```r
# title: Diagnosis and spatial and competiton models in forest
genetic trials using breedR: an example in Douglas-fir
# author: Eduardo Pablo Cappa
# date: "June 26th, 2015"

#install.packages('devtools')
#library(devtools)
#install_github('famuvie/breedR', ref = github_release())
#install_github('famuvie/breedR')

library(breedR)

## Loading required package: sp

# 1. DATA
data<-douglas
head(data)

##    self dad mum orig site block  x    y H02 H03 H04 H05 C13   AN   BR
## 1  135  41  21   pA   s1 s1:11  6   81  NA  NA  NA 634 586 <NA> <NA>
## 2  136  41  21   pA   s1 s1:44 27  135  NA  NA  NA 581 474 <NA> <NA>
## 3  137  41  21   pA   s1 s1:24 45   90  NA  NA  NA 611 715 <NA> <NA>
## 4  138  41  21   pA   s1 s1:28 57   45  NA  NA  NA 370 372 <NA> <NA>
## 5  139  41  21   pA   s1 s1:13 57  327  NA  NA  NA 721 665 <NA> <NA>
## 6  140  41  21   pA   s1 s1:35 60  474  NA  NA  NA 488 558 <NA> <NA>

str(data)

## 'data.frame':    9630 obs. of  15 variables:
##  $ self : num  135 136 137 138 139 140 141 142 143 144 ...
##  $ dad  : num  41 41 41 41 41 41 41 41 41 41 ...
##  $ mum  : num  21 21 21 21 21 21 21 21 21 21 ...
##  $ orig : Factor w/ 11 levels "pA","pB","pC",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ site : Factor w/ 3 levels "s1","s2","s3": 1 1 1 1 1 1 1 1 1 1 ...
##  $ block: Factor w/ 127 levels "s1:1","s1:2",..: 11 44 24 28 13 35 8 40 3 15 ...
##  $ x    : num  6 27 45 57 57 60 63 66 66 75 ...
##  $ y    : num  81 135 90 45 327 474 450 21 234 483 ...
##  $ H02  : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ H03  : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ H04  : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ H05  : int  634 581 611 370 721 488 574 498 528 620 ...
##  $ C13  : int  586 474 715 372 665 558 490 372 527 612 ...
##  $ AN   : Factor w/ 5 levels "1","2","3","4",..: NA NA NA NA NA NA NA NA NA NA ...
##  $ BR   : Factor w/ 5 levels "1","2","3","4",..: NA NA NA NA NA NA NA NA NA NA ...

# 1.1. Choose the site to be analysed
data<-droplevels(subset(douglas, site == "s3"))
head(data)
```

```
##        self dad mum orig site block    x     y H02 H03 H04 H05 C13 AN BR
## 8172 8306  41  21   pA   s3 s3:11 17.5 101.5 260 337 388  NA 481  2  3
## 8173 8307  41  21   pA   s3 s3:24 30.0 143.5 197 231 268  NA 457  4  3
## 8174 8308  41  21   pA   s3  s3:7 40.0 189.0 108 138 163  NA 151  4  3
## 8175 8309  41  21   pA   s3 s3:16 42.5 115.5 252 324 387  NA 514  4  2
## 8176 8310  41  21   pA   s3 s3:14 85.0   0.0 262 299 337  NA 417  3  3
## 8177 8311  41  21   pA   s3 s3:15 85.0  84.0 310 395 476  NA 632  3  3
```

```r
str(data)
```

```
## 'data.frame':    1459 obs. of  15 variables:
##  $ self : num  8306 8307 8308 8309 8310 ...
##  $ dad  : num  41 41 41 41 41 41 41 41 41 41 ...
##  $ mum  : num  21 21 21 21 21 21 21 21 21 21 ...
##  $ orig : Factor w/ 9 levels "pA","pB","pC",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ site : Factor w/ 1 level "s3": 1 1 1 1 1 1 1 1 1 1 1 1 ...
##  $ block: Factor w/ 34 levels "s3:1","s3:2",..: 11 24 7 16 14 15 23 17 33 13 ...
##  $ x    : num  17.5 30 40 42.5 85 ...
##  $ y    : num  102 144 189 116 0 ...
##  $ H02  : int  260 197 108 252 262 310 290 208 128 147 ...
##  $ H03  : int  337 231 138 324 299 395 364 270 155 193 ...
##  $ H04  : int  388 268 163 387 337 476 442 305 171 214 ...
##  $ H05  : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ C13  : int  481 457 151 514 417 632 550 338 121 221 ...
##  $ AN   : Factor w/ 5 levels "1","2","3","4",..: 2 4 4 4 3 3 3 3 2 3 ...
##  $ BR   : Factor w/ 5 levels "1","2","3","4",..: 3 3 3 2 3 3 4 3 3 3 ...
```

```r
# 1.2. Description of the data
library(psych)
suppressWarnings(describe(data))
```

```
##         vars    n    mean     sd median trimmed    mad  min  max range
## self       1 1459 9035.00 421.32 9035.0 9035.00 541.15 8306 9764  1458
## dad        2  635   52.52  25.13   51.0   49.22  22.24   19  117    98
## mum        3 1459   65.96  48.94   59.0   65.52  72.65    1  133   132
## orig*      4 1459     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
## site*      5 1459     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
## block*     6 1459     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
## x          7 1459  117.67  48.65  120.0  120.65  48.18    0  210   210
## y          8 1459   64.96  44.19   59.5   62.49  51.89    0  196   196
## H02        9 1445  244.54  64.60  251.0  246.97  65.23   51  424   373
## H03       10 1446  303.63  79.36  310.5  306.75  80.80   63  513   450
## H04       11 1459  345.73  96.49  352.0  349.07  97.85   62  610   548
## H05       12    0     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
## C13       13 1403  453.56 150.79  470.0  458.80 157.16   36  825   789
## AN*       14 1401     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
## BR*       15 1401     NaN     NA     NA     NaN     NA  Inf -Inf  -Inf
##         skew kurtosis    se
## self    0.00    -1.20 11.03
## dad     1.06     0.84  1.00
## mum     0.17    -1.60  1.28
```

```
## orig*      NA       NA    NA
## site*      NA       NA    NA
## block*     NA       NA    NA
## x        -0.46    -0.21  1.27
## y         0.53    -0.36  1.16
## H02      -0.35    -0.18  1.70
## H03      -0.35    -0.24  2.09
## H04      -0.29    -0.23  2.53
## H05        NA       NA    NA
## C13      -0.29    -0.41  4.03
## AN*        NA       NA    NA
## BR*        NA       NA    NA
```

```r
# 1.3. Choose the phenotype to be analysed
data$phe_X <-data$C13

# 1.4. Remove missing values
data<- subset(data, phe_X != "NA")
head(data)
```

```
##       self dad mum orig site block    x     y H02 H03 H04 H05 C13 AN BR
## 8172 8306  41  21   pA   s3 s3:11 17.5 101.5 260 337 388  NA 481  2  3
## 8173 8307  41  21   pA   s3 s3:24 30.0 143.5 197 231 268  NA 457  4  3
## 8174 8308  41  21   pA   s3  s3:7 40.0 189.0 108 138 163  NA 151  4  3
## 8175 8309  41  21   pA   s3 s3:16 42.5 115.5 252 324 387  NA 514  4  2
## 8176 8310  41  21   pA   s3 s3:14 85.0   0.0 262 299 337  NA 417  3  3
## 8177 8311  41  21   pA   s3 s3:15 85.0  84.0 310 395 476  NA 632  3  3
##      phe_X
## 8172   481
## 8173   457
## 8174   151
## 8175   514
## 8176   417
## 8177   632
```

```r
# 1.5. Some plots of the data
par(mfrow = c(2, 2))
plot(data$phe_X)
hist(data$phe_X)
qqnorm(data$phe_X)
boxplot(data$phe_X)
```

Histogram of data$phe_X

Normal Q-Q Plot
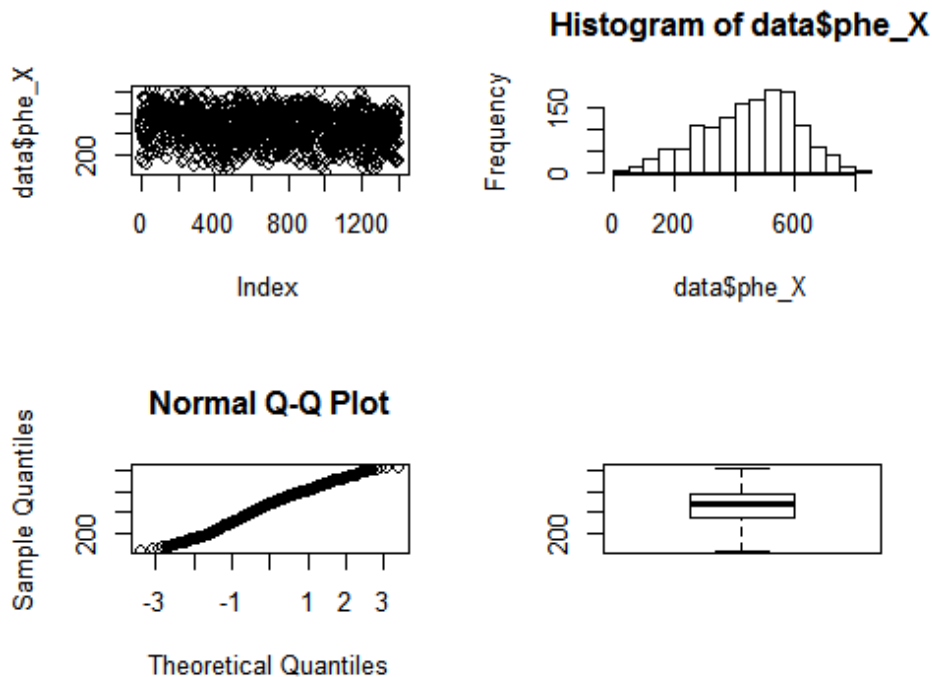
```
# 2.REGULAR ANALISIS FAMILY MODEL: The family additive model with block design
effects
res.stdflia <- remlf90(fixed = phe_X ~ orig,
                       random = ~ block + factor(mum),
                       data = data,
                       method = 'em') # either 'em' or 'ai'

## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.

summary(res.stdflia)

## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##     Data: data
##     AIC     BIC logLik
##   17885 unknown   -8940
##
## Parameters of special components:
##
##
## Variance components:
##             Estimated variances
## block                       1087
## factor(mum)                 1774
## Residual                   19910
##
## Fixed effects:
```

```
##          value    s.e.
## orig.pA 471.86 12.470
## orig.pB 501.58 19.925
## orig.pC 435.97 27.087
## orig.pF 444.08 14.372
## orig.pG 378.28 50.751
## orig.pH 389.80 46.891
## orig.pI 409.80 47.066
## orig.pJ 416.98 46.661
## orig.pK 445.68 46.510
```

```
#Narrow-sense individual-tree heritability
with(res.stdflia, (4*var["factor(mum)",1]) / sum(var))
```

```
## [1] 0.3116244
```

```
# 3. REGULAR ANALYSIS INDIVIDUAL-TREE MIXED MDOEL: The additive individual-tree model
with block design effects
res.blk <- remlf90(fixed = phe_X ~ orig,
                   genetic = list(model = 'add_animal',
                                  pedigree = data[, c('self','dad','mum')],
                                  id = 'self'),
                   spatial = list(model = 'blocks',
                                  coord = data[, c('x','y')],
                                  id = "block"),
                   data = data,
                   method = 'em')
```

```
## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').
```

```
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
```

```
summary(res.blk)
```

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC      BIC logLik
##  17882 unknown  -8938
##
## Parameters of special components:
## spatial: n.blocks: 34
##
## Variance components:
##          Estimated variances
## genetic                 5468
## spatial                 1107
## Residual               16240
##
## Fixed effects:
```

```
##          value    s.e.
## orig.pA 466.96 14.422
## orig.pB 493.66 20.049
## orig.pC 435.60 25.255
## orig.pF 444.01 13.458
## orig.pG 378.21 46.747
## orig.pH 389.83 42.429
## orig.pI 409.72 42.627
## orig.pJ 417.02 42.169
## orig.pK 445.65 41.999
```

```r
#Narrow-sense individual-tree heritability
(h2N_blk<- with(res.blk, var["genetic",1] / sum(var)))
```

```
## [1] 0.2396669
```

```r
# 4. Model without design effects. In this dataset only block design effects
res.stdSB <- remlf90(fixed = phe_X ~ orig,
                     genetic = list(model = 'add_animal',
                                    pedigree = data[, c('self','dad','mum')],
                                    id = 'self'),
                     data = data,
                     method = 'em')
```

```
## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').
```

```
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
```

```r
summary(res.stdSB)
```

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC     BIC logLik
##  17917 unknown  -8956
##
## Parameters of special components:
##
##
## Variance components:
##         Estimated variances
## genetic                5142
## Residual              17610
##
## Fixed effects:
##          value    s.e.
## orig.pA 465.30 12.994
## orig.pB 495.48 19.261
## orig.pC 434.32 24.450
## orig.pF 444.56 12.066
```

```
## orig.pG 376.42 45.945
## orig.pH 391.78 41.307
## orig.pI 411.22 41.515
## orig.pJ 417.24 41.023
## orig.pK 445.14 40.850

Residuals_stdSB<-residuals(res.stdSB)


################################################################################
# 5. DIAGNOSIS
# 5.1. Plots of median of phenoypes and residuals along rows and column
ByRow_P<-describeBy(x=data$phe_X,group=data$y, mat=TRUE)
ByCol_P<-describeBy(x=data$phe_X,group=data$x, mat=TRUE)
ByRow_R<-describeBy(x=Residuals_stdSB,group=data$y, mat=TRUE)
ByCol_R<-describeBy(x=Residuals_stdSB,group=data$x, mat=TRUE)
plot(as.numeric(ByRow_P$group1), ByRow_P$median, pch=19)
plot(as.numeric(ByCol_P$group1), ByCol_P$median, pch=19)
plot(as.numeric(ByRow_R$group1), ByRow_R$median, pch=19)
plot(as.numeric(ByCol_R$group1), ByCol_R$median, pch=19)
```
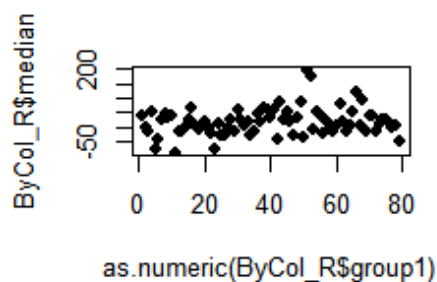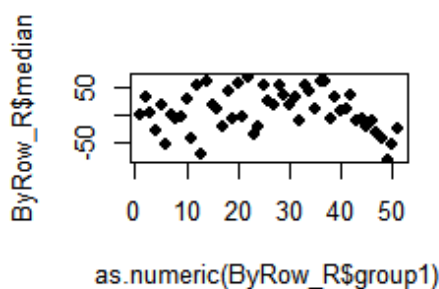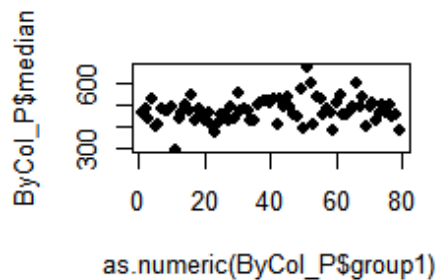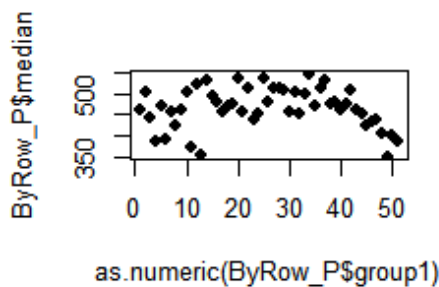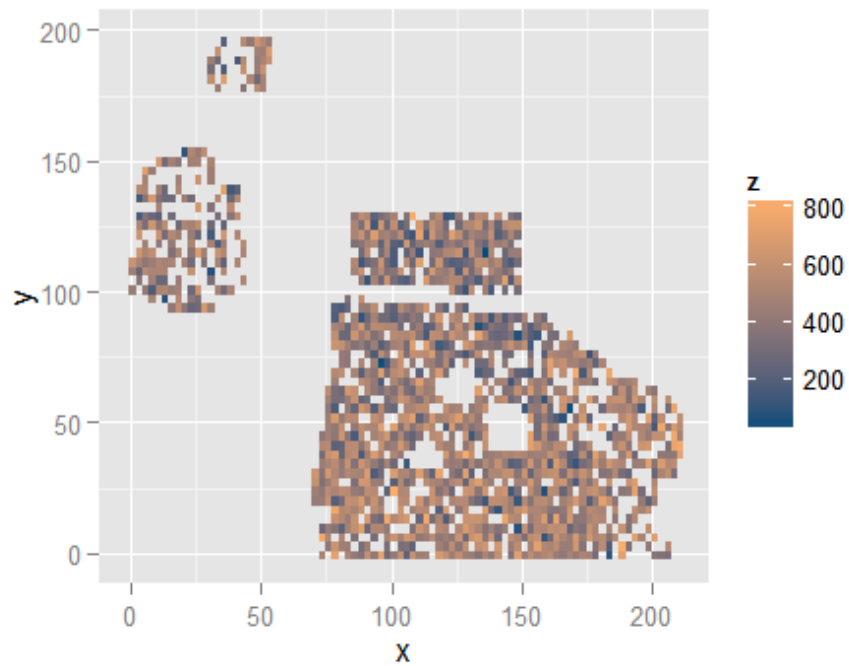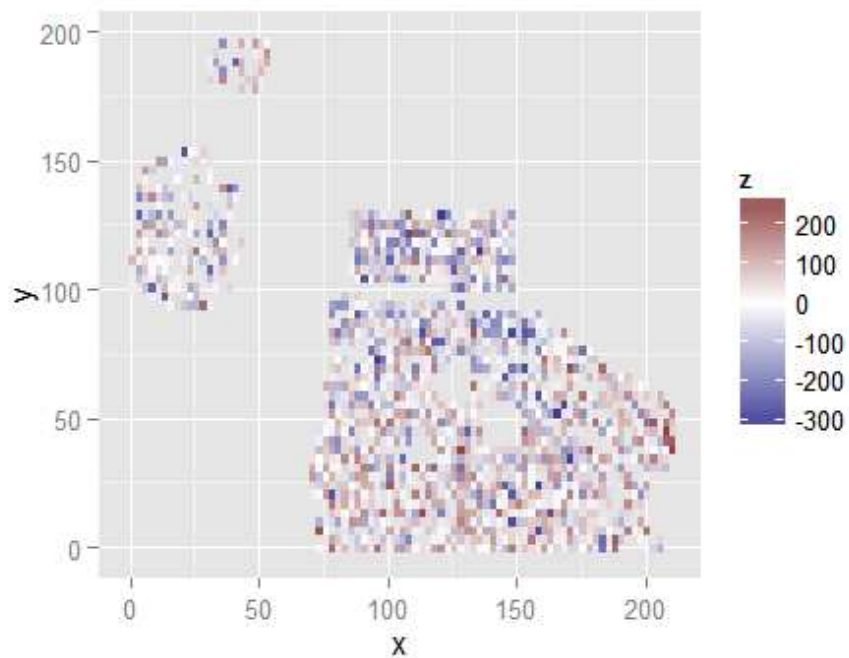


```
# 5.2. Plots the phenotypes and residuals by rows and columns using breedR
coordinates(res.stdSB) <- data[, c('x','y')]
# If you would like change the default colors
#breedR.setOption(col.seq = c('yellow', 'red'))
#breedR.setOption(col.div = c('yellow', 'red'))
plot(res.stdSB, type = 'phenotype')
```

```
plot(res.stdSB, type = 'residuals')
```



```
# 5.2.1. Other way to plot the residuals by rows and columns
# Transform rows and columns in meters to sequential numbers
```

```r
mRow <- 2.5 # Distance between row in meters
mCol<- 3.5 # Distance between column in meters
Row<-((data[,c('x')]-mRow)/mRow)+2 # 1,2,,3,...
Col<-((data[,c('y')]-mCol)/mCol)+2 # 1,2,,3,...
grid<-cbind(expand.grid(1:max(Row), 1:max(Col)),NA)
names(grid) <- c('Row', 'Col', 'Residual')
res<-cbind(data,Row,Col,Residuals_stdSB)
resc<-merge(res,grid, by=c('Row','Col'),all=TRUE)
resc.matrix<-matrix(resc$Residuals, nrow=max(Row),byrow=T)
library(fields)

## Loading required package: spam
## Loading required package: grid
## Spam version 1.0-1 (2014-09-09) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.
##
## Attaching package: 'spam'
##
## The following objects are masked from 'package:base':
##
##     backsolve, forwardsolve
##
## Loading required package: maps
##
## Attaching package: 'fields'
##
## The following object is masked from 'package:psych':
##
##     describe

Rows <- seq(1, max(Row), length= max(Row))
Columns <- seq(1,max(Col), length= max(Col))
par(mfrow = c(1, 1))
image.plot(x=Rows,y=Columns,z=resc.matrix)
```
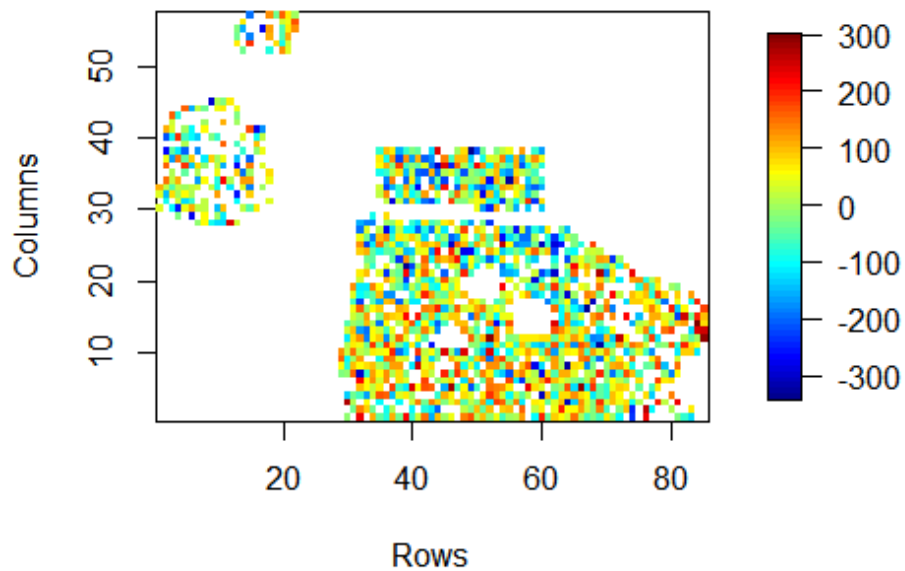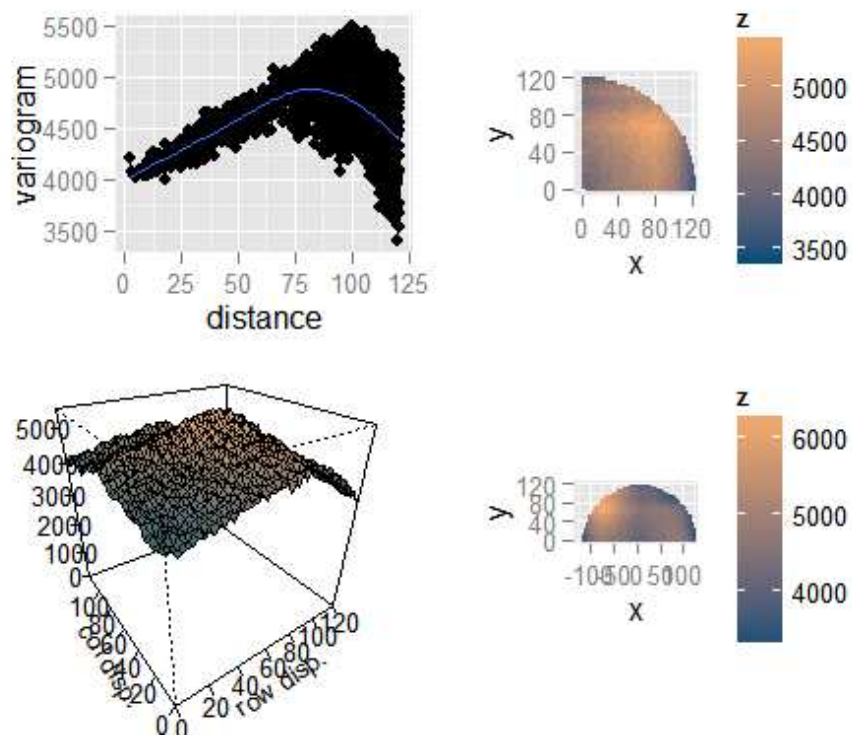
```
# 5.2.Variograms of residuals
variogram(res.stdSB)
```



```
variogram(res.stdSB, plot = 'perspective')
```
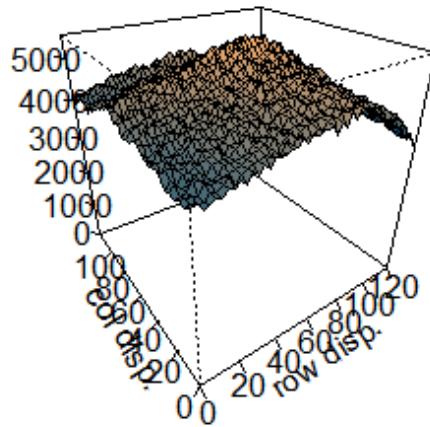
```
variogram(res.stdSB, plot = 'perspective', R=35)
```
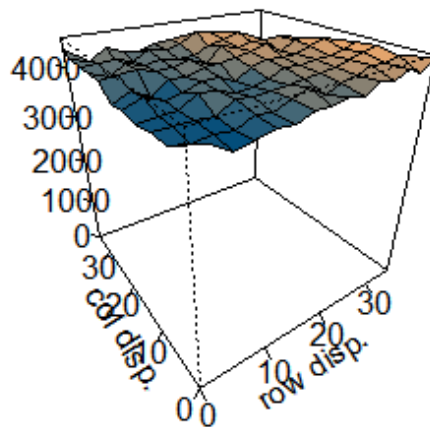


```
# 5.3.Residuals against row and column position
library(lattice)
```

```
xyplot(Residuals_stdSB ~ Col | Row,as.table=2,strip = strip.custom(strip.names =
TRUE, strip.levels = TRUE),
       panel = function(x, y) {
       panel.xyplot(x, y)
       panel.loess(x,y, span= 0.6,degree = 2)
       })
```
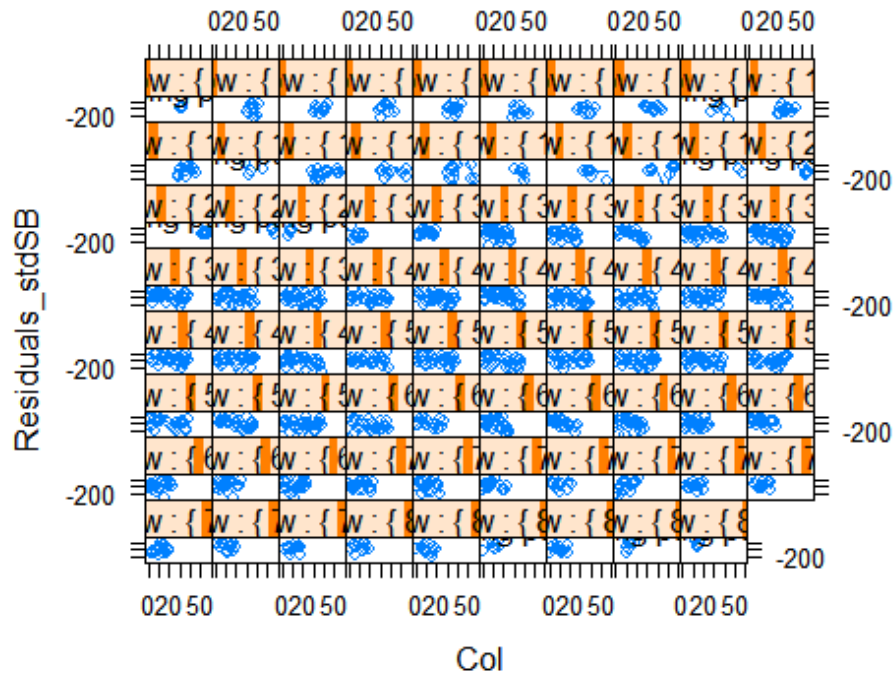


```
xyplot(Residuals_stdSB ~ Row | Col,as.table=2,strip = strip.custom(strip.names =
TRUE, strip.levels = TRUE),
       panel = function(x, y) {
       panel.xyplot(x, y)
       panel.loess(x,y, span= 0.6,degree = 2)
       })
```

```r
################################################################################
# 6. SPATIAL ANALISIS using individual-tree mixed model with two-dimensional B-
spline: The B-Spline model
res.spl <- remlf90(fixed = phe_X ~ orig,
                   genetic = list(model = 'add_animal',
                                  pedigree = data[, c('self','dad','mum')],
                                  id = 'self'),
                   spatial = list(model = 'splines',
                                  coord = data[, c('x','y')]),
                   data = data,
                   method = 'em')

## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').

## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.

summary(res.spl)

## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC     BIC logLik
##  17861 unknown  -8927
##
## Parameters of special components:
## spatial: n.knots: 13 13
```

```
## 
## Variance components:
##          Estimated variances
## genetic                5426
## spatial                1167
## Residual              16210
## 
## Fixed effects:
##            value   s.e.
## orig.pA 471.81 19.357
## orig.pB 496.26 23.795
## orig.pC 441.95 28.337
## orig.pF 448.04 18.616
## orig.pG 384.14 48.366
## orig.pH 394.08 44.173
## orig.pI 412.29 44.398
## orig.pJ 421.61 43.952
## orig.pK 448.73 43.830

(variogram(res.spl,plot = 'perspective'))
```
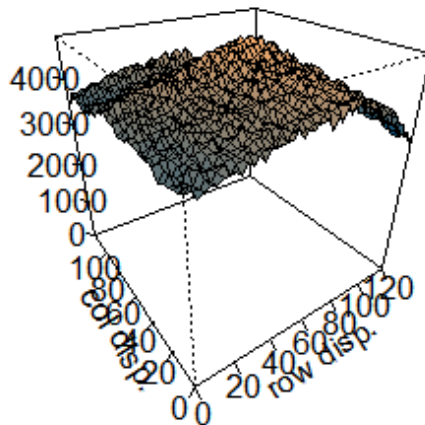


```
#Narrow-sense individual-tree heritability
(h2N_spl<- with(res.spl, var["genetic",1] / sum(var)))

## [1] 0.2379511

# 7. SPATIAL ANALISIS using individual-tree mixed model separable kronecker product
of First order
```

```
#    Autoregressive processes on the rows and the colums: The autoregressive model
# 7.1 Without block effects
res.ar1 <- remlf90(fixed = phe_X ~ orig,
#                   random = ~ block,
                   genetic = list(model = 'add_animal',
                                   pedigree = data[, c('self','dad','mum')],
                                   id = 'self'),
                   spatial = list(model = 'AR',
                                   coord = data[, c('x','y')],
                                   rho = c(.8,.8)),
data = data,
                   method = 'em')

## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').

## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.

summary(res.ar1)

## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC     BIC logLik
## 17879 unknown  -8936
##
## Parameters of special components:
## spatial: rho: 0.8 0.8
##
## Variance components:
##         Estimated variances
## genetic             5613
## spatial             1341
## Residual           15610
##
## Fixed effects:
##          value    s.e.
## orig.pA 467.27 14.733
## orig.pB 493.71 20.308
## orig.pC 437.33 25.580
## orig.pF 443.79 13.718
## orig.pG 381.10 47.238
## orig.pH 390.88 42.917
## orig.pI 408.63 43.111
## orig.pJ 417.51 42.667
## orig.pK 445.64 42.525

# 7.2 With block effects
res.ar1 <- remlf90(fixed = phe_X ~ orig,
                   random = ~ block,
```

```r
              genetic = list(model = 'add_animal',
                             pedigree = data[, c('self','dad','mum')],
                             id = 'self'),
              spatial = list(model = 'AR',
                             coord = data[, c('x','y')],
                             rho = c(-.2,-.2)),
              data = data,
              method = 'em')
```

```
## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').

## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
```

```r
summary(res.ar1)
```

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC      BIC logLik
##  17880 unknown  -8936
##
## Parameters of special components:
## spatial: rho: -0.2 -0.2
##
## Variance components:
##          Estimated variances
## block                   1164
## genetic                 5252
## spatial                 4222
## Residual               12130
##
## Fixed effects:
##           value    s.e.
## orig.pA 466.84 14.248
## orig.pB 492.35 19.874
## orig.pC 435.09 24.966
## orig.pF 444.49 13.335
## orig.pG 375.00 46.124
## orig.pH 389.01 41.763
## orig.pI 411.58 41.976
## orig.pJ 416.22 41.503
## orig.pK 443.98 41.330
```

```r
#Narrow-sense individual-tree heritability
(h2N_ar1<- with(res.ar1, var["genetic",1] / sum(var)))
```

```
## [1] 0.2306746
```

```r
# Full table of combinations and likelihoods
#res.ar1$rho
```

```
#Visualize log-likelihoods
#library(ggplot2)
#qplot(rho_r, rho_c,
#      fill = loglik,
#      geom = 'tile',
#      data = res.ar1$rho)

# 8. Plots comparing the diferent spatial models - we preserve the scale by using
compare.plots() -
# 8.1. Comparison of residuals
compare.plots(
list(`Individual-tree model only` = plot(res.stdSB, 'residuals'),
    `Individual-tree/blocks model` = plot(res.blk, 'residuals'),
    `Individual-tree/splines model` = plot(res.spl, 'residuals'),
    `Individual-tree/AR1 model` = plot(res.ar1, 'residuals'))
    )
```
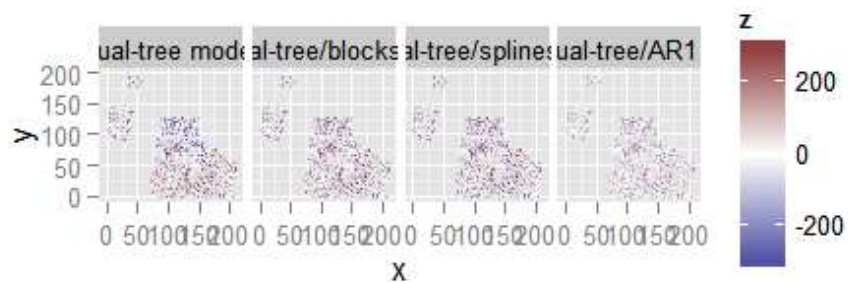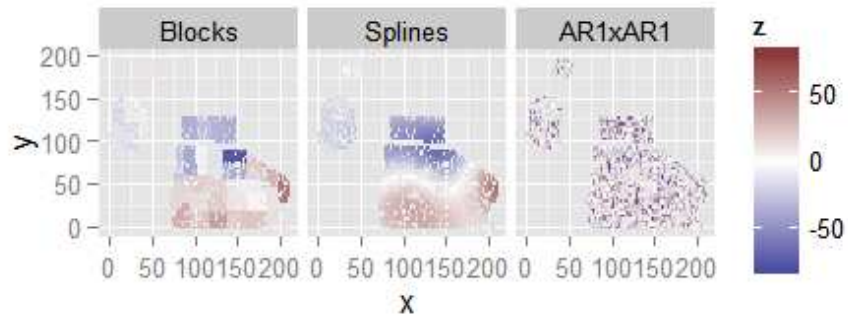


```
# 8.2. Comparison of spatial components
compare.plots(
list(Blocks = plot(res.blk, type = 'spatial'),
            Splines = plot(res.spl, type = 'spatial'),
            AR1xAR1 = plot(res.ar1, type = 'spatial'))
    )
```
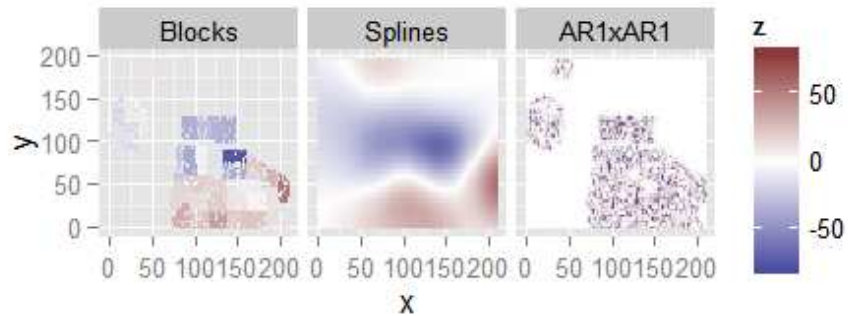
```
# 8.3. Prediction of the spatial effect in unobserved locations.
# The type fullspatial fills the holes (when possible)
compare.plots(
list(Blocks = plot(res.blk, type = 'fullspatial'),
                Splines = plot(res.spl, type = 'fullspatial'),
                AR1xAR1 = plot(res.ar1, type = 'fullspatial'))
    )
```

```r
# 9. Spearman correlations and plots of breeding values (BVs) for parents and
offspring between regular and spatial analyses.
# 9.1. Number of parents and offspring
parents<-as.matrix(summary(as.data.frame(get_pedigree(res.blk))$dam))
nparents<-parents["Max.",1]
progenies<-as.matrix(summary(as.data.frame(get_pedigree(res.blk))$self))
nprogenies<-progenies["Max.",1] - nparents

# 9.2. BVs
BVs_ind_parents<-res.blk$ranef$genetic$value[1:nparents]
BVs_ind_progenies<-res.blk$ranef$genetic$value[nparents+1:nprogenies]
BVs_spl_parents<-res.spl$ranef$genetic$value[1:nparents]
BVs_spl_progenies<-res.spl$ranef$genetic$value[nparents+1:nprogenies]
BVs_ar1_parents<-res.ar1$ranef$genetic$value[1:nparents]
BVs_ar1_progenies<-res.ar1$ranef$genetic$value[nparents+1:nprogenies]

# 9.3. Spearman correlations of BVs between the different models
cor(BVs_ind_parents,BVs_ar1_parents,method = c("spearman"))

## [1] 0.998538

cor(BVs_ind_parents,BVs_spl_parents,method = c("spearman"))

## [1] 0.9967001

cor(BVs_spl_parents,BVs_ar1_parents,method = c("spearman"))

## [1] 0.9954052
```

```r
cor(BVs_ind_progenies,BVs_ar1_progenies,method = c("spearman"))
```

```
## [1] 0.9985183
```

```r
cor(BVs_ind_progenies,BVs_spl_progenies,method = c("spearman"))
```

```
## [1] 0.9969548
```

```r
cor(BVs_spl_progenies,BVs_ar1_progenies,method = c("spearman"))
```
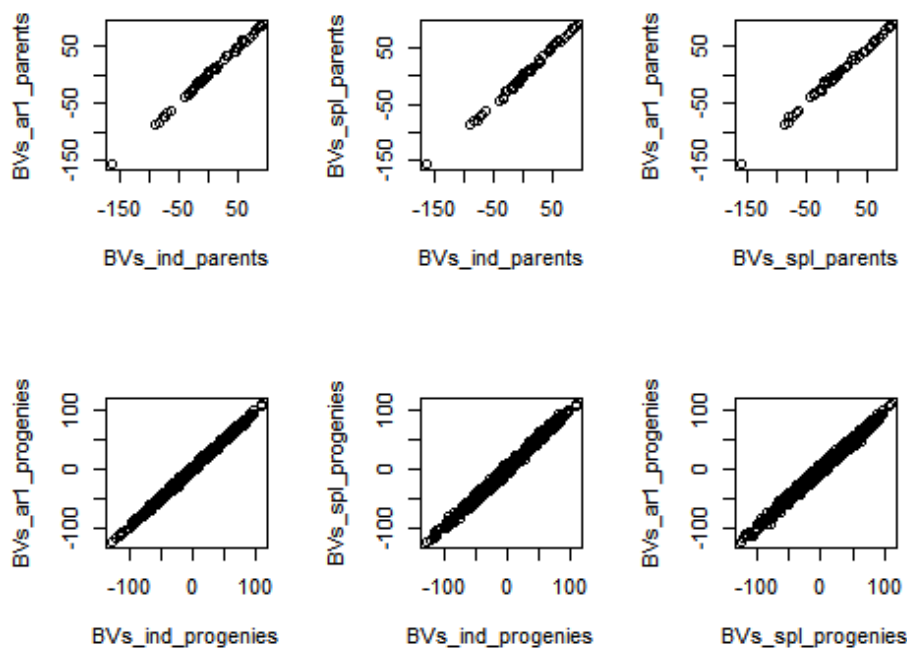
```
## [1] 0.9956844
```

```r
# 9.4. Plots of BVs between the different models
par(mfrow = c(2, 3))
plot(BVs_ind_parents,BVs_ar1_parents)
plot(BVs_ind_parents,BVs_spl_parents)
plot(BVs_spl_parents,BVs_ar1_parents)
plot(BVs_ind_progenies,BVs_ar1_progenies)
plot(BVs_ind_progenies,BVs_spl_progenies)
plot(BVs_spl_progenies,BVs_ar1_progenies)
```



```r
# 10. COMPETITION ANALISIS
res.comp <- remlf90(fixed = phe_X ~ orig,
                    genetic = list(model = c('comp'),
                                   pedigree = data[, c('self','dad','mum')],
                                   id = 'self',
                                   coord = data[, c('x', 'y')],
                                   competition_decay = 2, # IC decay 1/distance
                                   pec = list(present = TRUE)), #envirmonetal
```

```
                    spatial = list(model = 'blocks',
                                   coord = data[, c('x','y')],
                                   id = "block"),
                    data = data,
                    method = 'em',
                    debug = F)
```

```
## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').

## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
```

summary(res.comp)

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC     BIC logLik
##  17882 unknown  -8935
##
## Parameters of special components:
## spatial: n.blocks: 34
##
## Variance components:
## $genetic
##                     genetic_direct genetic_competition
## genetic_direct                5528              -1290.0
## genetic_competition          -1290                435.1
##
## $pec
## [1] 398.4
##
## $spatial
## [1] 1113
##
## $Residual
## [1] 15390
##
##
## Fixed effects:
##           value   s.e.
## orig.pA 465.08 12.262
## orig.pB 486.30 19.112
## orig.pC 436.69 24.679
## orig.pF 448.82 13.023
## orig.pG 359.03 45.377
## orig.pH 379.61 39.670
## orig.pI 434.82 40.384
```

```
## orig.pJ 428.41 39.295
## orig.pK 431.27 39.212

# Direct and competition additive correlation
Var_d<-res.comp$var$genetic["genetic_direct",1]
Var_dc<-res.comp$var$genetic["genetic_competition",2]
(res.comp$var$genetic["genetic_direct",2] / sqrt(Var_d*Var_dc))

## [1] -0.8317851

###############################################################################
# 11. Additional diagnosis of competition effects:
#     Plot of phenotypic and residual values after fitting genetic effects plotted
against means
#     of the 8 nearest neighbour trees. Means are weight by IC factor.
# Desing additive genetic competition matrix
Zc <-
as.matrix(model.matrix(res.comp)$"genetic_competition")[1:length(data$phe_X),(nparent
s+1):(nparents+nprogenies)]
# Phenotype values
phe_X<-as.matrix(data$phe_X)
# Phenotypic means of the 8 nearest neighbour trees
Nei_mean_pheno<- Zc%*%phe_X
# Residual means of the 8 nearest neighbour trees
Nei_mean_res<- Zc%*%Residuals_stdSB

# 11.1 Plot of the phenotypic values of each tree against the phenotypic means of the
neighbouring trees.
# Means are weight by IC factor.
par(mfrow = c(1, 2))
plot(phe_X, Nei_mean_pheno)
abline(lm(Nei_mean_pheno~phe_X), col="red") # regression line (y~x)

# 11. 2. Plot of the residual values of each tree after fitting genetic effects
against the phenotypic means of the neighbouring trees.
#Means are weight by IC factor.
plot(phe_X, Nei_mean_res)
abline(lm(Nei_mean_res~phe_X), col="blue") # regression line (y~x)
```
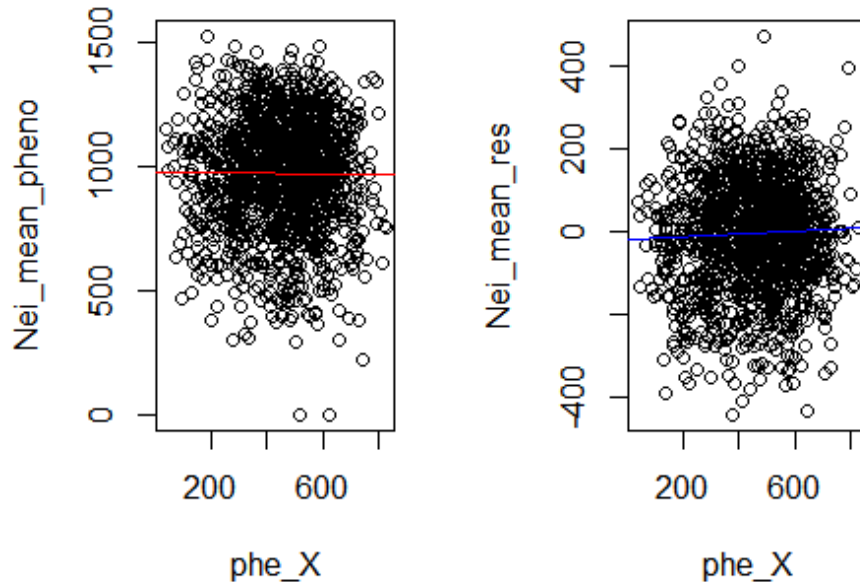
```
################################################################################
# 12. COMPETITION + SPATIAL ANALISIS (using an autorregresive model)
res.comp.ar1 <- remlf90(fixed = phe_X ~ orig,
                        genetic = list(model = c('comp'),
                                       pedigree = data[, c('self','dad','mum')],
                                       id = 'self',
                                       coord = data[, c('x', 'y')],
                                       competition_decay = 2, # IC decay 1/distance
                                       pec = list(present = TRUE)), #envirmonetal
```
compettion effect
```
                        spatial = list(model = 'AR',
                                       coord = data[, c('x','y')],
                                       rho = c(.8,.8)),
                        data = data,
                        method = 'em',
                        debug = F)

## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').

## No specification of initial variances.
##       Using default value of 1 for all variance components.
##       See ?breedR.getOption.

summary(res.comp.ar1)

## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##     Data: data
```

```
##     AIC     BIC logLik
##  17875 unknown  -8932
##
## Parameters of special components:
## spatial: rho: 0.8 0.8
##
## Variance components:
## $genetic
##                    genetic_direct genetic_competition
## genetic_direct               6128              -1608.0
## genetic_competition         -1608               525.2
##
## $pec
## [1] 197.6
##
## $spatial
## [1] 1507
##
## $Residual
## [1] 14380
##
##
## Fixed effects:
##            value    s.e.
## orig.pA 465.15 12.589
## orig.pB 484.83 19.543
## orig.pC 439.05 25.459
## orig.pF 449.25 13.480
## orig.pG 357.24 46.722
## orig.pH 380.19 40.554
## orig.pI 437.05 41.335
## orig.pJ 433.22 40.121
## orig.pK 425.25 40.172
```

```r
# COMPETITION + SPATIAL ANALISIS (using two-dimensional B-spline)
res.comp.spl <- remlf90(fixed = phe_X ~ orig,
                        genetic = list(model = c('comp'),
                                       pedigree = data[, c('self','dad','mum')],
                                       id = 'self',
                                       coord = data[, c('x', 'y')],
                                       competition_decay = 2, # IC decay 1/distance
                                       pec = list(present = TRUE)), #envirmonetal
competition effect
                        spatial = list(model = 'splines',
                                       coord = data[, c('x','y')]),
                        data = data,
                        method = 'em',
                        debug = F)
```

```
## Warning in build_pedigree(1:3, data = ped.df): The pedigree has been
## recoded. Check attr(ped, 'map').
```

```
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
```

`summary`(res.comp.spl)

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##    Data: data
##    AIC      BIC logLik
##  17860 unknown  -8924
##
## Parameters of special components:
## spatial: n.knots: 13 13
##
## Variance components:
## $genetic
##                       genetic_direct genetic_competition
## genetic_direct                  5606              -1346.0
## genetic_competition            -1346                475.3
##
## $pec
## [1] 386.8
##
## $spatial
## [1] 1161
##
## $Residual
## [1] 15250
##
##
## Fixed effects:
##            value    s.e.
## orig.pA 470.63 17.844
## orig.pB 488.14 23.025
## orig.pC 444.00 27.858
## orig.pF 452.53 18.247
## orig.pG 365.79 47.240
## orig.pH 383.37 41.614
## orig.pI 435.35 42.334
## orig.pJ 433.65 41.259
## orig.pK 430.97 41.290
```

```
# 13. TABLE WITH THE RESULTS OF THE FITTED MODELS: LogL, AIC, VAriance components and
heritabili
# 13.1 Fit of each model: logL
logL.blk<-res.blk$fit$`-2logL`
logL.spl<-res.spl$fit$`-2logL`
logL.ar1<-res.ar1$fit$`-2logL`
logL.comp<-res.comp$fit$`-2logL`
logL.comp.ar1<-res.comp.ar1$fit$`-2logL`
logL.comp.spl<-res.comp.spl$fit$`-2logL`
```

```
# 13.2 Fit of each model: AIC
AIC.blk<-res.blk$fit$AIC
AIC.spl<-res.spl$fit$AIC
AIC.ar1<-res.ar1$fit$AIC
AIC.comp<-res.comp$fit$AIC
AIC.comp.ar1<-res.comp.ar1$fit$AIC
AIC.comp.spl<-res.comp.spl$fit$AIC

# 12.3 Variance components
(res.blk$var)

##          Estimated variances
## genetic              5468
## spatial              1107
## Residual            16240

(res.spl$var)

##          Estimated variances
## genetic              5426
## spatial              1167
## Residual            16210

(res.ar1$var)

##          Estimated variances
## block                1164
## genetic              5252
## spatial              4222
## Residual            12130

(res.comp$var)

## $genetic
##                     genetic_direct genetic_competition
## genetic_direct                5528             -1290.0
## genetic_competition          -1290               435.1
##
## $pec
## [1] 398.4
##
## $spatial
## [1] 1113
##
## $Residual
## [1] 15390

(res.comp.ar1$var)

## $genetic
##                     genetic_direct genetic_competition
## genetic_direct                6128             -1608.0
```

```
## genetic_competition              -1608                   525.2
##
## $pec
## [1] 197.6
##
## $spatial
## [1] 1507
##
## $Residual
## [1] 14380

(res.comp.spl$var)

## $genetic
##                      genetic_direct genetic_competition
## genetic_direct                 5606             -1346.0
## genetic_competition            -1346              475.3
##
## $pec
## [1] 386.8
##
## $spatial
## [1] 1161
##
## $Residual
## [1] 15250
```

```r
All<-
c(logL.blk,logL.spl,logL.ar1,logL.comp,logL.comp.ar1,logL.comp.spl,AIC.blk,AIC.spl,AI
C.ar1,AIC.comp,AIC.comp.ar1,AIC.comp.spl,h2N_blk,h2N_spl,h2N_ar1,".",".",".")

Final_Results <- matrix(All,ncol=6,byrow=TRUE)
rownames (Final_Results) <- c("logL","AIC","Heretabilities")
colnames (Final_Results) <-
c("Clasical","Splines","AR1","Comp","Spatial_ar1+Comp","Spatial_sp+Comp")
(Final_Results <- as.table(Final_Results))
```

```
##                Clasical        Splines             AR1
## logL            17876.09  17854.68  17872.42
## AIC             17882.09  17860.68  17880.42
## Heretabilities 0.24 0.24 0.23
##                Comp             Spatial_ar1+Comp Spatial_sp+Comp
## logL            17869.74 17863.48  17847.62
## AIC             17881.74 17875.48  17859.62
## Heretabilities .               .                .
```