

```
# title: Diagnosis of spatial and competition effects in forest genetic trials using breedR: an example in Eucalyptus globulus
# 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<-globulus
```

```
head(data)
```

```
##   self dad mum gen gg bl phe_X x y
## 1   69  0  64  1 14 13 15.756 0 0
## 2   70  0  41  1  4 13 11.141 3 0
## 3   71  0  56  1 14 13 19.258 6 0
## 4   72  0  55  1 14 13  4.775 9 0
## 5   73  0  22  1  8 13 19.099 12 0
## 6   74  0  50  1 14 13 19.258 15 0
```

```
str(data)
```

```
## 'data.frame': 1021 obs. of 9 variables:
## $ self : int 69 70 71 72 73 74 75 76 77 78 ...
## $ dad : int 0 0 0 0 0 0 0 0 0 4 ...
## $ mum : int 64 41 56 55 22 50 67 59 49 8 ...
## $ gen : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...
## $ gg : Factor w/ 14 levels "1","2","3","4",...: 14 4 14 14 8 14 14 14 11 ...
## $ bl : Factor w/ 15 levels "1","2","3","4",...: 13 13 13 13 13 13 13 13 9 9 ...
## $ phe_X: num 15.76 11.14 19.26 4.78 19.1 ...
## $ x : int 0 3 6 9 12 15 18 21 24 27 ...
## $ y : int 0 0 0 0 0 0 0 0 0 0 ...
## - attr(*, "comment")= chr "Eucalyptus Globulus dataset" "Thanks to Eduardo Cappa and Pablo Pathauer" "Variables:" "self = id of the tree" ...
```

```
# 1.1. Description of the data
```

```
library(psych)
```

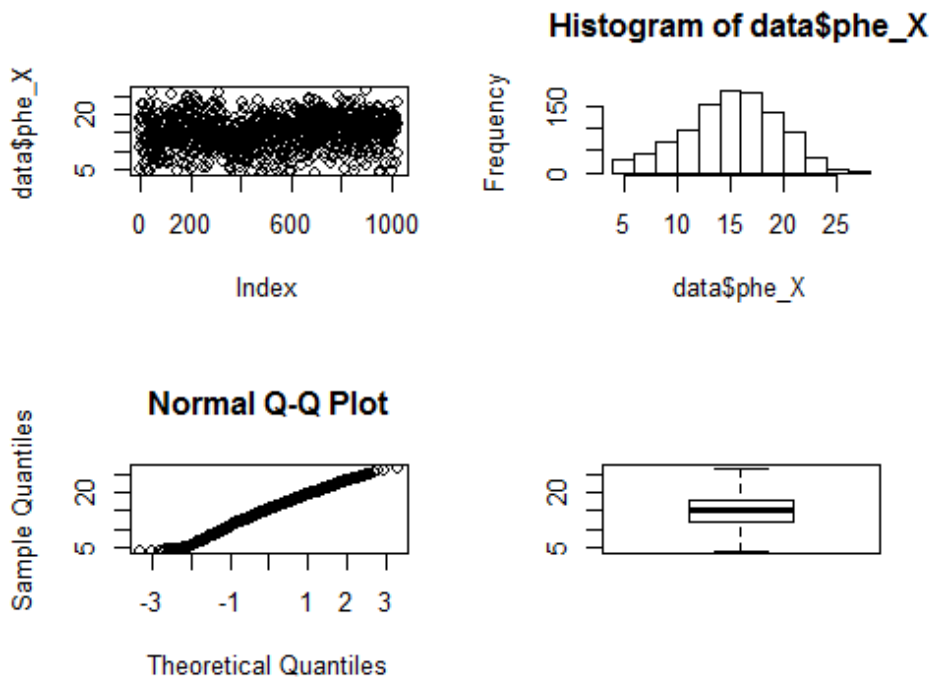
```
suppressWarnings(describe(data))
```

```
##      vars      n  mean      sd median trimmed      mad      min      max      range
## self      1 1021 579.00 294.88 579.00 579.00 378.06 69.00 1089.0 1020.00
## dad       2 1021  0.22  0.87  0.00  0.00  0.00  0.00  5.0  5.00
## mum       3 1021 32.88 20.71 33.00 33.00 26.69 0.00 68.0 68.00
```

```
## gen*      4 1021    NaN    NA    NA    NaN    NA    Inf    -Inf    -Inf
## gg*      5 1021    NaN    NA    NA    NaN    NA    Inf    -Inf    -Inf
## bl*      6 1021    NaN    NA    NA    NaN    NA    Inf    -Inf    -Inf
## phe_X    7 1021   15.08   4.39  15.28   15.21   4.48   4.14   26.9   22.76
## x        8 1021   49.47  26.75  51.00   49.96  31.13   0.00   93.0   93.00
## y        9 1021   49.82  30.44  48.00   49.34  40.03   0.00  105.0  105.00
##          skew kurtosis  se
## self    0.00    -1.20  9.23
## dad     4.25    17.60  0.03
## mum    -0.04    -1.19  0.65
## gen*     NA      NA    NA
## gg*     NA      NA    NA
## bl*     NA      NA    NA
## phe_X  -0.24    -0.27  0.14
## x      -0.11    -1.10  0.84
## y       0.09    -1.14  0.95
```

1.2. 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)
```



2. REGULAR ANALYSIS FAMILY MODEL: The family additive model with block design effects

```
res.stdflia <- remlf90(fixed = phe_X ~ gg,
```

```

        random = ~ bl + factor(mum),
        data = data,
        method = 'em')

## 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
## 5677 unknown -2836
##
## Parameters of special components:
##
##
## Variance components:
##           Estimated variances
## bl                2.644
## factor(mum)       1.101
## Residual           14.390
##
## Fixed effects:
##      value   s.e.
## gg.1  13.533 1.2165
## gg.2  14.027 1.3384
## gg.3  16.116 0.6618
## gg.4  11.863 0.8546
## gg.5  15.885 0.7222
## gg.6  10.211 1.6501
## gg.7  13.995 1.4955
## gg.8  15.694 0.6422
## gg.9  16.474 0.7308
## gg.10 12.845 1.5185
## gg.11 16.723 0.7603
## gg.12 16.922 1.0493
## gg.13 16.297 1.4955
## gg.14 14.424 0.5262

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

## [1] 0.2428453

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

```

```

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

## 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
## 5675 unknown -2835
##
## Parameters of special components:
## spatial: n.blocks: 15
##
## Variance components:
##           Estimated variances
## genetic           4.996
## spatial            2.656
## Residual          10.490
##
## Fixed effects:
##      value   s.e.
## gg.1 13.533 0.6287
## gg.2 14.027 0.8548
## gg.3 16.117 0.6753
## gg.4 11.863 0.8748
## gg.5 15.885 0.7385
## gg.6 10.208 1.6902
## gg.7 13.995 1.5412
## gg.8 15.691 0.6546
## gg.9 16.474 0.7468
## gg.10 12.845 1.1333
## gg.11 16.717 0.9150
## gg.12 16.945 1.0975
## gg.13 16.297 1.5412
## gg.14 14.424 0.5331

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

## [1] 0.2753831

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

```

```

                                id = 'self'),
                                data = data,
                                method = 'em')

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

summary(res.stdSB)

## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
##   Data: data
##   AIC    BIC logLik
## 5799 unknown -2898
##
## Parameters of special components:
##
##
## Variance components:
##      Estimated variances
## genetic              3.397
## Residual              14.450
##
## Fixed effects:
##      value   s.e.
## gg.1  13.591 0.5014
## gg.2  14.085 0.7984
## gg.3  16.112 0.5028
## gg.4  11.972 0.7354
## gg.5  15.894 0.5767
## gg.6  10.329 1.5967
## gg.7  13.995 1.4081
## gg.8  15.684 0.4782
## gg.9  16.470 0.5891
## gg.10 12.742 1.1292
## gg.11 16.697 0.7421
## gg.12 16.955 0.9868
## gg.13 16.297 1.4081
## gg.14 14.450 0.3120

Residuals_stdSB<-residuals(res.stdSB)

#####

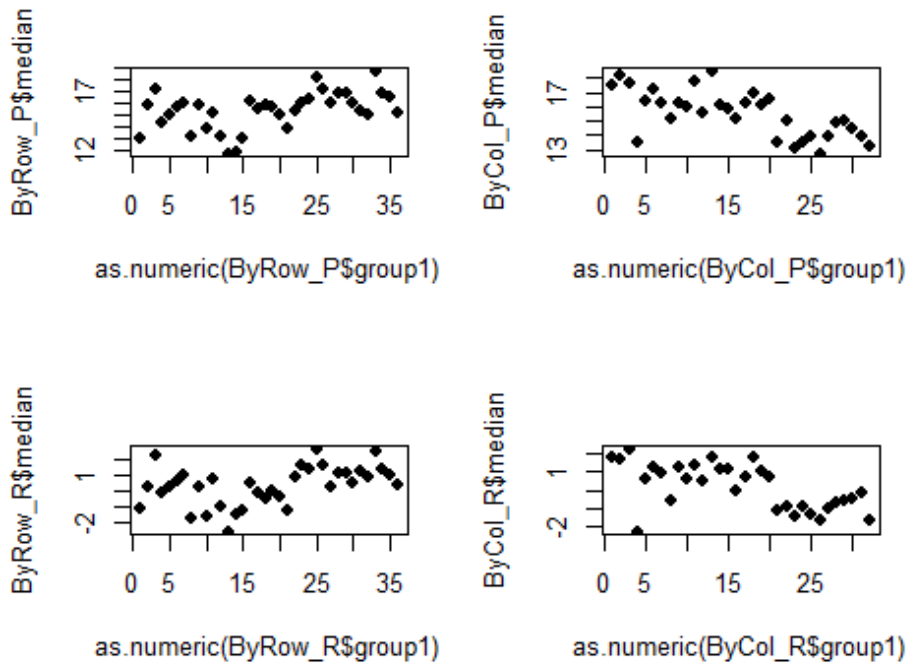
# 5. DIAGNOSIS
# 5.1. Plots of median of phenotypes and residuals along rows and column
ByRow_P<-describeBy(x=data$phe_X,group=data$y, mat=TRUE)
ByCol_P<-describeBy(x=data$phe_X,group=data$x, mat=TRUE)
ByRow_R<-describeBy(x=Residuals_stdSB,group=data$y, mat=TRUE)
ByCol_R<-describeBy(x=Residuals_stdSB,group=data$x, 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)

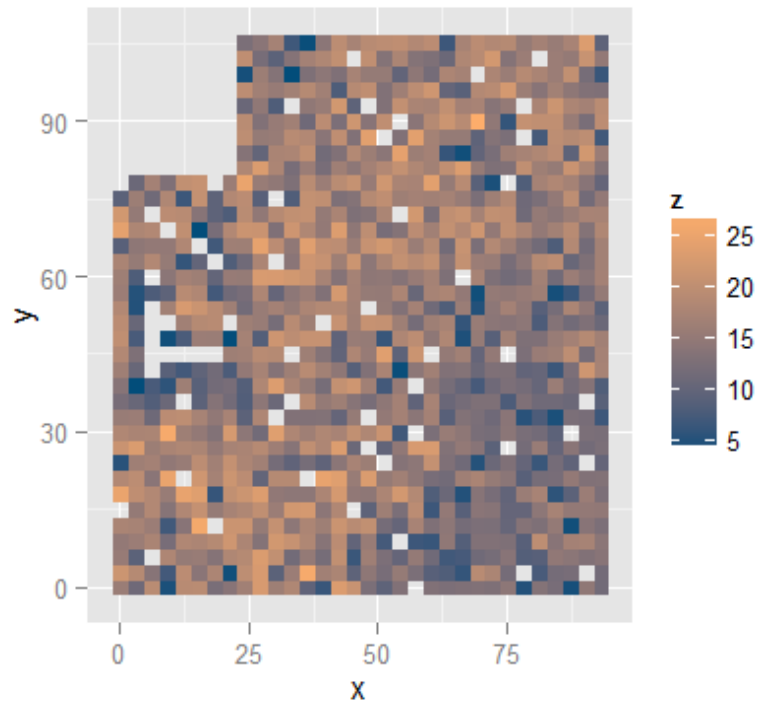
```



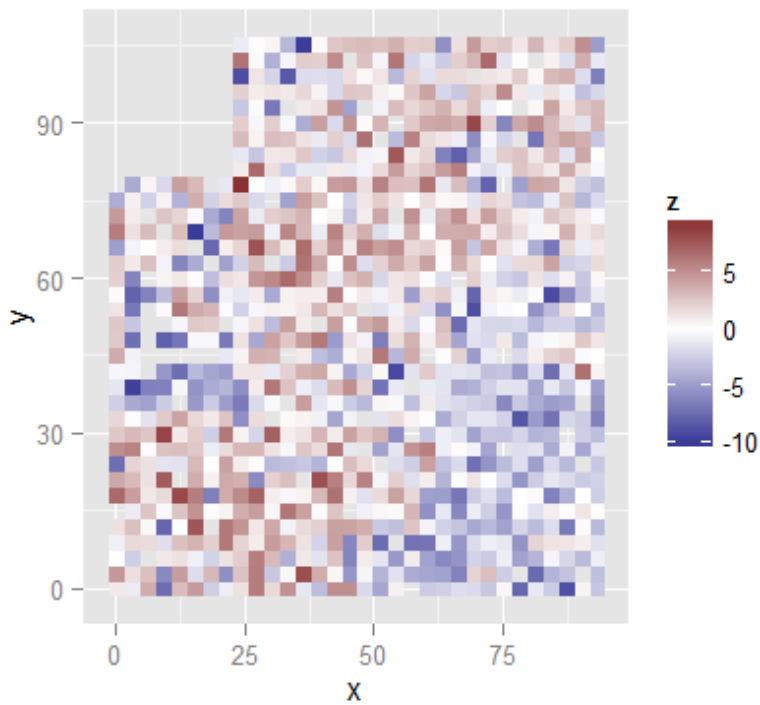
```

# 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
```

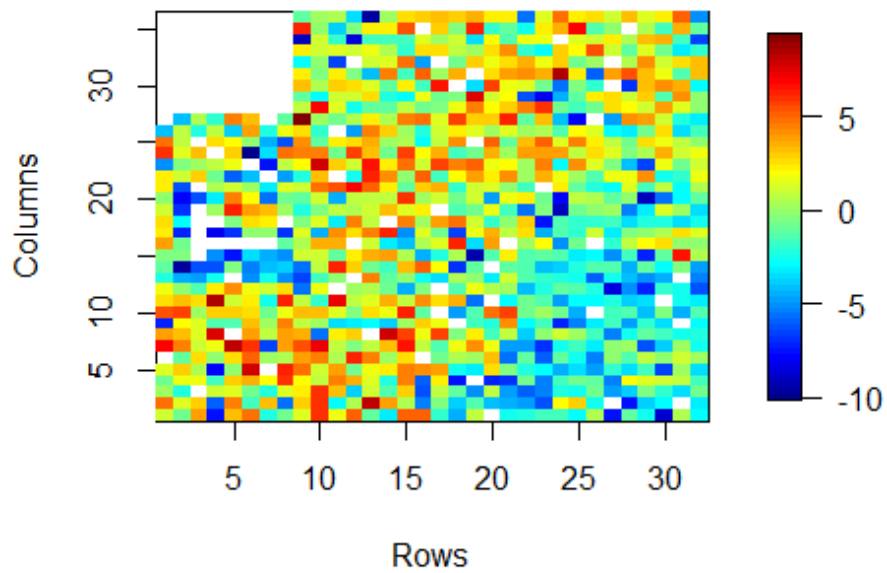
```

mRow <- 3 # Distance between row in meters
mCol<- 3 # 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

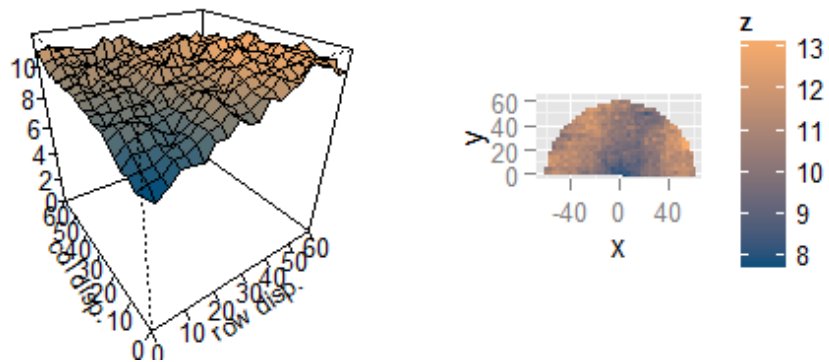
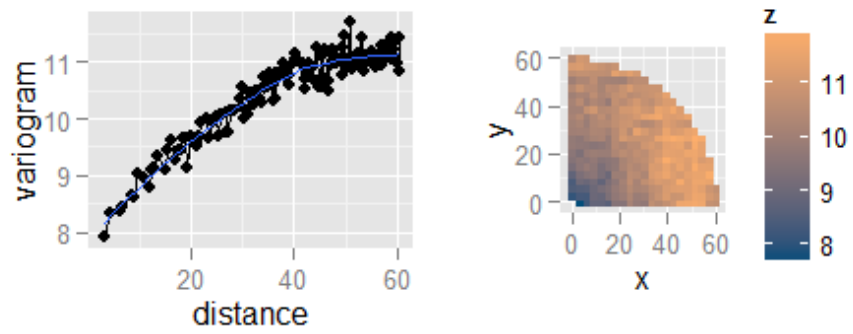
Rows <- seq(1, max(Row), length= max(Row))
Columns <- seq(1,max(Col), length= max(Col))
par(mfrow = c(1, 1))
image.plot(x=Rows,y=Columns,z=resc.matrix)

```

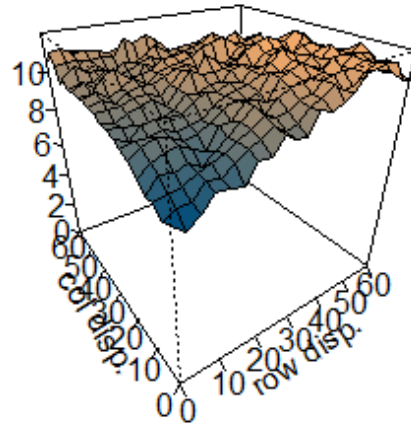



5.3. Variograms of residuals

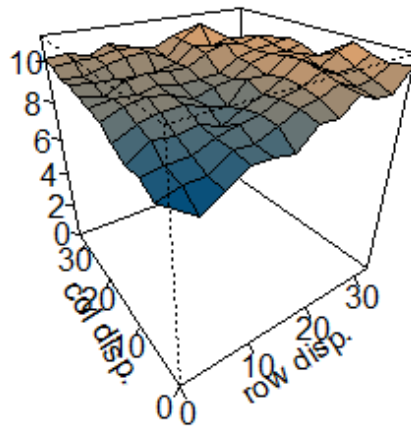
```
variogram(res.stdSB)
```



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



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

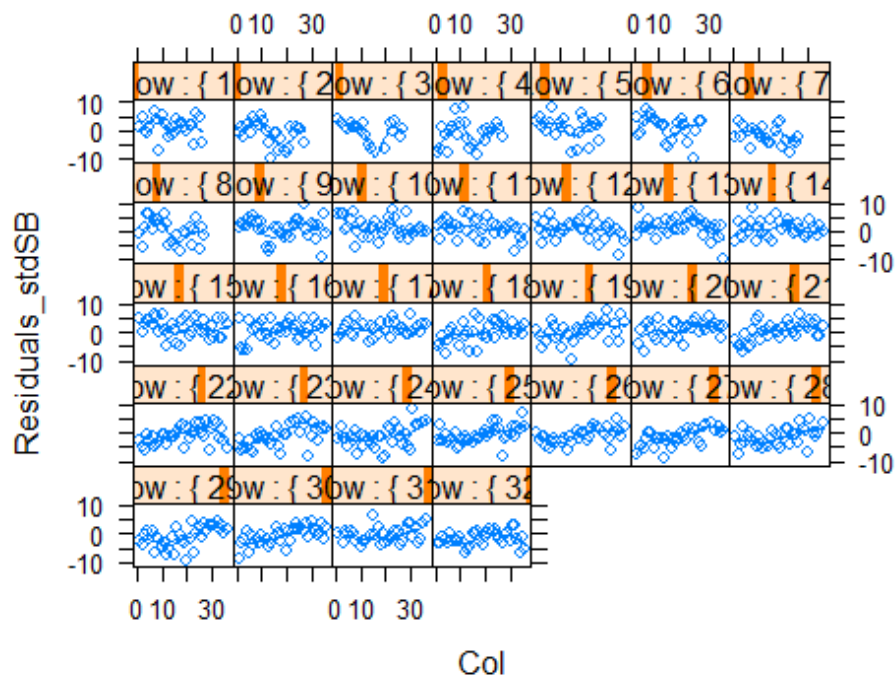


```
# 5.4. Residuals against row and column position  
library(lattice)
```

```

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)
  })

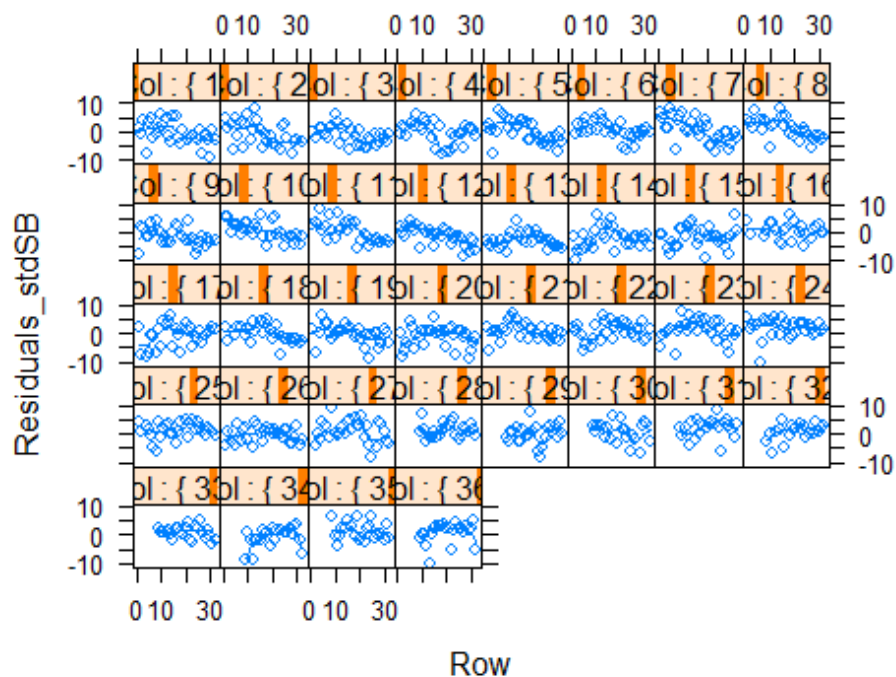
```



```

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)
  })

```



#####

6. SPATIAL ANALYSIS using individual-tree mixed model with two-dimensional B-spline: The B-Spline model

```
res.spl <- remlf90(fixed = phe_X ~ gg,
  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')
```

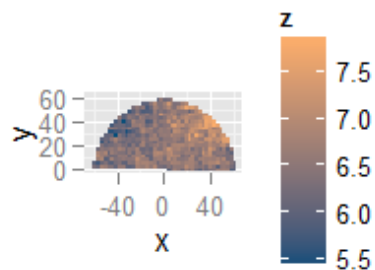
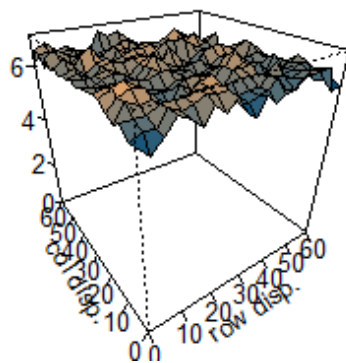
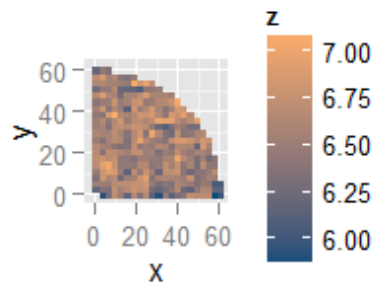
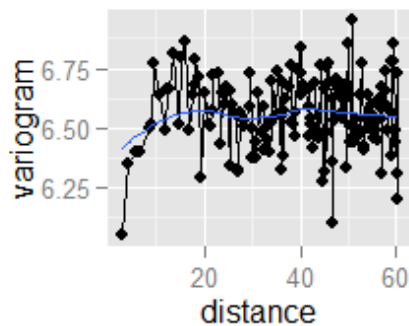
```
## No specification of initial variances.
## Using default value of 1 for all variance components.
## See ?breedR.getOption.
```

```
summary(res.spl)
```

```
## Linear Mixed Model with pedigree and spatial effects fit by REMLF90 ver. 1.78
## Data: data
## AIC BIC logLik
## 5626 unknown -2810
##
## Parameters of special components:
## spatial: n.knots: 12 12
##
```

```
## Variance components:
##           Estimated variances
## genetic           4.281
## spatial           4.203
## Residual          10.230
##
## Fixed effects:
##           value  s.e.
## gg.1  13.3480 0.9034
## gg.2  13.9542 1.0610
## gg.3  15.7997 0.9302
## gg.4  11.6422 1.0632
## gg.5  15.5900 0.9645
## gg.6   9.8466 1.7409
## gg.7  13.6490 1.6097
## gg.8  15.4733 0.9109
## gg.9  16.3469 0.9706
## gg.10 12.3430 1.2855
## gg.11 16.3881 1.0937
## gg.12 16.7726 1.2436
## gg.13 15.8154 1.6098
## gg.14 14.1499 0.8358
```

```
Residuals_spl<-residuals(res.spl)
(variogram(res.spl))
```




```

##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## No specification of initial variances.
##      Using default value of 1 for all variance components.
##      See ?breedR.getOption.
##
## 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
## 5605 unknown -2800
##
## Parameters of special components:
## spatial: rho: 0.8 0.8
##
## Variance components:
##      Estimated variances
## genetic          4.889
## spatial          4.907
## Residual         7.572
##
## Fixed effects:
##      value   s.e.
## gg.1 13.4090 0.6660
## gg.2 14.3653 0.8675
## gg.3 15.9931 0.7151

```

```

## gg.4 11.6325 0.8917
## gg.5 15.9467 0.7679
## gg.6 9.6901 1.6603
## gg.7 13.7737 1.5280
## gg.8 15.5745 0.6932
## gg.9 16.3533 0.7742
## gg.10 12.7766 1.1194
## gg.11 16.5054 0.9363
## gg.12 16.8501 1.0999
## gg.13 15.8195 1.5265
## gg.14 14.2556 0.5862

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

## [1] 0.2814947

# Full table of combinations and Likelihoods
res.ar1$rho

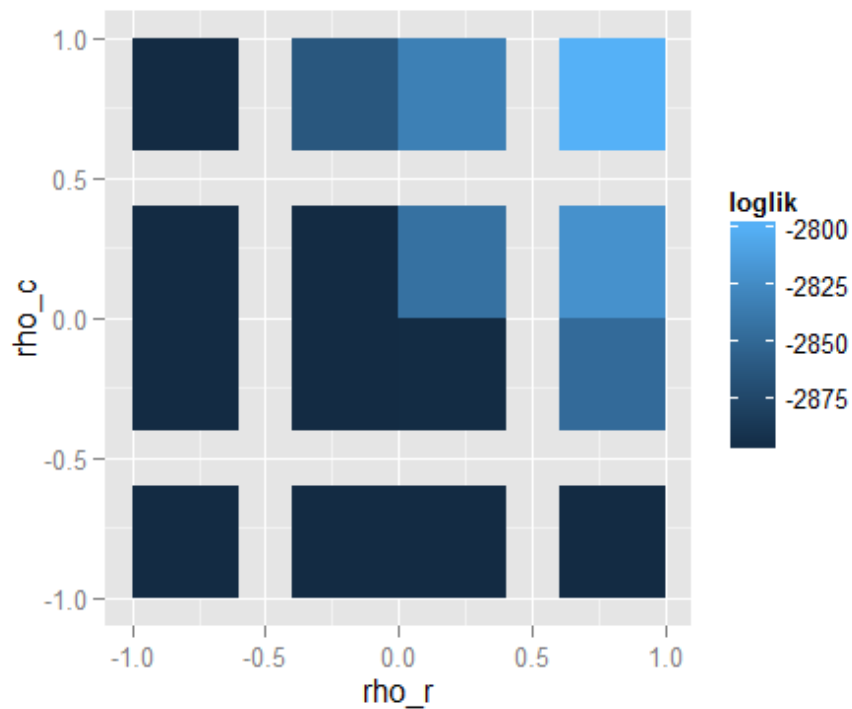
## rho_r rho_c loglik
## 1 -0.8 -0.8 -2898.094
## 2 -0.2 -0.8 -2898.017
## 3 0.2 -0.8 -2898.006
## 4 0.8 -0.8 -2897.701
## 5 -0.8 -0.2 -2898.079
## 6 -0.2 -0.2 -2897.948
## 7 0.2 -0.2 -2897.029
## 8 0.8 -0.2 -2848.278
## 9 -0.8 0.2 -2898.016
## 10 -0.2 0.2 -2897.768
## 11 0.2 0.2 -2843.505
## 12 0.8 0.2 -2821.058
## 13 -0.8 0.8 -2897.761
## 14 -0.2 0.8 -2862.547
## 15 0.2 0.8 -2832.748
## 16 0.8 0.8 -2799.521

#Visualize Log-Likelihoods
library(ggplot2)

##
## Attaching package: 'ggplot2'
##
## The following object is masked from 'package:psych':
##
## %+%

qplot(rho_r, rho_c,
      fill = loglik,
      geom = 'tile',
      data = res.ar1$rho)

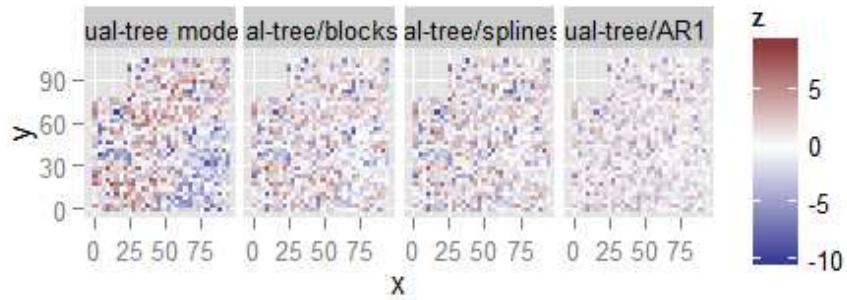
```

8. Plots comparing the different spatial models - we preserve the scale by using `compare.plots()` -

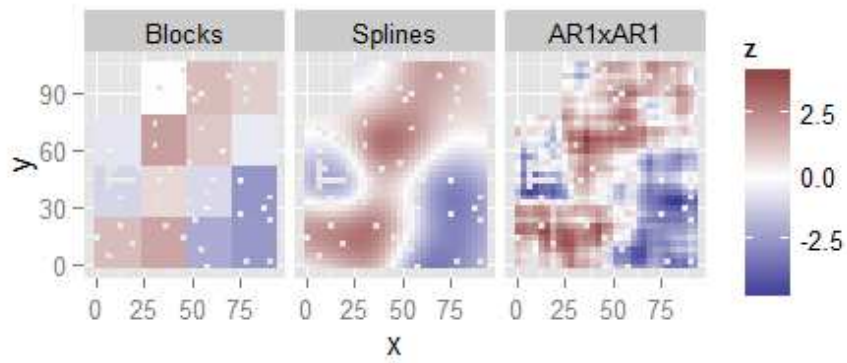
8.1. Comparison of residuals

```
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

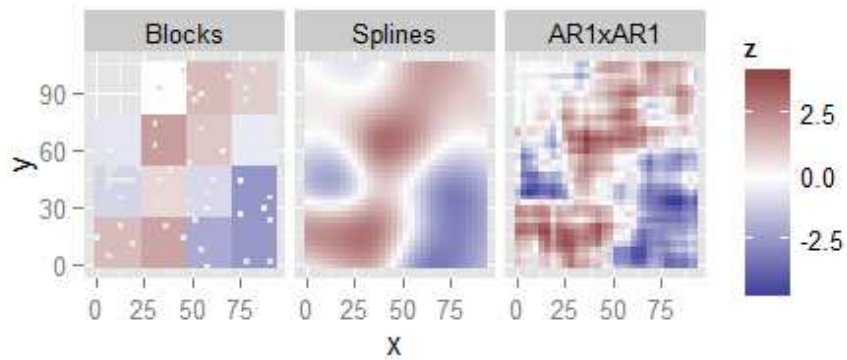
```
compare.plots(
  list(Blocks = plot(res.blk, type = 'spatial'),
       Splines = plot(res.spl, type = 'spatial'),
       AR1xAR1 = plot(res.ar1, type = 'spatial'))
)
```



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'))
)
```



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] 0.9643798
```

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

```
## [1] 0.985416
```

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

```
## [1] 0.9873249
```

```

cor(BVs_ind_progenies,BVs_ar1_progenies,method = c("spearman"))
## [1] 0.948575
cor(BVs_ind_progenies,BVs_spl_progenies,method = c("spearman"))
## [1] 0.9764063
cor(BVs_spl_progenies,BVs_ar1_progenies,method = c("spearman"))
## [1] 0.975546

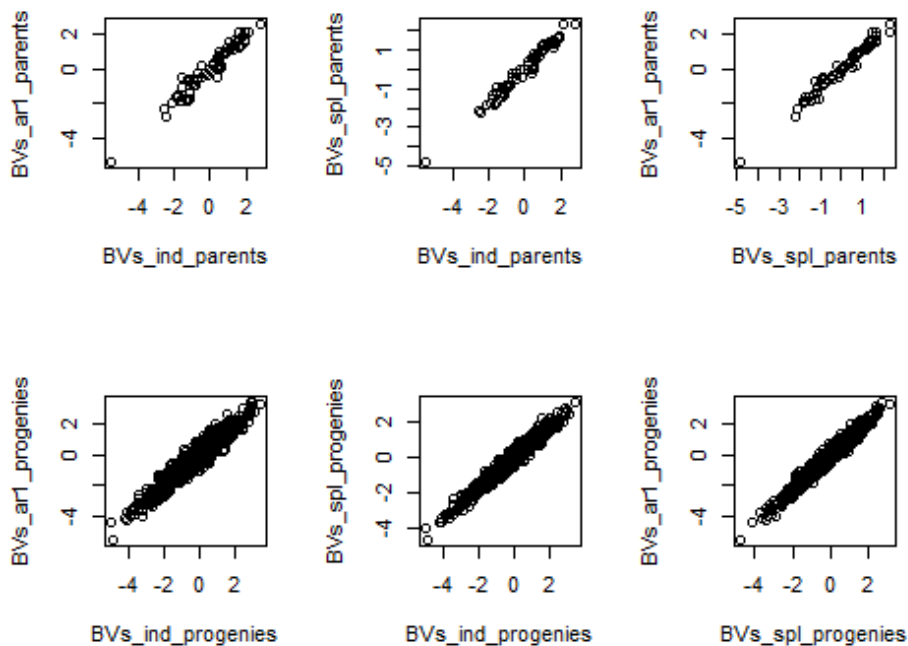
```

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)

```



10. COMPETITION ANALYSIS

```

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

```

competition effect

```
spatial = list(model = 'blocks',
               coord = data[, c('x','y')],
               id = "b1"),
data = data,
method = 'em',
debug = F)
```

```
## 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
## 5645 unknown -2817
##
## Parameters of special components:
## spatial: n.blocks: 15
##
## Variance components:
## $genetic
## genetic_direct genetic_competition
## genetic_direct 5.5670 0.7467
## genetic_competition 0.7467 0.2113
##
## $pec
## [1] 2.644
##
## $spatial
## [1] 1.952
##
## $Residual
## [1] 7.44
##
##
## Fixed effects:
## value s.e.
## gg.1 13.565 0.6034
## gg.2 14.329 0.8259
## gg.3 16.175 0.6710
## gg.4 11.632 0.8667
## gg.5 16.077 0.7332
## gg.6 10.009 1.6791
## gg.7 13.724 1.5376
## gg.8 15.691 0.6505
## gg.9 16.480 0.7380
## gg.10 12.679 1.0968
## gg.11 16.680 0.9194
```

```

## gg.12 16.884 1.0897
## gg.13 15.915 1.5376
## gg.14 14.328 0.5270

# 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] 0.6884712

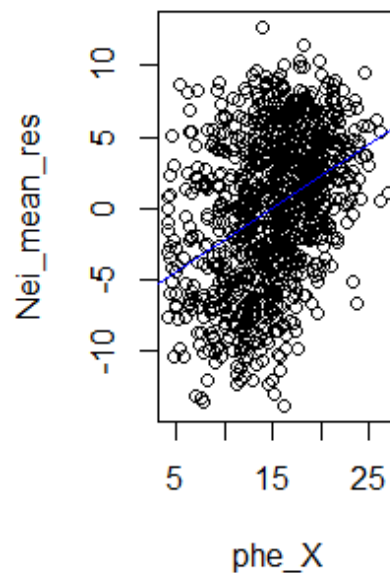
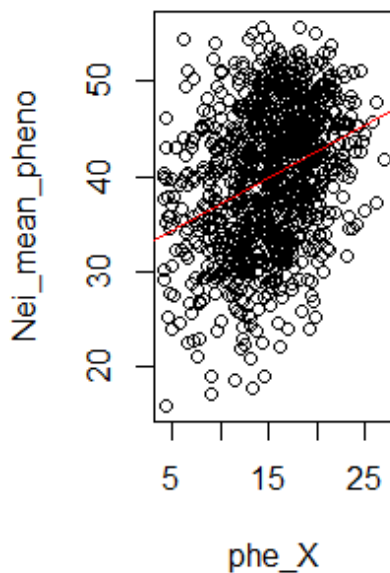
#####

# 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),(nparen
ts+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. TABLE WITH THE RESULTS OF THE FITTED SPATIAL MODELS: LogL, AIC, VAriance components and heritabili

12.1 Fit of each model: LogL

logL.blk<-res.blk\$fit\$`-2logL`

logL.spl<-res.spl\$fit\$`-2logL`

logL.ar1<-res.ar1\$fit\$`-2logL`

12.2 Fit of each model: AIC

AIC.blk<-res.blk\$fit\$AIC

AIC.spl<-res.spl\$fit\$AIC

AIC.ar1<-res.ar1\$fit\$AIC

12.3 Variance components

(Var.blk<-res.blk\$var)

Estimated variances

genetic 4.996

spatial 2.656

Residual 10.490

(Var.spl<-res.spl\$var)

Estimated variances

genetic 4.281


```

## spatial          4.203
## Residual         10.230

(Var.ar1<-res.ar1$var)

##           Estimated variances
## genetic          4.889
## spatial          4.907
## Residual         7.572

All<-c(logL.blk,logL.spl,logL.ar1,AIC.blk,AIC.spl,AIC.ar1,h2N_blk,h2N_spl,h2N_ar1)

Final_Results <- matrix(All,ncol=3,byrow=TRUE)
rownames (Final_Results) <- c("logL","AIC","Heretabilities")
colnames (Final_Results) <- c("Clasical","Splines","AR1")
(Final_Results <- as.table(Final_Results))

##           Clasical      Splines      AR1
## logL          5669.4013369 5620.1890498 5599.0410099
## AIC           5675.4013369 5626.1890498 5605.0410099
## Heretabilities 0.2753831 0.2287592 0.2814947

```