorax Difference", main="Attachment time Differences vs biteforce and thorax width", col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```

Attachment time Differences vs biteforce and thorax width



```
filled.contour(data.output0, plot.axes = {
  axis(1)
  axis(2)
  contour(data.output0, add = TRUE, lwd = 2)
})
```



#2nd pairing

```
trials.fitness00 <- Tps(cbind(bitediff,thoraxdiff),attachtime2)
summary(trials.fitness00)
```

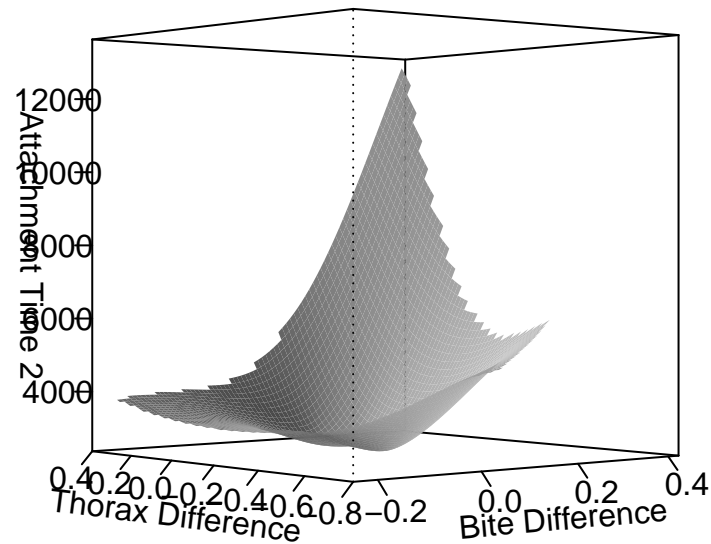
```
## CALL:
## Tps(x = cbind(bitediff, thoraxdiff), Y = attachtime2)
##
## Number of Observations:      15
## Number of unique points:     15
## Number of parameters in the null space 3
## Parameters for fixed spatial drift 3
## Effective degrees of freedom: 6.5
## Residual degrees of freedom: 8.5
## MLE tau      2084
## GCV tau      2254
## MLE sigma    717100000
## Scale passed for covariance (sigma) <NA>
## Scale passed for nugget (tau^2) <NA>
## Smoothing parameter lambda    0.006059
##
## Residual Summary:
##      min   1st Q   median   3rd Q    max
## -2778.0 -1363.0   240.3  1279.0  2432.0
##
## Covariance Model: Rad.cov
## Names of non-default covariance arguments:
##      p
##
## DETAILS ON SMOOTHING PARAMETER:
## Method used:  GCV    Cost: 1
##      lambda      trA      GCV  GCV.one GCV.model   tauHat
## 6.059e-03 6.460e+00 8.925e+06 8.925e+06      NA 2.254e+03
##
## Summary of all estimates found for lambda
##      lambda      trA      GCV tauHat -lnLike Prof converge
```

```
## GCV      0.006059 6.460 8925412 2254      112.9      17
## GCV.model      NA      NA      NA      NA      NA      NA
## GCV.one  0.006059 6.460 8925412 2254      NA      17
## RMSE      NA      NA      NA      NA      NA      NA
## pure error      NA      NA      NA      NA      NA      NA
## REML      0.004118 7.062 9010481 2184      112.8      2
```

```
data.output00 <- predictSurface(trials.fitness00)
```

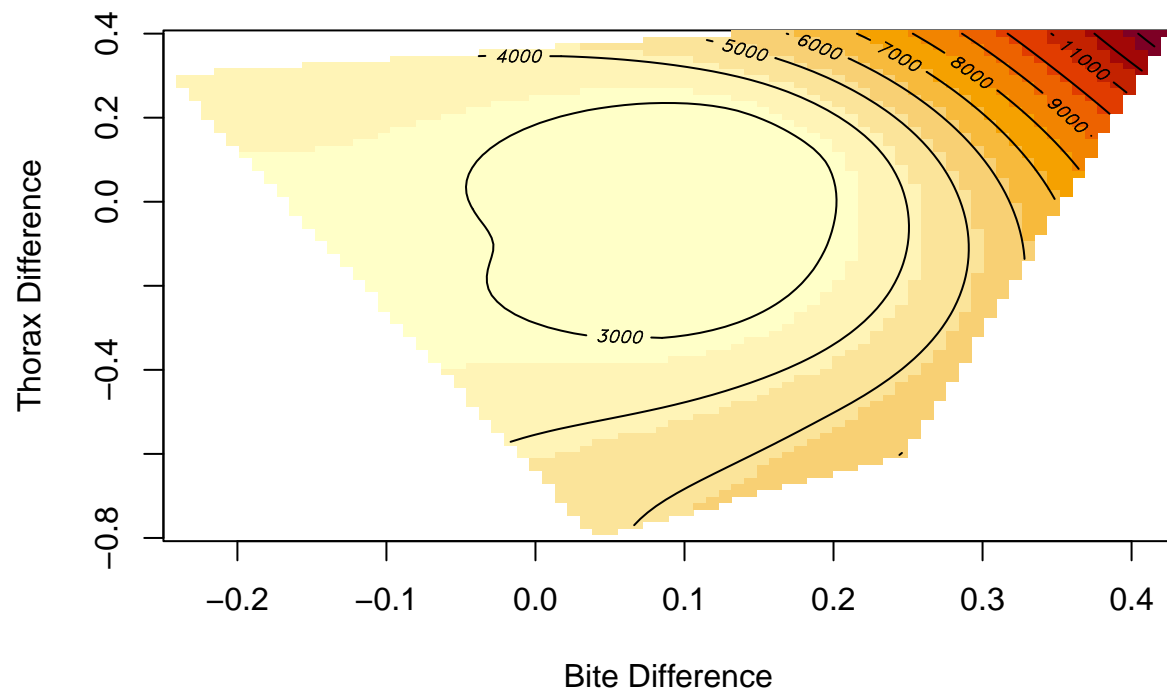
```
persp(data.output00,col="lightgrey",border=NA,shade=0.75,theta=320,phi=360,d=5,axes=T,ticktype="detailed")
```

Attachment time Differences of 2nd pairing based on bite force and thorax

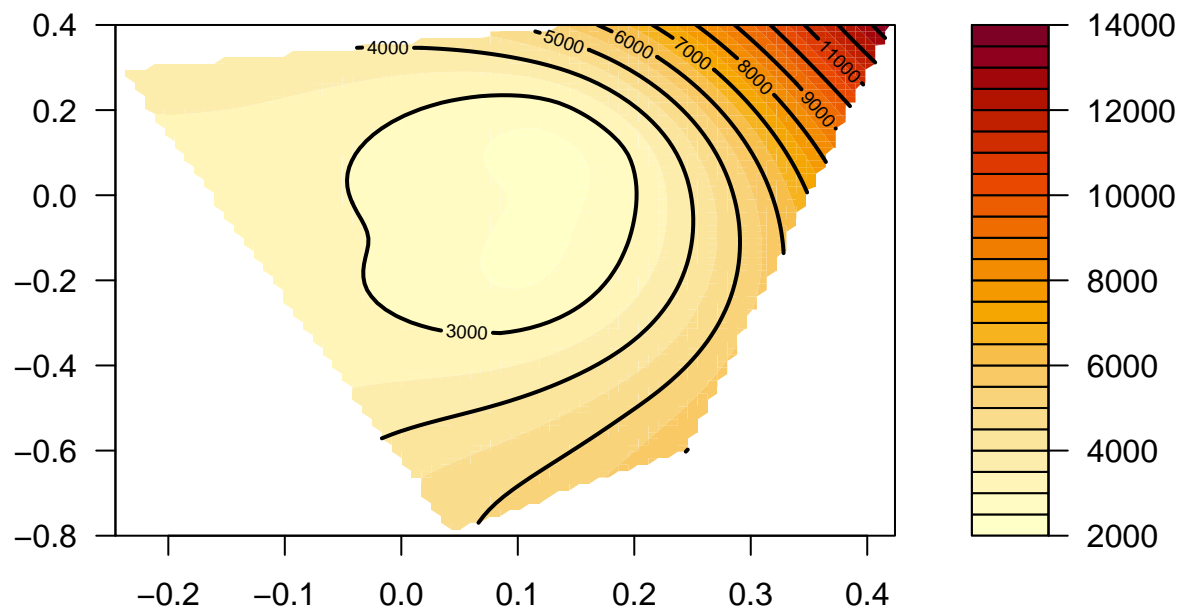


```
image(data.output00, xlab="Bite Difference",ylab="Thorax Difference", main="Attachment time Differences of 2nd pairing based on bite force and thorax",
contour(data.output00,col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```


Attachment time Differences of 2nd pairing vs Bite Force and Thorax V



```
filled.contour(data.output00, plot.axes = {
  axis(1)
  axis(2)
  contour(data.output00, add = TRUE, lwd = 2)
})
```



```
##initiation times compared with biteforce and thorax parameters
trials.fitnessa <- Tps(cbind(bitediff,thoraxdiff),init)
summary(trials.fitnessa)
```

```

## CALL:
## Tps(x = cbind(bitediff, thoraxdiff), Y = init)
##
## Number of Observations:          27
## Number of unique points:         27
## Number of parameters in the null space 3
## Parameters for fixed spatial drift 3
## Effective degrees of freedom:      6.6
## Residual degrees of freedom:       20.4
## MLE tau                           2114
## GCV tau                           2257
## MLE sigma                         3.32e+08
## Scale passed for covariance (sigma) <NA>
## Scale passed for nugget (tau^2)    <NA>
## Smoothing parameter lambda        0.01347
##
## Residual Summary:
##      min   1st Q   median   3rd Q    max
## -4175.0 -1397.0   633.3  1524.0  2790.0
##
## Covariance Model: Rad.cov
## Names of non-default covariance arguments:
##      p
##
## DETAILS ON SMOOTHING PARAMETER:
## Method used:   GCV   Cost: 1
##      lambda      trA      GCV   GCV.one GCV.model   tauHat
## 1.347e-02 6.602e+00 6.742e+06 6.742e+06      NA 2.257e+03
##
## Summary of all estimates found for lambda
##      lambda      trA      GCV tauHat -lnLike Prof converge
## GCV      0.01347 6.602 6741811 2257      221.7      17
## GCV.model      NA      NA      NA      NA      NA      NA
## GCV.one      0.01347 6.602 6741811 2257      NA      17
## RMSE      NA      NA      NA      NA      NA      NA
## pure error      NA      NA      NA      NA      NA      NA
## REML      0.02025 5.831 6761418 2302      221.7      3

```

```

data.outputa <- predictSurface(trials.fitnessa)

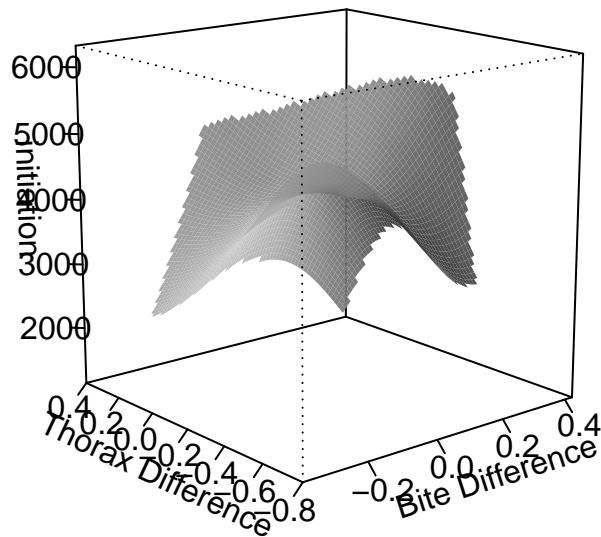
```

```

persp(data.outputa,col="lightgrey",border=NA,shade=0.75,theta=320,phi=15,d=5,axes=T,ticktype="detailed"

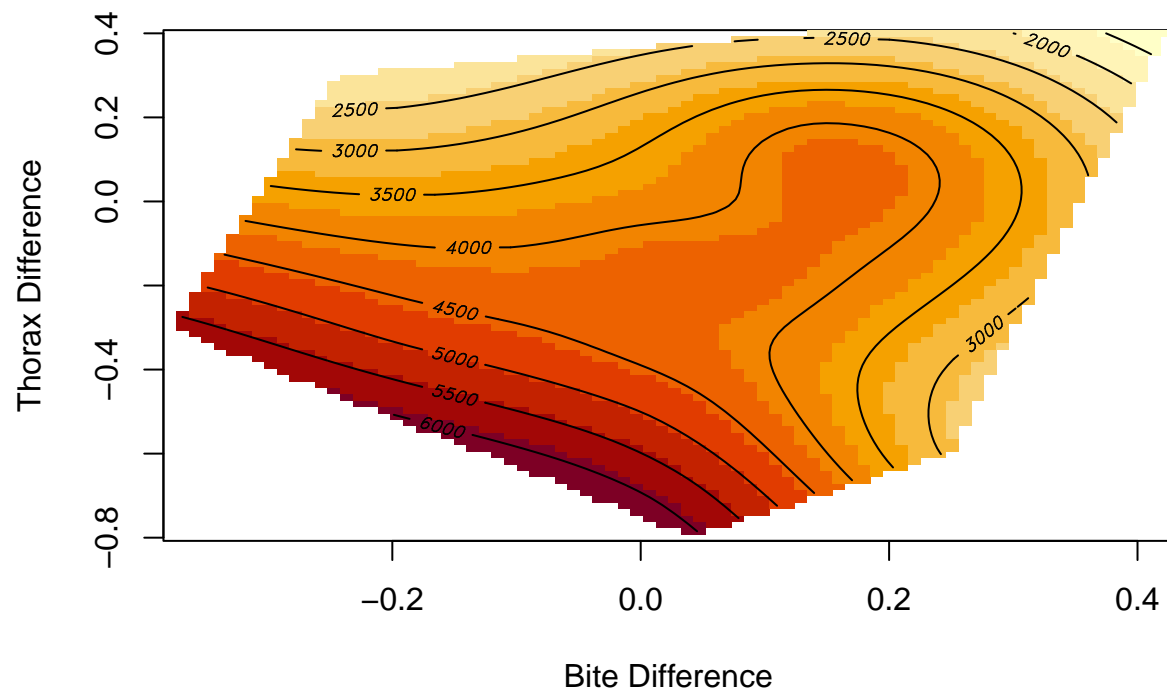
```

Initiation time of mating based on biteforce and thorax width



```
image(data.outputa, xlab="Bite Difference", ylab="Thorax Difference", main="Initiation time of mating vs  
contour(data.outputa, col = "black", add=T, labelcex = 7, vfont=c("sans serif", "bold italic"))
```

Initiation time of mating vs biteforce and thorax width



```
filled.contour(data.outputa, plot.axes = {  
  axis(1)  
  axis(2)  
  contour(data.outputa, add = TRUE, lwd = 2)  
})
```

