1er Coloquio de

Agricolae: Librería R Para la investigación Agrícola

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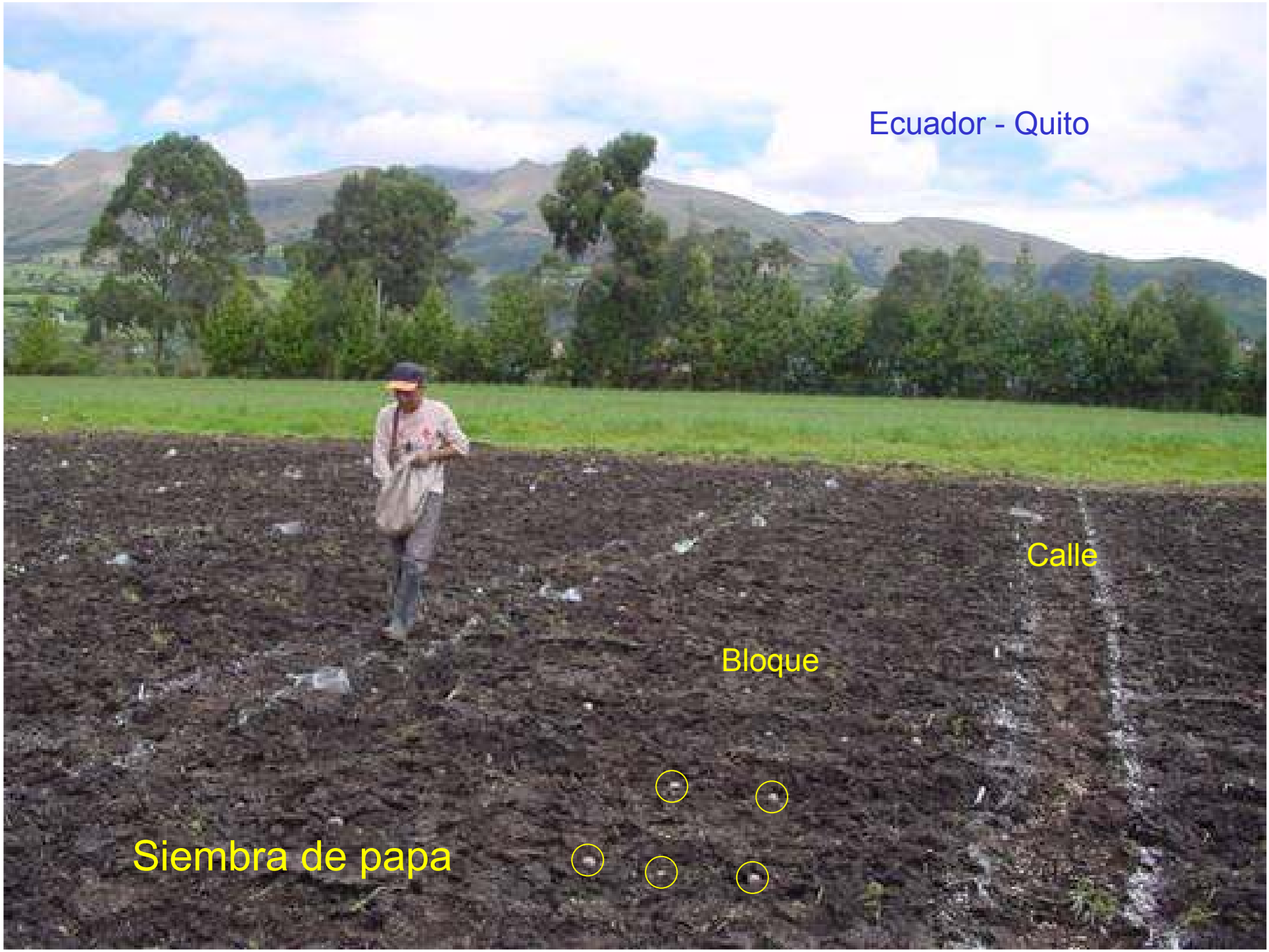
http://www.cipotato.org

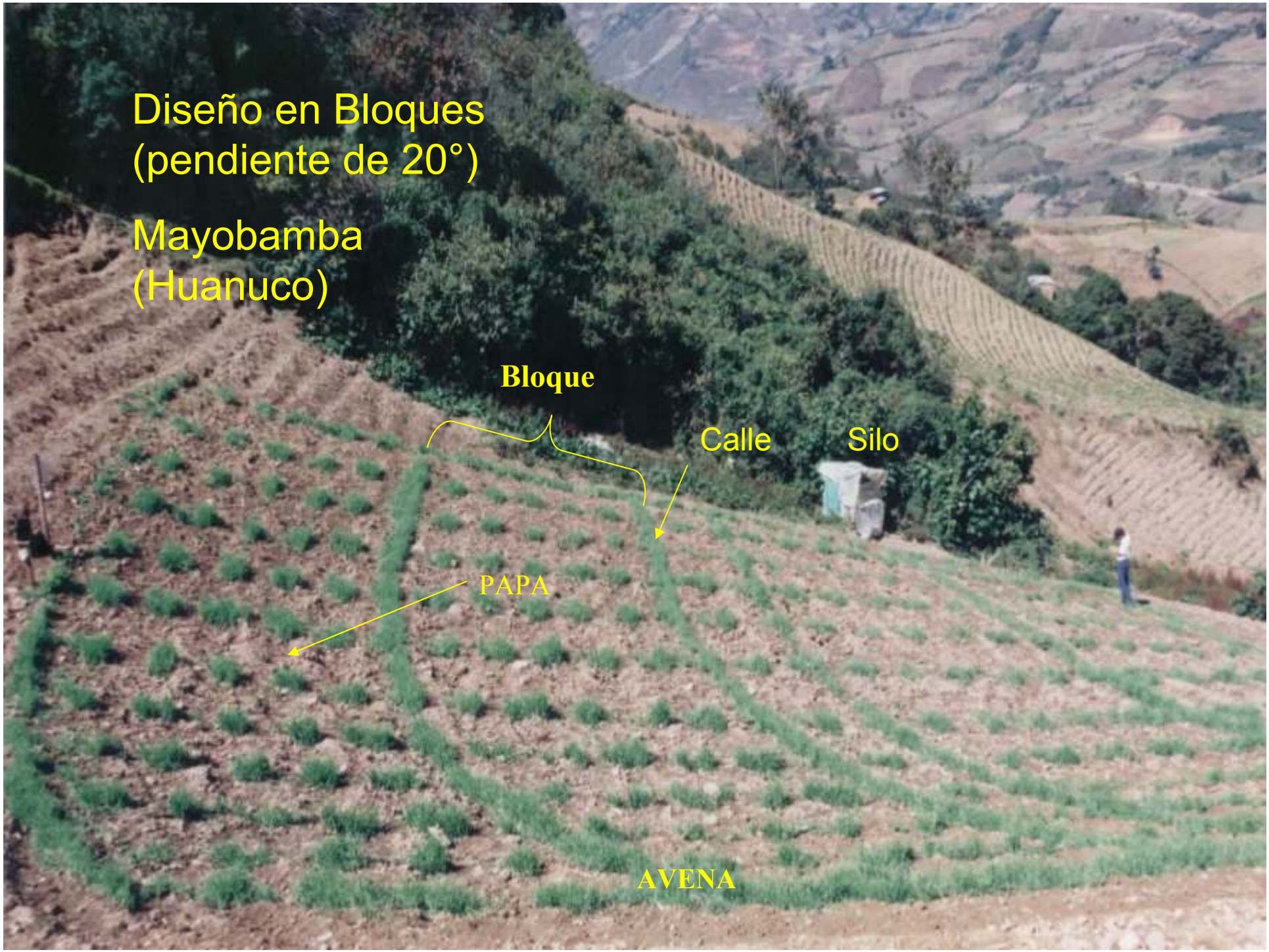
El CIP es un centro de investigacion con orientacion a cultivos de raices y tuberculos como la papa, el camote y otros cultivos andinos.

Los estudios usan mayormente los diseños de experimentos para analisis comparativo,

Son muchas las areas que realizan estas actividades que usan los diseños y analisis estadistico: Recursos Geneticos, Entomologia, Virologia, Patologia, Biodiversidad, Mejoramiento genetico de plantas y otras. Esto fue el ingrediente para desarrollar una libreria en R para apoyar a los investigadores del CIP.


Invernadero


Ecuador - Quito
Calle
Bloque
Siembra de papa


Diseño en Bloques
(pendiente de 20°)
Mayobamba
(Huanuco)
Bloque
Calle
Silo
PAPA
AVENA


Busqueda de resistencia a Rancha en clones de papa
Barrera
Barrera
Barrera
Surco infestada


Rotación de cultivos en Carhuaz para marchitez bacteriana: Pedro Aley.
Zanahoria
Papa
Col


Experimento para el control de rancha
Strip Plot: 4 variedades y 5 tratamientos con 4 rep
Variedad i
Trat j
Repeticion I

Las banderas indican el tipo de aplicacion de fungicida en la parcela


Parcelas de Observacion:
Banco de Germoplasma de
papa nativa (6000 clones)
Objetivo: Caracterizacion y
mantenimientos del material genetico
Analisis: Cluster y
dendrogramas

agricolae: Statistical Procedures for Agricultural Research

These functions are currently utilized by the International Potato Center Research (CIP), the Statistics and Informatics Instructors and the Students of the Universidad Nacional Agraria La Molina Peru, and the Specialized Master in "Bosques y Gestion de Recursos Forestales" (Forest Resource Management). This package contains functionality for the statistical analysis of experimental designs applied specially for field experiments in agriculture and plant breeding. Planning of field experiments: Lattice, factorial, RCBD, CRD, Latin Square, Greaco, BIB, PBIB, Alpha design. Comparison of multi-location trials: AMMI (biplot and triplot), Stability. Comparison between treatments: LSD, Bonferroni, HSD, Waller, Kruskal, Friedman, Durbin, Van Der Waerden. Resampling and simulation: resampling.model, simulation.model, analysis Mother and baby trials, Ecology: Indices Biodiversity, path analysis, consensus cluster, Uniformity Soil: Index Smith's.

Version:	1.0-4
Suggests:	akima, klaR, SuppDists, corpcor
Date:	2007-09-11
Author:	Felipe de Mendiburu
Maintainer:	Felipe de Mendiburu
License:	GPL
URL:	http://tarwi.lamolina.edu.pe/~fmendiburu

Downloads:

Package source:	agricolae_1.0-4.tar.gz
MacOS X binary:	agricolae_1.0-4.tgz
Windows binary:	agricolae_1.0-4.zip
Reference manual:	agricolae.pdf

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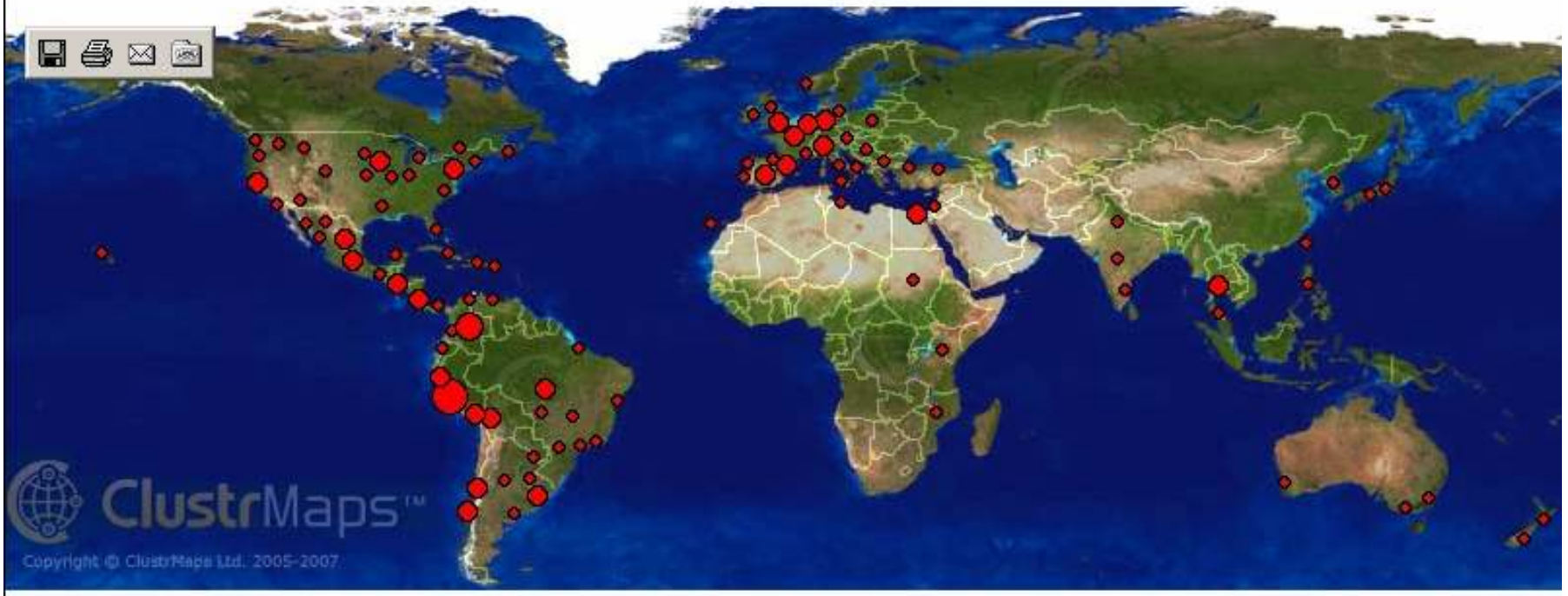
Visitors to tarwi.lamolina.edu.pe/~fmendiburu (dates below)

Navigation: Map with smaller clustrs | Maps Archive | Notes | Full Map Key



⊢ distance in which individuals are clustered

Dot sizes: ● = 1,000+ ● = 100 - 999 ● = 10 - 99 ○ = 1 - 9 visits

The above map depicts: 3,545 visits from 17 Jan 2007 to 13 Nov 2007
This map is normally updated *daily* (latest: 2007-11-13 05:50:43 GMT)

¿Por qué crear un paquete R?

Hay tres buenas razones:

- Obliga a documentar el código y proporcionar ejemplos de prueba para asegurar que en realidad funciona. También será mucho más fácil usar el código como una funcion y compartir con todas las funciones de biblioteca.
- Permite difundir la investigación, esto es una manera ideal de asegurar que otros tenga acceso al trabajo. También aumenta la probabilidad que con el tiempo el trabajo será el correcto, y es posible aprender más acerca de las propiedades de su investigación mediante la experiencia de otros.
- Compromete como un sentido de culpa al devolver algo a esta increíble comunidad de voluntarios de R

Caracteristicas de Agricolae

1. Version 1.0 - Diciembre 10, del 2006
2. Version 1.0.4 Setiembre 11, del 2007 tiene un tamaño de 550 kb
3. 33 dataset y 69 funciones

Aplicaciones

1. Manipulacion de datos
2. Estadistica descriptiva
3. Diseño de experimentos
4. Comparación multiple de tratamientos
5. Pruebas no paramétricas
6. Diseños Geneticos
7. Análisis de Estabilidad, biodiversidad
8. Pruebas de uniformidad para tamaño y forma de parcela
9. Consensus en cluster

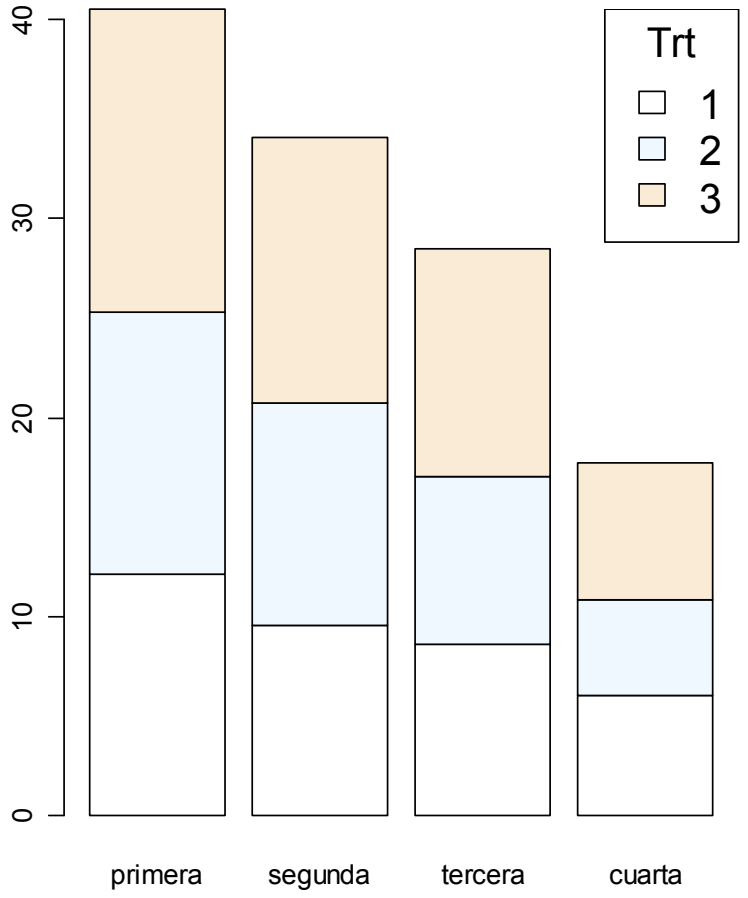
> TAPPLY.STAT(……)

```
tapply.stat(papa[,2],papa[,3:6],mean)
tapply.stat(papa[,2],papa[,3:6],function(x) sd(x)*100/mean(x))
```

```
> papa[,3:6] <-round(papa[,3:6],1)
> papa
   bloque tratamiento primera segunda tercera cuarta
1       1           1    10.0    11.2    11.3    8.3
2       2           1    13.0    12.1     8.8    7.7
3       3           1    17.6    10.7    10.5    5.1
4       4           1     9.3     7.9     6.6    5.1
5       5           1    10.7     5.9     6.0    4.1
6       1           2    12.4    13.3    11.6    7.5
7       2           2    20.3    14.1     9.6    4.7
8       3           2    19.0    12.6     8.2    3.9
9       4           2     6.5     7.2     6.6    3.8
10      5           2     7.7     8.6     5.9    4.1
11      1           3    12.1     9.8    11.5    9.8
12      2           3    15.0    15.5    13.0    7.7
13      3           3    18.4    13.4     9.4    6.4
14      4           3    15.4    13.0    11.2    6.3
15      5           3    15.1    15.2    12.0    4.2
```

```
> tapply.stat(papa[,2],papa[,3:6],mean)
  papa[, 2] primera segunda tercera cuarta
1         1   12.12    9.56    8.64   6.06
2         2   13.18   11.16    8.38   4.80
3         3   15.20   13.38   11.42   6.88
```

```
> barplot(as.matrix(medias[,-1]), col=colors()[1:3])
```



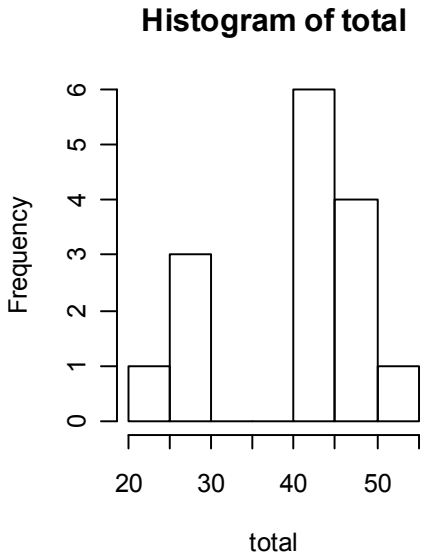

```
> legend("topright",as.character(medias[,1]),fill=colors()[1:3],cex=1.5,title="Trt")
```

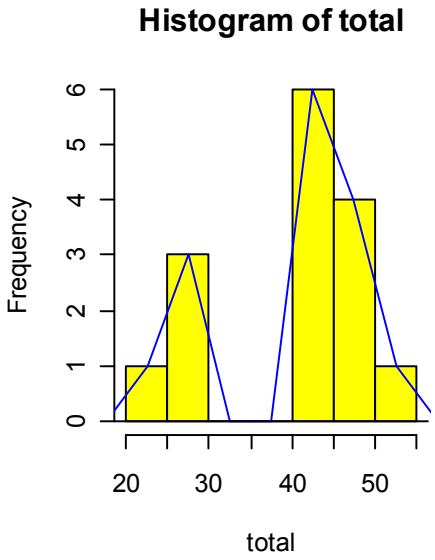
Estadistica descriptiva

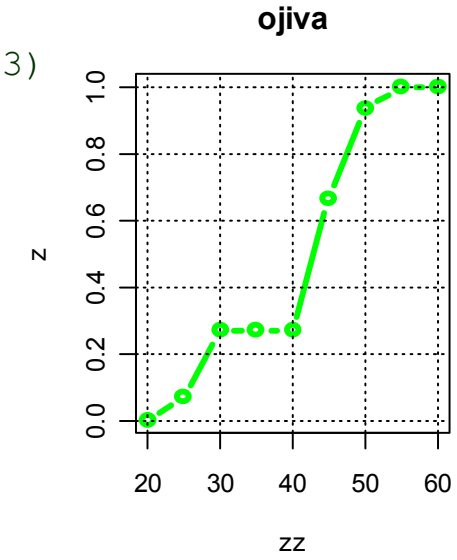
```
X<-cbind(c(1,1,1,1))
total <- as.matrix(papa[,3:6])%*%X
par(mfrow=c(2,2))
h<-hist(total)
plot(h,col="yellow")
polygon.freq(h,col="blue")
```

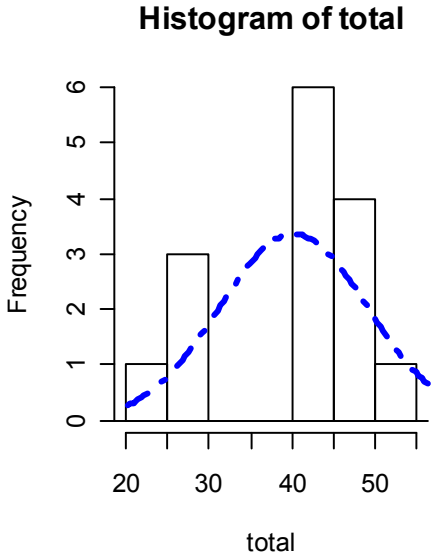
```
ojiva.freq(h,type="b",col="green",
main="ojiva",lwd=3)
stat.freq(h)
plot(h)
normal.freq(h,col="blue",lty=4,lwd=3)
```

```
> round(table.freq(h),2)
  Inf Sup   MC fi  fri Fi  Fri
   20  25 22.5  1 0.07  1 0.07
   25  30 27.5  3 0.20  4 0.27
   30  35 32.5  0 0.00  4 0.27
   35  40 37.5  0 0.00  4 0.27
   40  45 42.5  6 0.40 10 0.67
   45  50 47.5  4 0.27 14 0.93
   50  55 52.5  1 0.07 15 1.00
```









Diseño de experimentos
aleatorización y libro de campo

Alpha design, Graeco, latin square, CRD, RCBD , BIB.

La planificación de experimentos de campo es una de las principales tareas de la librería Agricolae.

- Soporta un diseño de latice simple (lattice.simple),
- Factorial en un diseño de bloques (design.ab),
- Alpha diseñó (alpha.design),
- Bloques incompleto balanceado (design.bib),
- Bloques completos al azar (design.rcbd).
- Completamente al azar (design.crd),
- Greco latino (design.graeco),
- Cuadrado latino (design.lsd).

Diseño Greco Latino

```
> T1<-c("a","b","c","d")
> T2<-c("v","w","x","y")
> Plan <-  design.graeco(T1,T2,number=101)
```

---

args: trt1, trt2, number = 1, seed = 0, kinds = "Super-Duper"

Parcelas

```
     [,1] [,2] [,3] [,4]
[1,]  101  102  103  104
[2,]  105  106  107  108
[3,]  109  110  111  112
[4,]  113  114  115  116
```

Tratamientos

```
     [,1]  [,2]  [,3]  [,4]
[1,] "d w" "b v" "a x" "c y"
[2,] "b y" "d x" "c v" "a w"
[3,] "a v" "c w" "d y" "b x"
[4,] "c x" "a y" "b w" "d v"
```

No es posible para: 6,10 y pares >= 14

Diseño Alfa (01)

(trt, k, r, number = 1, seed = 0, kinds = "Super-Duper“)

```
> trt <- letters[1:12]
> plan<-design.alpha(trt,k=3, r=2, number=101, seed=55)
```

```
alpha design (0,1) - Serie  I
Parameters Alpha design
=======================
treatmeans : 12
Block size : 3
Blocks     : 4
Replication: 3

Efficiency factor

(E ) 0.7096774

<<< Book >>>
```

Libro de campo

```
> plan
   plots cols block trt replication
1      1    1     1   c           1
2      2    2     1   a           1
3      3    3     1   d           1
4      4    1     2   j           1
...
35    35    2    12   g           3
36    36    3    12   d           3
```

Diseño alfa con semilla = 55

```
> fields<-plan[,4]
> dim(fields)<-c(k,s,r)
> for (i in 1:r) print(t(fields[,,i]))
```

I

```
     [,1] [,2] [,3]
[1,] c    a    d
[2,] j    f    k
[3,] i    l    g
[4,] b    h    e
```

II

```
     [,1] [,2] [,3]
[1,] j    c    b
[2,] k    g    h
[3,] a    i    f
[4,] l    d    e
```

III

```
[,1] [,2] [,3]
[1,] j    a    e
[2,] l    f    h
[3,] c    k    i
[4,] b    g    d
```

Diseño de bloques incompleto balanceado

```
> trt<-c("A","B","C","D","E")
> k<-3
> bib <-design.bib(trt,k,number=101,kinds ="Super-Duper")
```

```
Parameters BIB
==============
Lambda     : 3
treatmeans : 5
Block size : 3
Blocks     : 10
Replication: 6
Efficiency factor
0.8333333
<<< Book >>>
```

```
> field <-as.character(bib[,3])
> t(matrix(field,c(3,5)))
```

```
      [,1] [,2] [,3]
 [1,] "C"  "D"  "E"
 [2,] "E"  "B"  "D"
 [3,] "E"  "C"  "B"
 [4,] "B"  "A"  "D"
 [5,] "A"  "E"  "C"
 [6,] "B"  "C"  "D"
 [7,] "A"  "C"  "B"
 [8,] "C"  "A"  "D"
 [9,] "B"  "E"  "A"
[10,] "D"  "E"  "A"
```

Diseño de bloques completos y cuadrado latino

```
> trt<-c("A","B","C","D")
```

```
> rcbd <-design.rcbd(trt,5,45, kinds= "Super-Duper")
> plan <-as.character(rcbd[,3])
> dim(plan) <-c(4,5)
> print(t(plan))
```

Bloques →

```
     [,1] [,2] [,3] [,4]
[1,] "C"  "B"  "D"  "A"
[2,] "B"  "D"  "C"  "A"
[3,] "A"  "B"  "C"  "D"
[4,] "B"  "A"  "D"  "C"
[5,] "D"  "C"  "A"  "B"
```

```
> lsd <-design.lsd(trt,45,kinds="Super-Duper")
> plan <-as.character(lsd[,4])
> dim(plan) <-c(4,4)
> print(t(plan))
```

Latino { - Filas; - Columnas

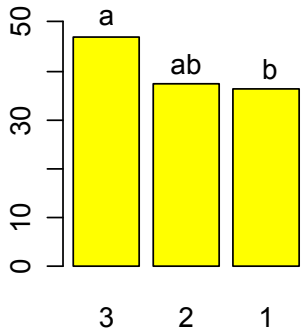
```
     [,1] [,2] [,3] [,4]
[1,] "C"  "A"  "B"  "D"
[2,] "D"  "B"  "C"  "A"
[3,] "A"  "C"  "D"  "B"
[4,] "B"  "D"  "A"  "C"
```

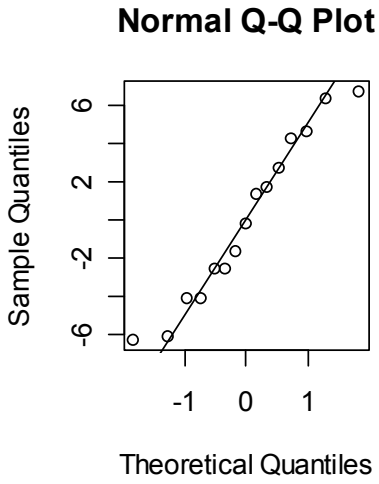
Comparación multiple

```
> modelo <- aov(primera+segunda+tercera+cuarta ~ bloque + tratamiento,papa)
> anova(modelo)
> cv.model(modelo)
```

```
> attach(papa)
```

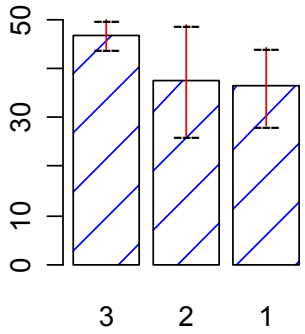
```
> comparacion<- HSD.test(primera +
segunda + tercera +
cuarta,tratamiento, 8, 33.08)
```

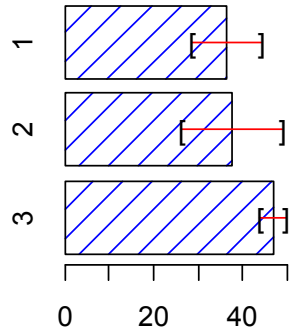





```
> bar.group(comparacion, ylim=c(0,55), col=”yellow”)
> error<-residuals(modelo)
> shapiro.test(error)
> qqnorm(error)
> qqline(error)
```

```
> bar.err(comparacion,
ylim=c(0,55),col="blue",density=4)
```






```
> bar.err(comparacion, xlim=c(0,55),col="blue",density=8,horiz=T)
```

AMMI : Estabilidad

```
> model <- AMMI(Localidad, Cip_Number,Rep, Fe,xlim=c(-3,3),ylim=c(-3,3)
,number=F, main="Hierro ppm")

ANALYSIS AMMI:  Fe

Number of observations:  120

model Y: Fe  ~ ENV + REP%in%ENV + GEN + ENV:GEN
Random effect REP%in%ENV


 Analysis of Variance Table

 Response: Y
           Df  Sum Sq Mean Sq  F value    Pr(>F)
 ENV        2 1273.82  636.91 169.3027  0.000823 ***
 REP(ENV)   3   11.29    3.76   1.6092  0.197280
 GEN       19  703.11   37.01  15.8293 3.143e-16 ***

 ENV:GEN   38  490.51   12.91   5.5215 4.463e-09 ***
 Residuals 57  133.26    2.34
 ---
 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Coeff var       Mean Fe
 9.914176         15.42227

 Analysis
     percent  acum Df   Sum.Sq   Mean.Sq F.value Pr.F
 CP1    66.3  66.3 20 325.4555 16.272773    6.96    0
 CP2    33.7 100.0 18 165.0577  9.169872    3.92    0
 CP3     0.0 100.0 16   0.0000  0.000000    0.00    1
```

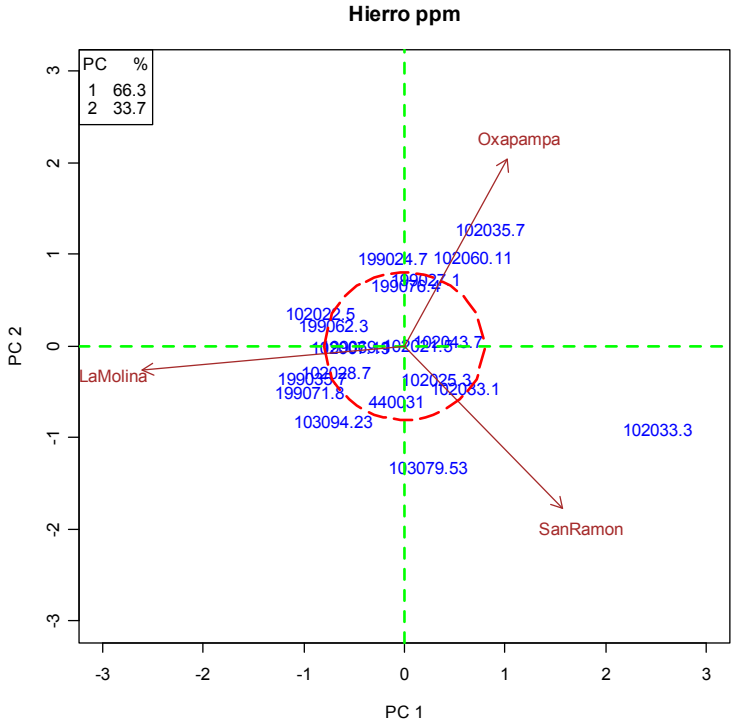
```
> AMMI.contour(model,distance=0.3,shape=20,col="red",lwd=2,lty=5)

Limit, radio: 0.8026402
Genotype  in: 11
Genotype out: 9

$`GENOTYPE IN`
 [1] "102007.19" "102021.5"  "102025.3"  "102028.7"  "102033.1"  "102043.7"
 [7] "199027.1"  "199062.3"  "199069.1"  "199076.4"  "440031"

$`GENOTYPE OUT`
[1] "102022.5"  "102033.3"  "102035.7"  "102060.11" "103079.53" "103094.23"
"199024.7"  "199035.7"  "199071.8"
```

	distance
102007.19	0.5363391
102021.5	0.1360669
102022.5	0.9136192
102025.3	0.4729085
102028.7	0.7337491
....	
199069.1	0.4897033
199071.8	1.0525786
199076.4	0.6850364
440031	0.5925231



Consensus cluster

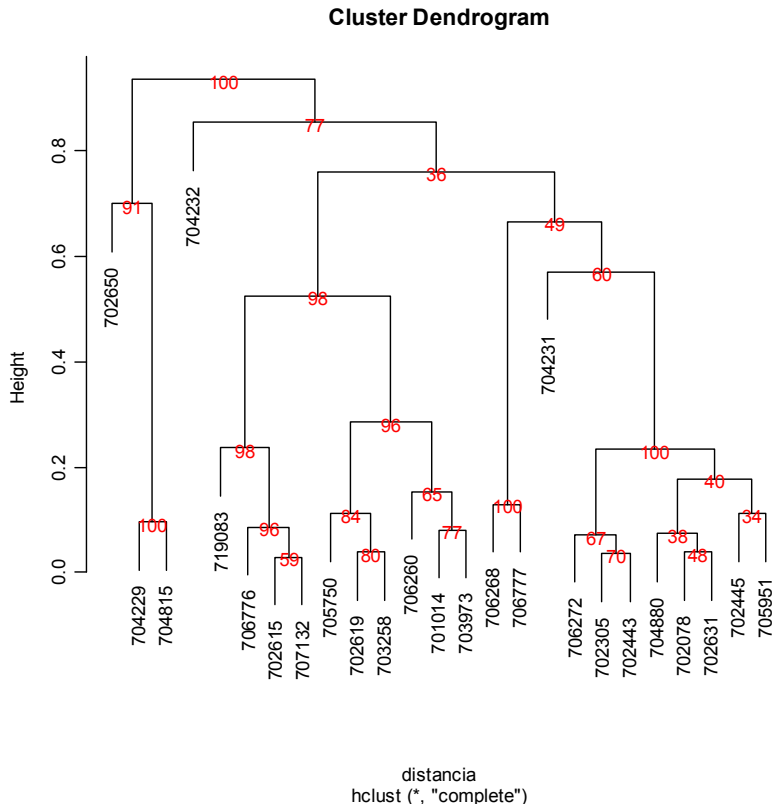
Methods distance and clustering of R, functions dist() and hclust().

```
(data, distance = c("binary", ..), method = c("complete", ..),
nboot = 500, duplicate = TRUE, cex.text = 1, col.text = "red",
...)
```

```
output<-consensus( pamCIP,distance="binary", method="complete", nboot=500)
```

```
Duplicates: 18
New data   : 25 Records
Consensus hclust
Method distance: binary
Method cluster : complete
rows and cols  : 25 107
n-boostrap     : 500

Run time       : 16.281 secs
```



Consensus cluster

Methods distance and clustering of R, functions dist() and hclust().

```
(data, distance = c("binary", ..), method = c("complete", ..),
nboot = 500, duplicate = TRUE, cex.text = 1, col.text = "red",
...)
```

OUTPUT

```
> names(output)
[1] "table.dend" "dendrogram" "duplicates"
```

to reproduce dendrogram

```
dend<-output$dendrogram
data<-output$table.dend
plot(dend)
text(data[,3],data[,4],data[,5],col="blue",cex=1)
```

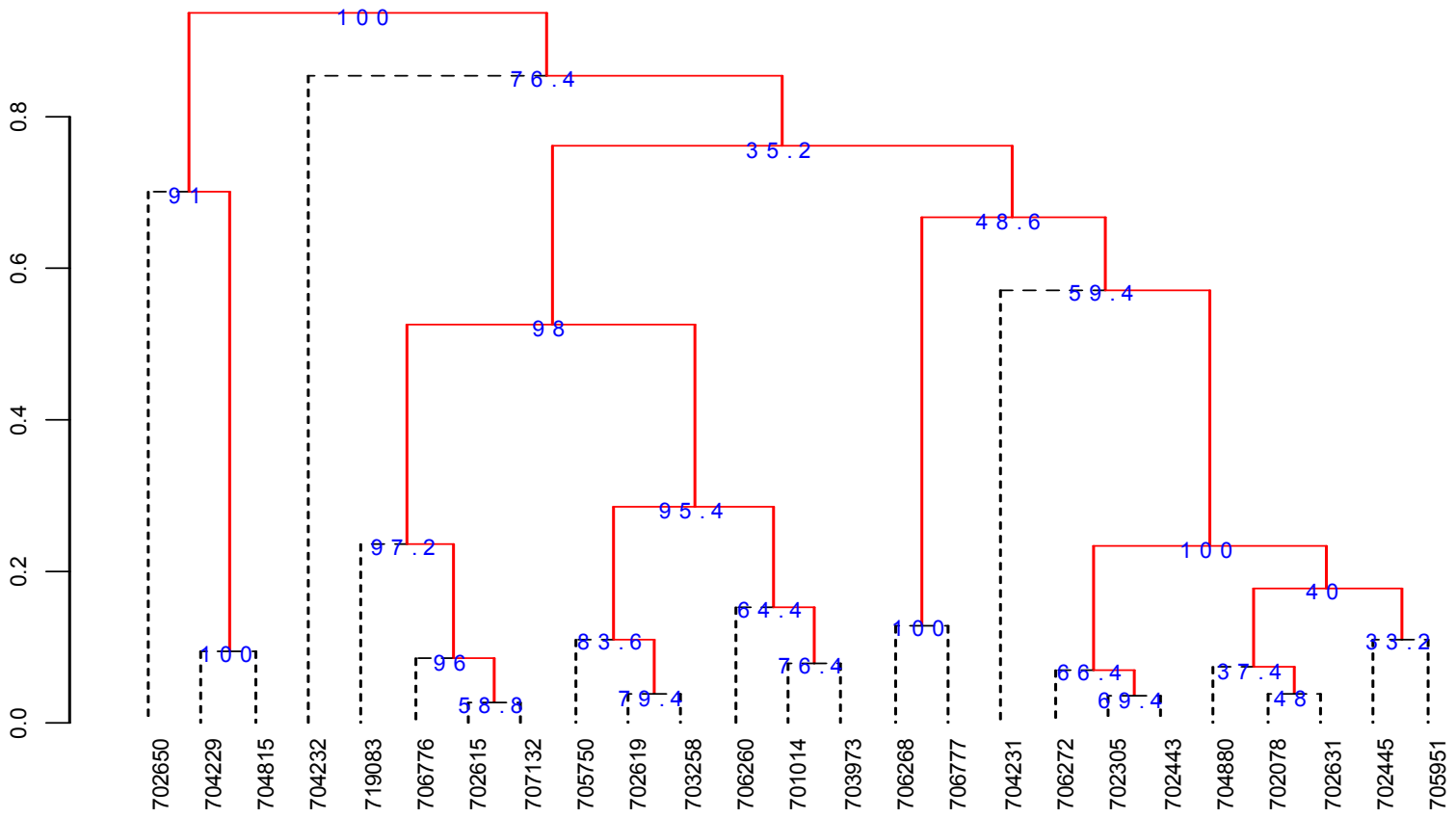
classical dendrogram

```
dend<-as.dendrogram(output$dendrogram)
plot(dend,type="r",edgePar = list(lty=1:2, col=2:1))
text(data[,3],data[,4],data[,5],col="blue",cex=1)
```

Consensus cluster

Methods distance and clustering of R, functions dist() and hclust().

```
(data, distance = c("binary", ..), method = c("complete", ..),
nboot = 500, duplicate = TRUE, cex.text = 1, col.text = "red",
...)
```



Consensus cluster

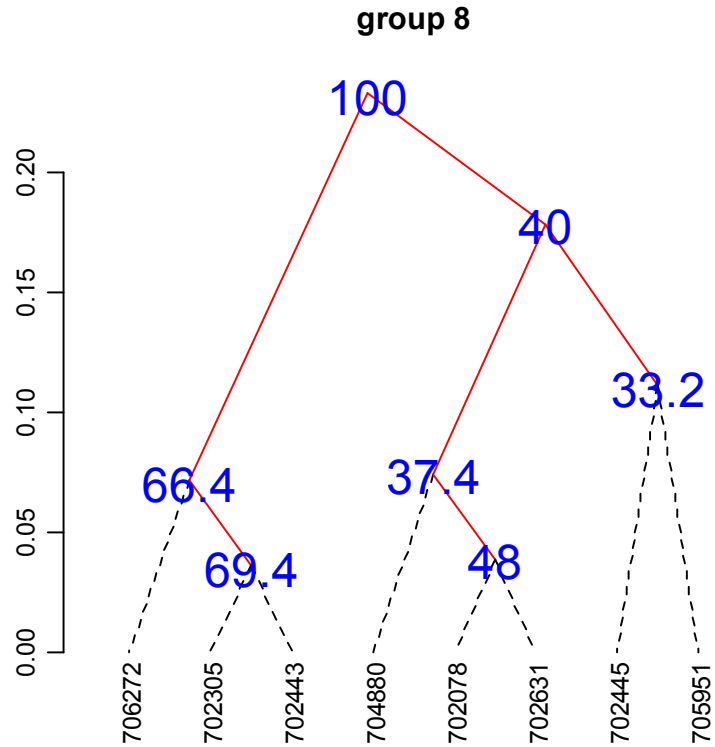
Input: output consensus

hcut()

```
(consensus, h, group, col.text = "blue", cex.text = 1, ...)
```

```
hcut(output,h=0.4,group=8,type="t",edgePar = list(lty=1:2,
col=2:1),main="group 8" ,col.text="blue",cex.text=2)
```

numbers	
1	1
2	2
3	1
4	4
5	6
6	2
7	1
8	8



Soil uniformity

```
Index.smith(data, ...)
```

```
table<-index.smith(rice, type="l",lty=4, lwd=3,
main="Relationship between CV\n per unit area and plot
size",col="red")
```

Smith's index of soil heterogeneity is used primarily to derive optimum plot size. The index gives a single value as a quantitative measure of soil heterogeneity in an area. The coefficient of variance is used to determine plot size and shape

> table

```
$model

lm(formula = CV ~
I(log(x)))

Coefficients:
(Intercept)     I(log(x))
    12.4782       -0.7009
```

```
$uniformity

      Size Width Length plots       Vx   CV
 [1,]    1     1      1   648 9044.539 13.0
 [2,]    2     1      2   324 7816.068 12.1
 [3,]    2     2      1   324 7831.232 12.1
 [4,]    3     1      3   216 7347.975 11.7
 [5,]    3     3      1   216 7355.216 11.7
 ...
[40,]  162     9     18     4 4009.765  8.6
```

Soil uniformity

```
Index.smith(data, ...)
```

```
table<-index.smith(rice, type="l",lty=4, lwd=3,
main="Relationship between CV\n per unit area and plot
size",col="red")
```

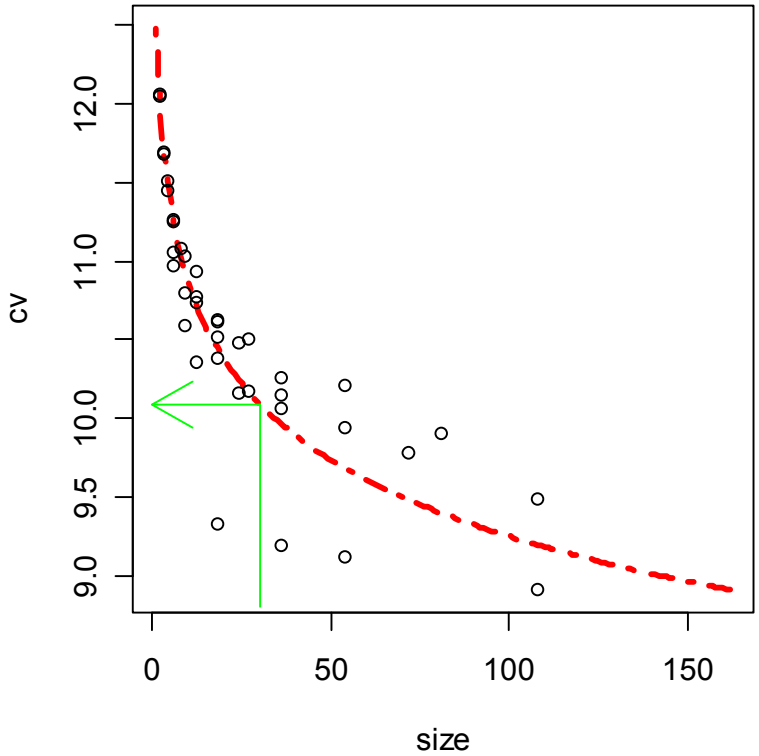
---

predict(table$model, new=data.frame(x=30))

[1] 10.09436

If plot size = 30 unit ^2
then CV = 10 %

Relationship between CV per unit area and plot size



`rice`

Data Editor

	V1	V2	V3	V4	V5
1	842	844	808	822	97
2	803	841	870	970	94
3	773	782	860	822	93
4	912	887	815	937	84
5	874	792	803	793	81
6	908	875	899	788	86
7	875	907	921	963	87
8	891	928	871	875	86
9	823	784	754	873	76

Other functions and data sets

Genetic design: north carolina design, line x tester.
Biodiversity index and confidence interval.
Descriptive statistical: cross tabulations,...
Model: simulation and resampling.

Data sets main in package 'agricolae':

ComasOxapampa	Data AUDPC Comas - Oxapampa
Glycoalkaloids	Data Glycoalkaloids
RioChillon	Data and analysis Mother and baby trials
clay	Data of Ralstonia population in clay soil
disease	Data evaluation of the disease overtime
huasahuasi	Data of yield in Huasahuasi
melon	Data of yield of melon in a Latin square experiment
natives	Data of native potato
pamCIP	Data Potato Wild
paracsho	Data of Paracsho biodiversity
ralstonia	Data of population bacterial Wilt: AUDPC
soil	Data of soil analysis for 13 localities
sweetpotato	Data of sweetpotato yield
trees	Data of species trees. Pucallpa
wilt	Data of Bacterial Wilt (AUDPC) and soil

Agricolae Version 1.0-4

http://tarwi.lamolina.edu.pe/~fmendiburu