Supplementary

Table S1. Geographical coordinates of goat breeds.

Breed	Country of origin	code	longitude	latitude
Abaza	Turkey	ABA	42.9	40.95
Swiss Alpine	Switzerland	ALP	8.22	46.72
French Alpine	France	ALP	5.64	45.19
Angora	Turkey	ANG	32.15	39.63
Argentata dell'eEna	Italy	ARG	15	37.99
German Alpine	Germany	BDE	9.08	49.87
Beshi	Saudi Arabia	BES	43.43	18.08
Bionda dell'Adamello	Italy	BIO	10.3	45.97
Brava	Portugal	BRA	-8.01	41.56
Polish Fawn Cloured Goat	Poland	BUK	18.2	52.47
Camosciata delle Alpi	Italy	CAM	9.82	46.01
Capore	Albany	CAP	20.62	40.88
Carpathian	Rumania	CAR	23.24	46.53
Corsican	France	COR	9.21	42.14
Dukati	Albany	DUK	19.5	40.29
Florida	Spain	FLR	-5.16	37.82
Cabra del Quadarrama	Spain	GDR	-4.11	40.55
Girgentana	Italy	GIR	13.87	37.51
Grigia molisana	Italy	GMO	14.4	41.52
Greek Goat	Greece	GRG	24.04	38.86
Grisons striped	Switzerland	GRS	8.41	46.77
Gurcu	Turkey	GUR	43.24	40.38
Hair	Turkey	HAI	38.42	38.74
Hasi	Albany	HAS	20.45	42.2
Liqenasi	Albany	LIQ	20.54	40.47
Makeras	Cyprus	MAK	33.38	35.16
Mati	Albany	MAT	20.08	41.92
Malague4a	Spain	MLG	-4.36	36.87
Muzhake	Albany	MUZ	20.21	40.09
Najrani	Saudi Arabia	NAG	44.59	18.43
Hungarian Native	Hungary	NAT	19.9	47.02
Orobica	Italy	ORO	9.56	45.88
Peacock goat	Switzerland	PCG	8.53	47.07
Pinzgauer	Austria	PIZ	12.77	47.35
Pyrenean	France	PYR	1.02	43.34
Payoya	Spain	PYY	-5.39	36.84
Rove	France	ROV	4.99	44.21
Sarda	Italy	SAR	9.16	39.55
St. Gallen Booted Goat	Switzerland	SGB	7.93	46.88
Skopelos	Greece	SKO	23.31	39.33
Tauernschecken	Austria	TAS	13.11	47.27
Thuringian Forest Goat	Germany	TWZ	10.31	50.84

Table S1. *Cont*.

Valdostana	Italy	VAL	7.43	45.71
Valais Black Neck	Switzerland	VBN	8.36	46.76
Verata	Spain	VRT	-5.64	40.11

Table S2. Geographical coordinates of cattle breeds.

Breed	Country of origin	code	longitude	latitude
Aberdeen Angus	Great-Britain	ABA	-2.63	57.13
Anatolian Black	Turkey	ABL	33.67	40.22
Alentejana	Portugal	ALE	-7.53	39.13
Alistano-Sanabressa	Spain	ALS	-6.8	42.1
Angeln	Germany	ANG	9.67	54.67
Arouquosa	Portugal	ARQ	-8.13	40.68
Asturiana de la Montana	Spain	ASM	-6.2	43.33
Aubrac	France	AUB	3	44.5
Avilena Negro Iberica	Spain	AVI	-4.67	40.72
Ayrshire	Great-Britain	AYR	-4.57	55.65
Baladi	Egypt	BAL	30.85	27.43
Bazadais	France	BAZ	0.22	44.43
Blonde d'Aquitaine	France	BDA	0.08	43.82
Betizu locations 2. 3	Spain	BET	-1.87	43.16
Bohemian Red	Tchechie	BOR	13.88	50
Bretonne-Pie-Noire	France	BPN	-2.57	47.83
German Black Pied	Germany	BPW	7.66	53.33
German Brown Bavaria, Wuerttemberg	Germany	BRG	10.1	47.72
German Brown Original	Germany	BRO	10.1	47.72
Belgian White-Blue	Belgium	BWB	4.43	50.45
Byelorussian Red	Byelorussia	BYR	27.3	53.53
Cabannina	Italy	CAB	9.33	44.48
Cardena	Spain	CAR	-4.33	38.26
Carinthian Blond	Austria	CBL	13.82	46.77
Charolais	France	CHA	4	46.5
Chianina	Italy	CHI	11.6	43.42
Casta Navarra	Spain	CNA	-1.65	42.63
Damascus	Syria	DAM	36.78	34.82
Danish Red	Denmark	DAR	11.55	54.45
Desi	India	DES	78	19
Dexter	Great-Britain	DEX	-7	53
Dutch Belted	Netherlands	DUB	5	52
East Anatolian Red	Turkey	EAR	40.4	40.17
Eastern Finn Cattle	Finland	EFC	26.67	62.92
Eringer	Switzerland	ERI	7.43	46.16
Evolene	Switzerland	EVO	7.5	46.12
Fries Hollands	Netherlands	FRD	5.57	52.97
Gasconne	France	GAS	1.67	43.17
Grigia Alpina	Italy	GRA	11.87	46.53

Table S2. *Cont*.

Guernsey	Great-Britain	GUE	-2.58	49.45
Groningen Whiteheaded	Netherlands	GWH	6.72	53.25
Hariana	India	HAR	78.05	26
Hereford	Great-Britain	HER	-2.82	52.05
Holstein Friesian	Netherlands, America	HFR	4.87	52.7
Hungarian Grey	Hungary	HGY	19	47
Hinterwaelder	Germany	HIW	8.05	47.73
Iraqi	Iraq	IRQ	45.35	31.75
Istrian	Croatia	IST	14.27	45.4
Jersey	Jersey	JER	-2.13	49.22
Jutland 1950	Denmark	JUT	10.33	55.3
Kalmyk	Russia	KAL	45.61	46.23
Kholmogor	Russia	KHO	41	64
Kurdi	Iraq	KUR	44.35	37
Limousin	France	LIM	2.2	45.8
Maine-Anjou	France	MAN	-1.14	47.5
Montbeliarde	France	MBE	6.4	47.17
Mertolenga	Portugal	MER	-7.8	38
Maremmana	Italy	MMA	11.62	42.35
Modicana	Italy	MOD	14.77	37.15
Monchina	Spain	MON	-3.28	43.12
Morucha	Spain	MOR	-6.38	40.68
Nelore	India	NEL	79.5	15.2
Northern Finn Cattle	Finland	NFC	25.41	66.29
Normand	France	NOR	-1	49
Ongole	India	ONG	79.5	15.2
Pajuna	Spain	PAJ	-5	38
Parthenaise	France	PAR	-0.72	46.77
Pechora (type of Kholmogor)	Russia	PCH	54	63.55
Pinzgauer	Austria	PIG	12.82	47.27
Piemontese	Italy	PIM	7.87	44.67
Podolica	Italy	POD	14.92	41.23
Polish Red	Poland	POR	19.9	50.15
Pustertaler	Austria	PUS	12	46.77
Rendena	Italy	REN	10.57	46.27
Retinta	Spain	RET	-6.33	39
Rubia Gallega	Spain	RGA	-7.84	43.17
Romagnola	Italy	ROM	12.08	44.58
Red pied	Netherlands, Germany	RP	5.77	51.77
Red Sindhi	India	RSI	67	25.6
Red Steppe	Ukraine	RST	32.2	48.35
Sahiwal	India	SAH	73.55	27.72
Salers	France	SAL	2.57	44.93
South Anatolian Red	Turkey	SAR	37	36.91
Sayaguesa	Spain	SAY	-6.05	41.34

Table S2. *Cont*.

Highland	Great-Britain	SHI	-5	56.47
Shorthorn	Great-Britain	SHN	-1.3	54.55
Simmental	Switzerland	SIM	7.47	46.47
Swedish Red Polled	Sweden	SRP	15.26	60.29
Suksun	Russia	SUK	57.1	58
Swiss Brown	Switzerland	SWB	8.78	47.01
Sykia	Greece	SYK	23.95	40.05
Turkish Grey	Turkey	TGY	27.5	41.2
Tharparkar	India	THK	71.68	23
Tudanca	Spain	TUD	-4.25	43.22
Ukrainian Grey	Ukraine	UGY	31	47.5
Ukrainian Whiteheaded	Ukraine	UWH	30.28	50.3
Vosgienne	France	VOSD	7.03	47.9
Waldviertler Blond	Austria	WBL	15.25	48.52
Western Finn Cattle	Finland	WFC	23.5	61.3
Yaroslavl	Russia	YAR	39.55	57.35
German Yellow	Germany	YEL	11.78	49.82

Table S3. Geographical coordinates of the sheep breeds.

Breed	Country of origin	code	longitude	latitude
Akkaraman	Turkey	AKK	40.31	39.86
Altamurana	Italy	ALT	15.48	41.13
Anogeiano	Greece	ANO	24.82	35.25
Bardhoka	Albany	BAR	19.73	42.02
Brown Mountain sheep	Germany	BBS	11.14	48.13
Pecora Bergamasca	Italy	BER	9.78	45.45
Churra Bragan ça na	Portugal	CHU	-8.34	41.78
Cikta	Hungary	CIK	18.45	47.62
Colmenareňa	Spain	CLM	-3.75	40.67
Daglic	Turkey	DAG	29.75	38.75
Exmoor horn	Great Britain	EXH	-3.75	51.16
Cypriot Fat Tailed	Cyprus	FTS	33.38	35.16
German Grey Heath	Germany	GGH	9.87	52.85
Polish Mountain	Poland	GOR	20.14	49.38
Kalarritiko	Greece	KAL	21.8	39.66
Karagouniko	Greece	KAR	21.83	39.48
Black karakul	Romania	KKL	26.4	47.4
Kefalleneas	Greece	KEF	20.57	38.32
Kymi	Greece	KIM	24.11	38.5
Karayaka	Turkey	KRY	37.5	40.5
Pecora delle langhe	Italy	LAN	8.04	44.49
Laticauda	Italy	LAT	14.24	41.2
Lesvos	Greece	LES	26.19	39.23
Manchega	Spain	MCG	-3.69	39.54
Morkaraman	Turkey	MOR	42.71	39.91
Spanish Merino	Spain	MRS	-5.99	39.16

Table S3. *Cont.*

Najdi	Saudi Arabia	NAJ	48	26.5
Orino	Greece	ORI	20.76	39.7
Ossimi	Egypt	OSS	31.21	30.08
Pilioritiko	Greece	PIL	23.02	39.31
Magyar racka	Hungary	RAC	20.88	47.04
Rubia del molar	Spain	RBM	-3.82	40.69
Rhönsheep	Germany	RHO	9.85	50.58
Ruda	Albany	RUD	20.28	41.5
Scottish Blackface	Great Britain	SBF	-3.16	55.5
Swaledale	Great Britain	SDL	-1.79	54.34
Sfakia	Greece	SFA	24.21	35.27
Segureña	Spain	SGR	-2.32	37.55
Shkodrane	Albany	SHK	19.43	42.27
Skopelos	Greece	SKO	23.23	39.16
Thones et Marthod	France	THM	6.62	45.62
Tsigaia	Hungary	TSI	22.38	46.47
Tsigaia	Rumania	RTS	24.79	46.19
Turcana	Rumania	TUR	23.66	46.26
Welsh Mountain	Great Britain	WMT	-3.63	52.4
Polish Heath	Poland	WRZ	19.81	53.33

Figure S1. Locations of the breeds.

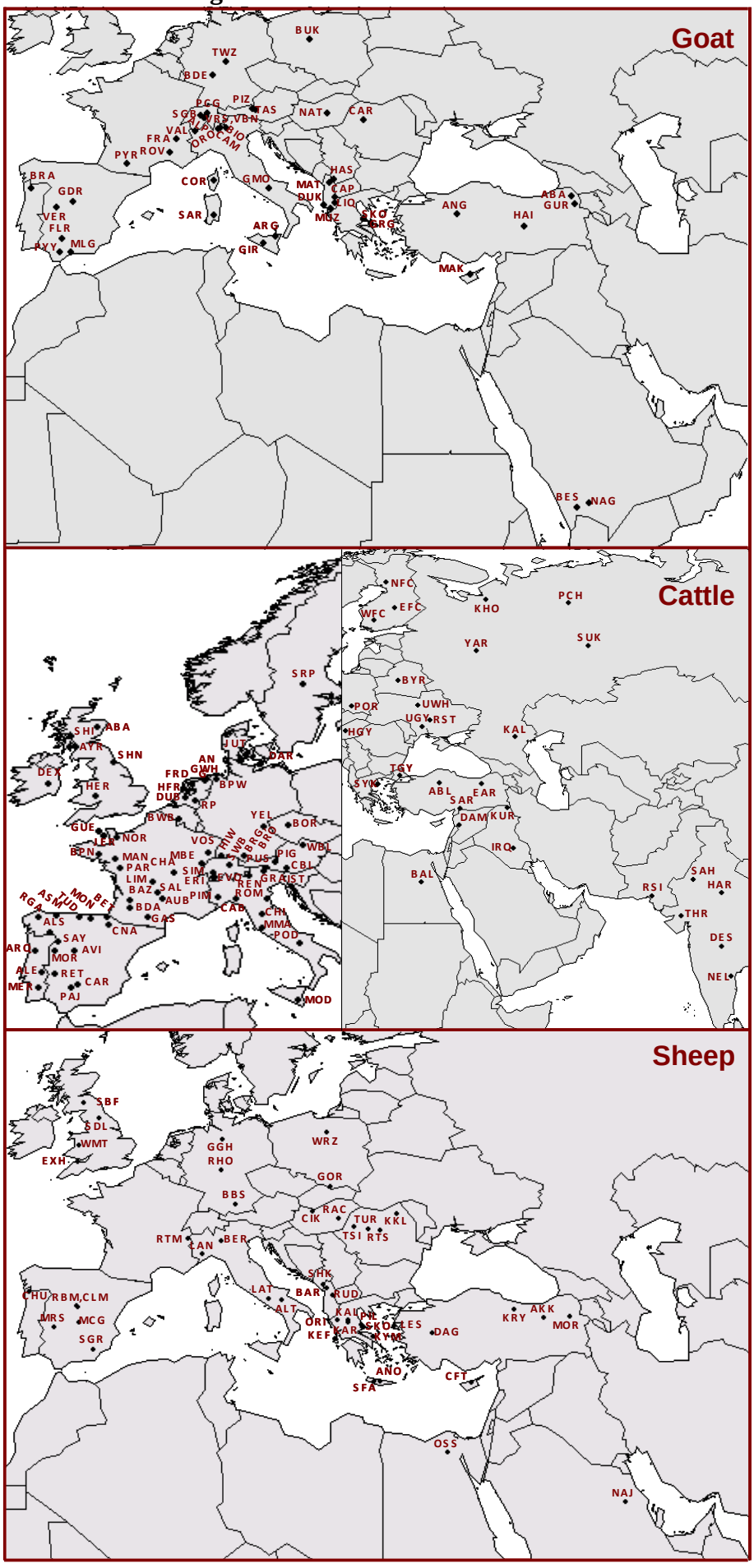


Figure. S2. Three neighboring graphs modeling the spatial structure of goat populations, the Delaunay graph (green), the Gabriel graph (red), and the first nearest neighbor graph (black).

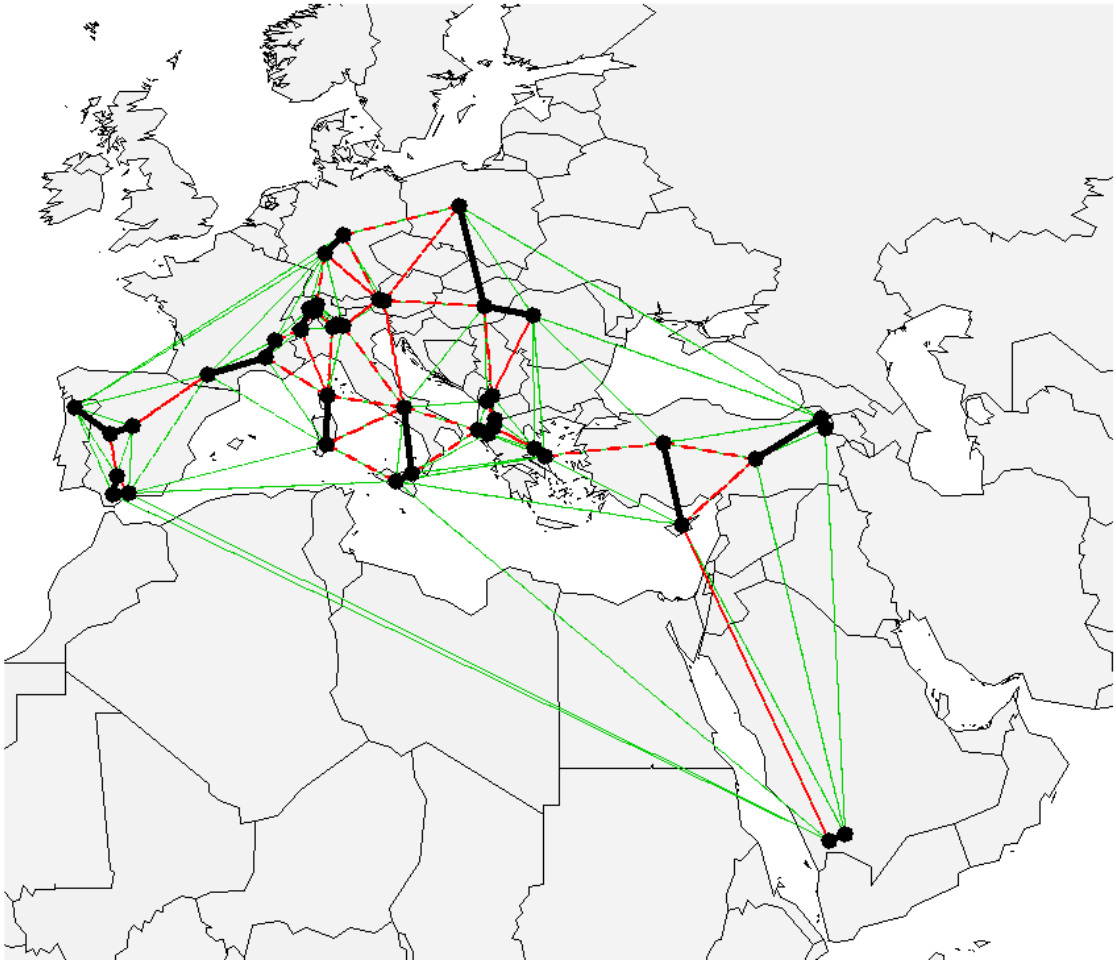


Figure S3. Projection of the goat breeds scores of five sPC's onto the geographical map. The areas of the squares are proportional to the absolute value of the score. The color of the square (black or white) corresponds to the sign of the score.

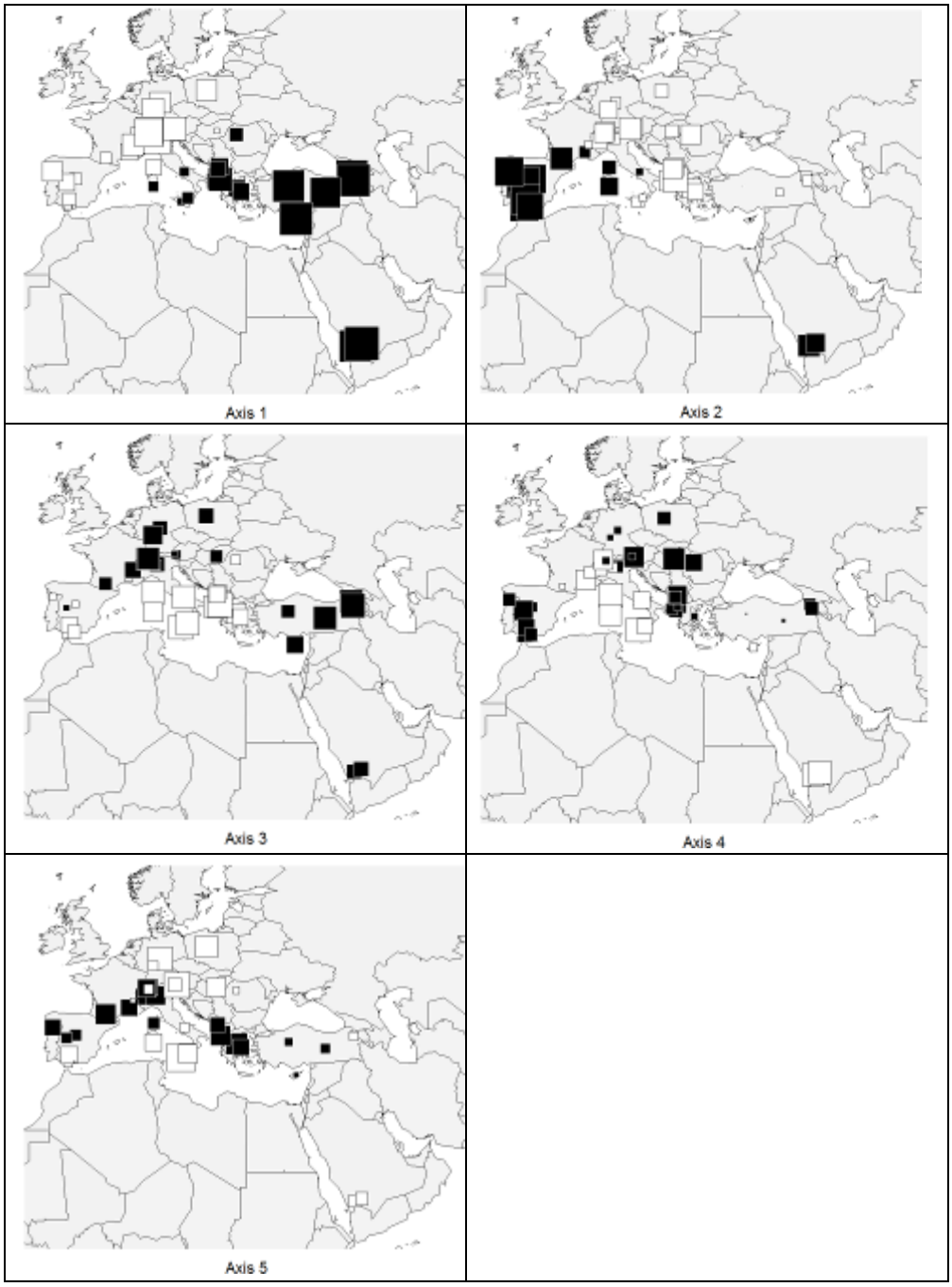
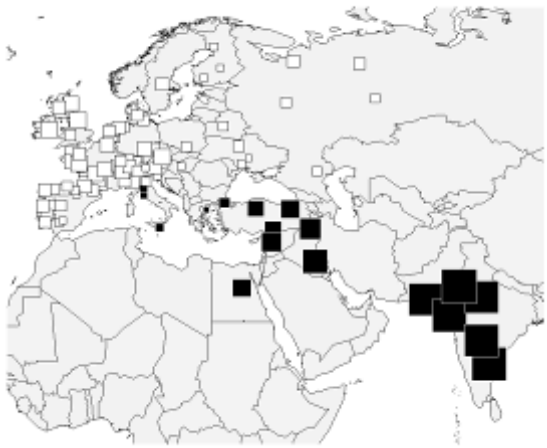


Figure. S4. Projection of the cattle breed scores of five sPC's onto the geographical map. The areas of the squares are proportional to the absolute value of the score. The color of the square (black or white) corresponds to the sign of the score.



Axis 1

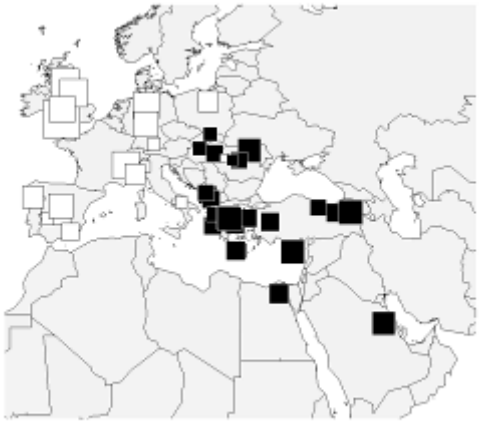
Axis 2

Axis 3

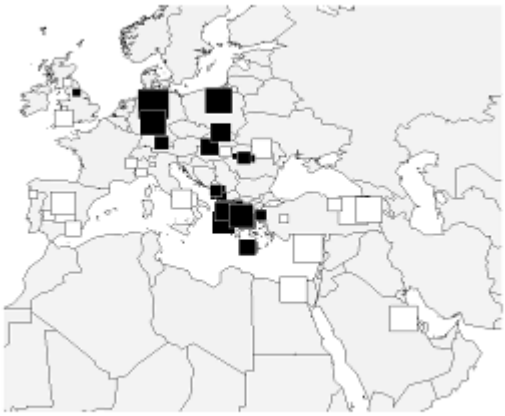
Axis 4

Axis 5

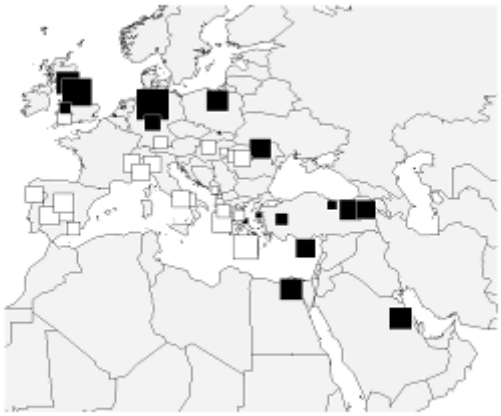
Figure S5. Projection of the sheep breed scores of five sPC's onto the geographical map. The areas of the squares are proportional to the absolute value of the score. The color of the square (black or white) corresponds to the sign of the score.



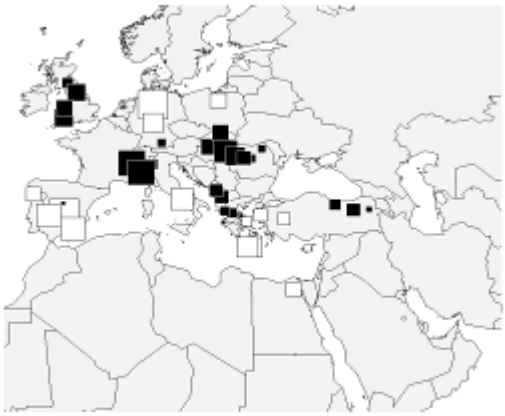
Axis 1



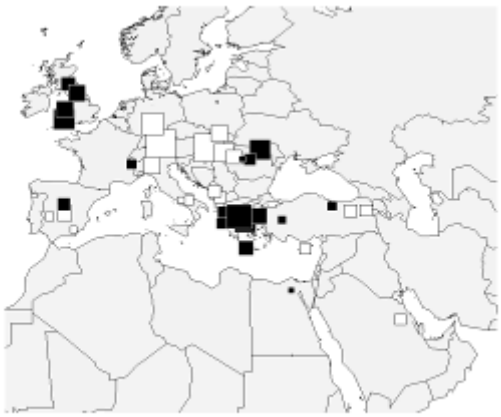
Axis 2



Axis 3



Axis 4



Axis 5

Figure S6. Projection of the sheep breed scores of the 45th sPC onto the geographical map. Figures indicate allelic richness [22].

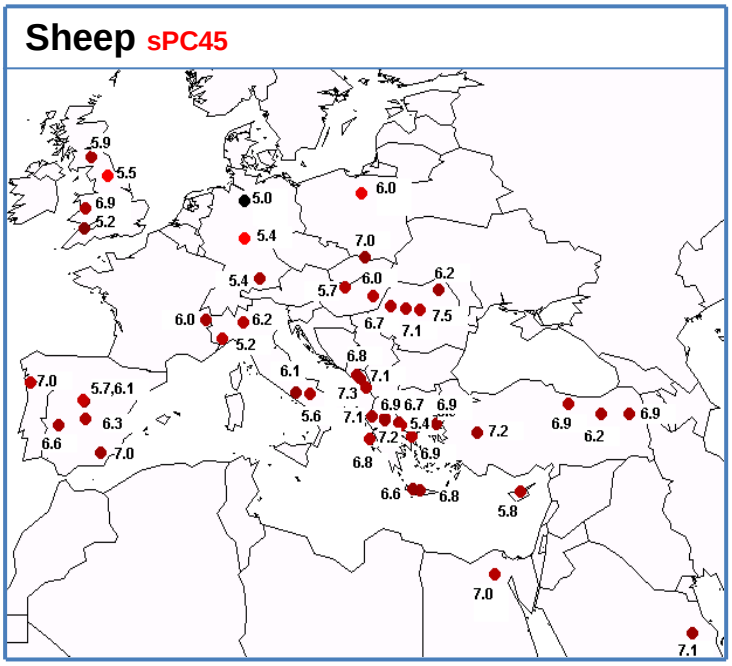


Table S4. Correlation between goat breed scores generated by sPCA with different graph types.

	Gabriel *vs.* Delaunay	Gabriel / 1st Neighbor	Delaunay / 1st Neighbor	Gabriel . sPCA *vs.* sMDS
sPC1	0.998	0.999	0.998	0.995
sPC2	0.995	0.994	0.987	0.995
sPC3	0.979	0.983	0.970	0.995
sPC4	0.743	0.825	0.432	0.995
sPC5	0.686	0.033	0.365	0.962

Table S5. PCA and sPCA analyses on goat allelic frequencies.

a. Decomposition of PCA eigenvalues.

Axis	Variance %	Cumulated Variance %	Moran's I
1	15.9	15.9	0.89
2	9.1	25.0	0.82
3	6.3	31.3	0.48
4	5.4	36.7	-0.06
5	5.3	42.0	0.29

b. Decomposition of sPCA eigenvalues.

Axis	Variance %	Cumulated Variance %	Moran's I
1	15.7	15.7	0.92
2	8.8	24.5	0.90
3	5.5	29.9	0.79
4	3.4	33.4	0.72
5	3.9	37.3	0.59

Table S6. Spatial MDS analysis on goat Reynolds distances.

a. Decomposition of MDS eigenvalues.

Axis	Var %	Cumulated Variance %	moran
1	19.1	19.1	0.88
2	10.2	29.3	0.79
3	7.3	36.6	0.28
4	6.5	43.1	0.10
5	5.8	48.8	0.20

b. Decomposition of spatial MDS.

Axis	Var %	Cumulated Variance %	Moran's I
1	18.6	18.6	0.91
2	9.8	28.4	0.89
3	5.9	34.3	0.75
4	3.6	37.9	0.68
5	4.3	42.2	0.49

Table S7. PCA and sPCA analyses on cattle allelic frequencies.

a. Decomposition of PCA eigenvalues.

Axis	Variance %	Cumulated Variance %	Moran's I
1	26.2	26.2	0.89
2	5.9	32.0	0.58
3	4.9	36.9	0.26
4	4.1	41.0	0.19
5	3.6	44.6	0.50

b. Decomposition of sPCA eigenvalues.

Axis	Variance %	Cumulated Variance %	Moran's I
1	26.1	26.1	0.89
2	5.5	31.6	0.68
3	3.6	35.1	0.74
4	3.0	38.2	0.71
5	3.1	41.2	0.64

Table S8. PCA and sPCA analyses on sheep allelic frequencies.

a. Decomposition of PCA eigenvalues.

Axis	Variance %	Cumulated Variance %	moran
1	9.5	9.5	0.76
2	8.4	17.8	-0.18
3	7.3	25.1	0.49
4	5.1	30.2	0.39
5	4.7	34.9	0.01

b. Decomposition of sPCA eigenvalues.

Axis	Variance %	Cumulated Variance %	moran
1	9.0	9.0	0.87
2	6.5	15.5	0.73
3	4.7	20.2	0.65
4	4.1	24.3	0.59
5	3.1	27.4	0.68
45	6 .4	33.8	-0.62

Figure S7. Goat marker contribution to the sPCA components.

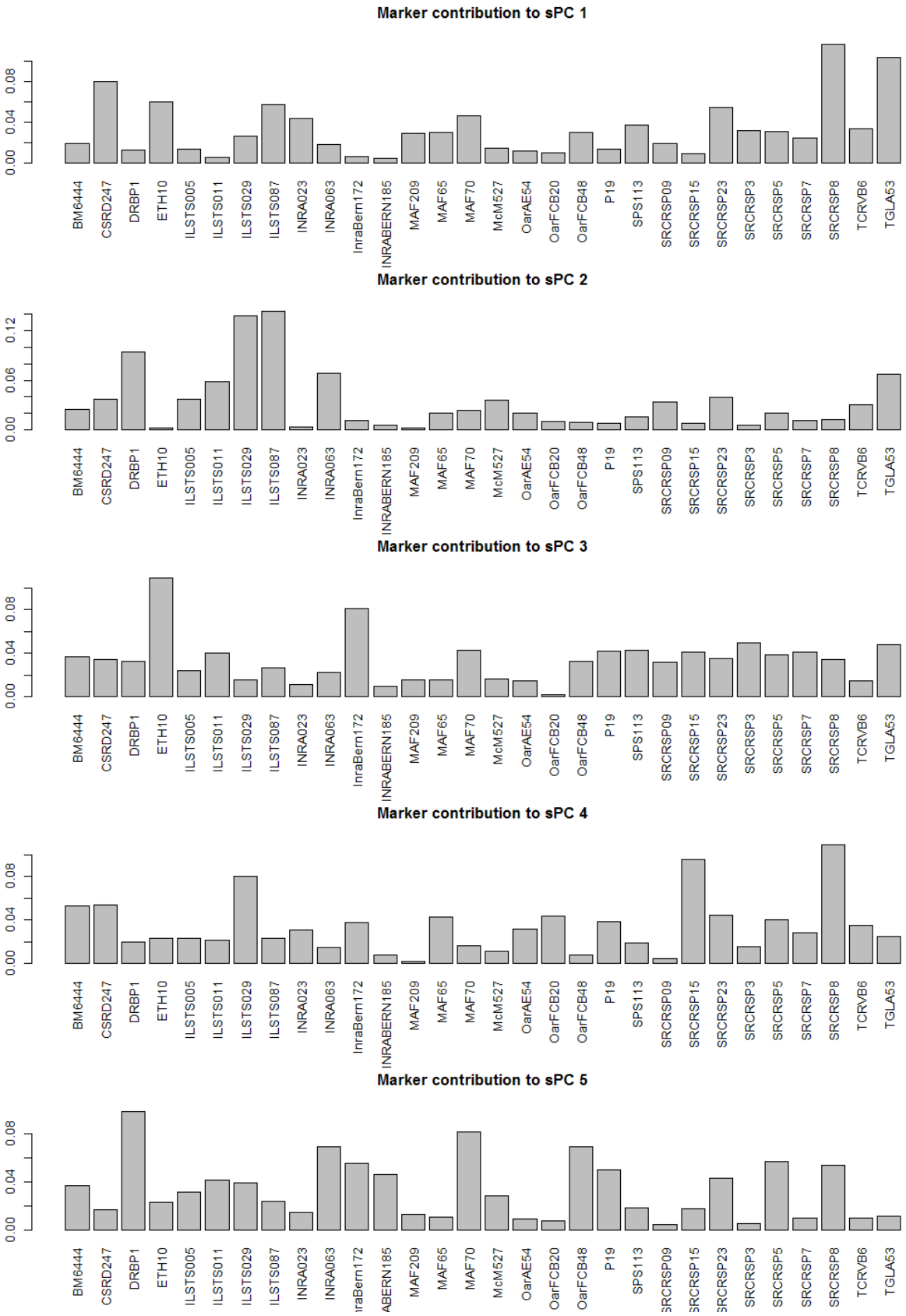


Figure S8. Cattle marker contribution to the sPCA components.

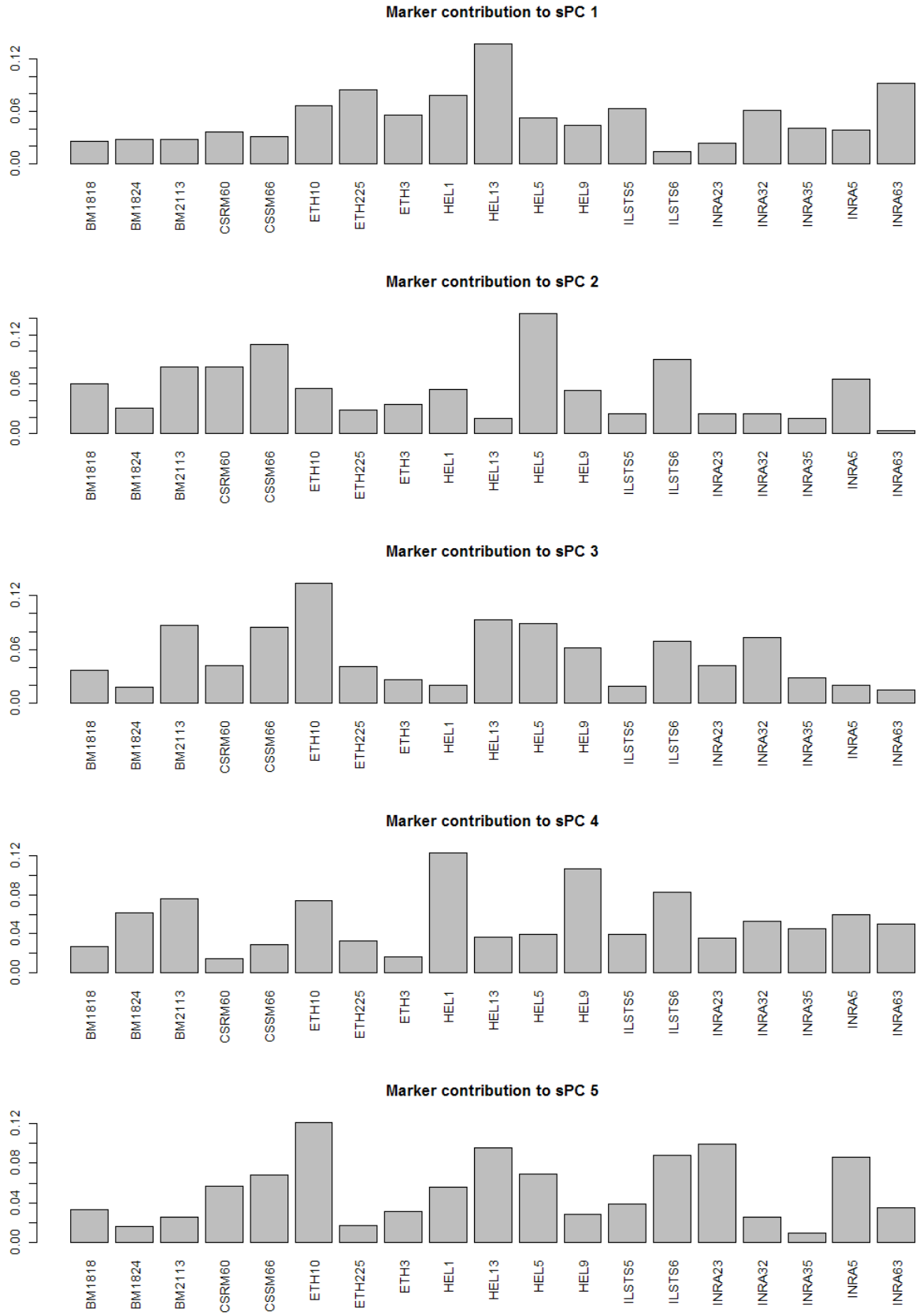
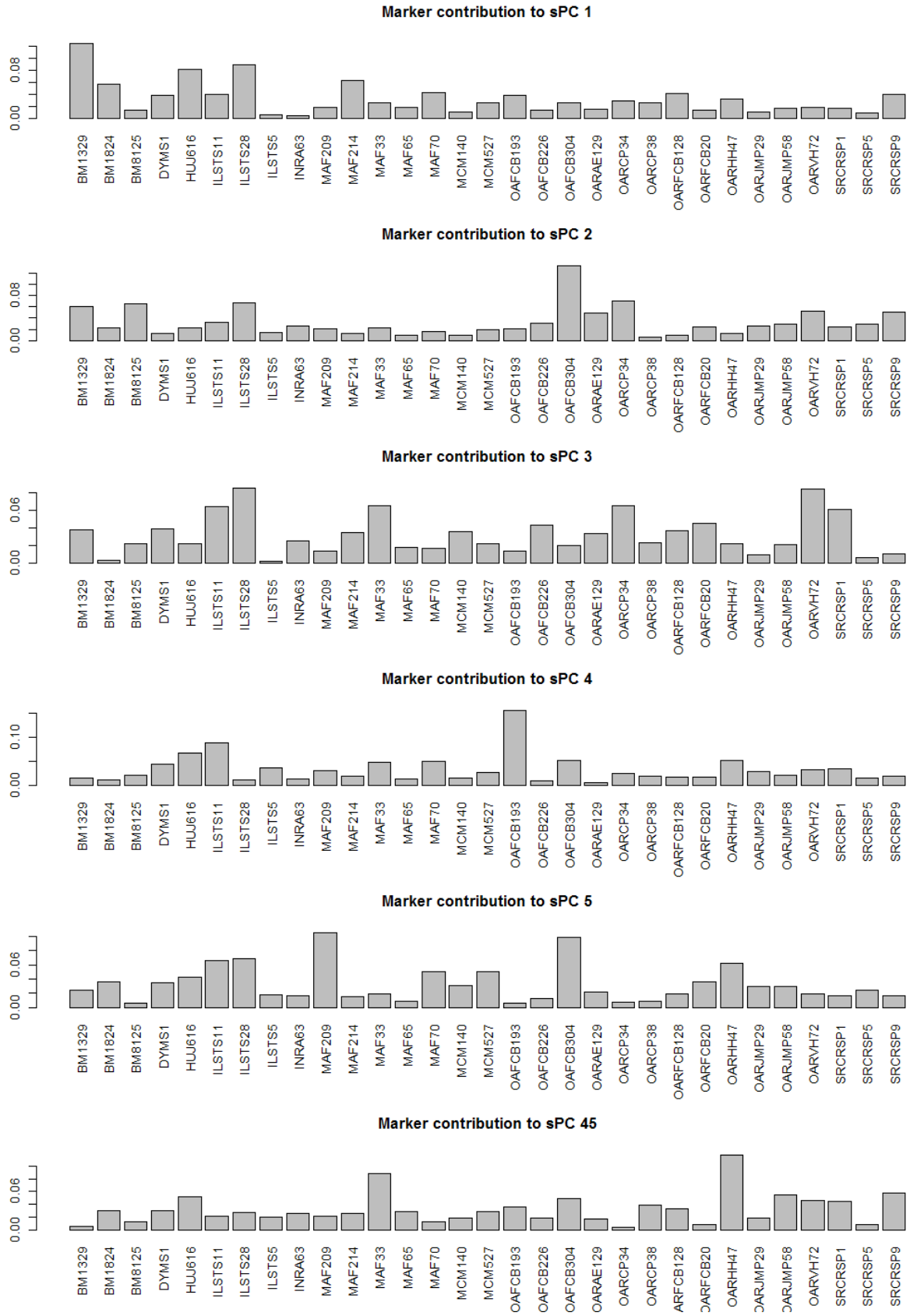


Figure S9. Sheep marker contribution to the sPCA components.



An R session

Microbov is a data set available in the adegenet package [1]. Details may be found in [2]. It gives the genotypes of 704 cattle individuals for 30 microsatellites recommended by the FAO. The individuals are divided into two countries (Africa, France), two species (Bos taurus and Bos indicus), and 15 breeds.

Coordinates of breeds are in the dataframe "coord" that is to be created. The R script is in red italic. Results are in black. Lines of comments begin by "#"

Here is the content of the dataframe. Geographic coordinates of the African breeds are approximate.

coord :

	breed	Northern.longitude	Eastern.latitude
4	Borgou	4.0000	10.00
14	Zebu	2.0000	8.00
8	Lagunaire	1.0000	6.00
16	NDama	2.5000	9.00
13	Somba	1.0000	10.00
1	Aubrac	3.0000	44.50
2	Bazadais	0.2167	44.43
3	BlondeAquitaine	0.0833	43.82
5	BretPieNoire	-2.5667	47.83
6	Charolais	4.0000	46.50
7	Gascon	1.6667	43.17
9	Limousin	2.2000	45.80
10	MaineAnjou	-1.1333	47.50
11	Montbeliard	6.4000	47.17
12	Salers	2.5667	44.93

```
# Loading of the required packages
require(ade4)
require(adegenet)
require(maptools)
gpclibPermit()

# Loading of data
data(microbov) # genetic data set supplied in the adegenet package :
data(wrld_simpl) # map

# plotting breeds on a geographical map – see Figure 1
plot(wrld_simpl,xlim=c(-10,20),ylim=c(0,50),col=grey(950:951/1000))
   s.label(coord[,2:3],include.ori=F,add.p=T,label=coord$breed,clab=.4)
```

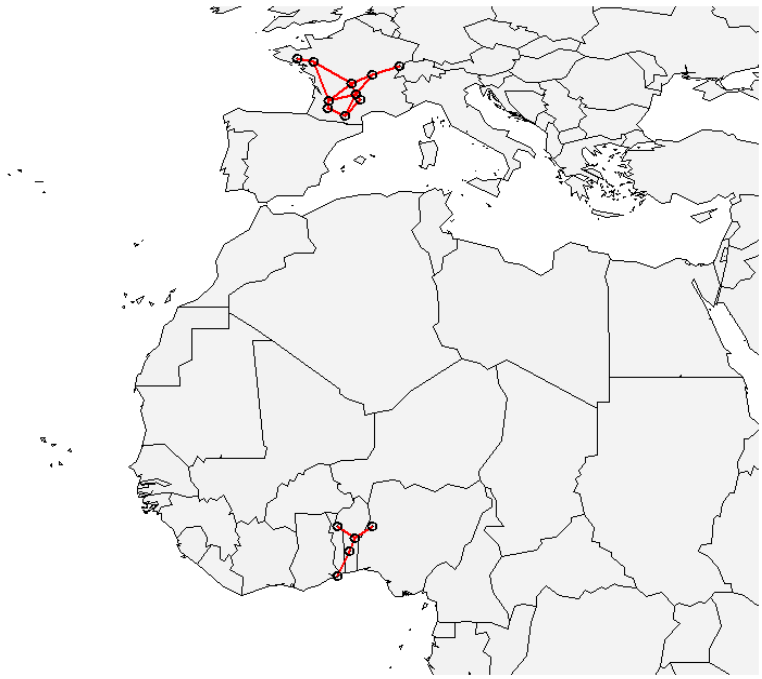
Figure 1. General map and (approximate) location of breeds.

```
# make Y, a genpop object
Y <- genind2genpop(microbov)

# build and edit tt (edit.nb=T), the Gabriel graph (type=2. Links between French and African
  # breeds are deleted
tt<-chooseCN(coord[,2:3],edit.nb=T,type=2)
Identifying contiguity for deletion ...
Delete this line (y/n) y
deleted contiguity between point 1 and 11
Options: quit[q] refresh[r] continue[c] r
Options: quit[q] continue[c]c
Identifying contiguity for deletion ...
Delete this line (y/n) y
deleted contiguity between point 5 and 11
Options: quit[q] refresh[r] continue[c] q

# drawing the neighbour graph : Figure 2
plot(wrld_simpl,xlim=c(-10,20),ylim=c(0,50),col=grey(950:951/1000))
  s.label(coord[,2:3],include.ori=F,add.p=T,label=coord$breed,clab=0,cpoint=.5)
  plot(tt,coord[,2:3],add=T,col="red",lwd=2)
```

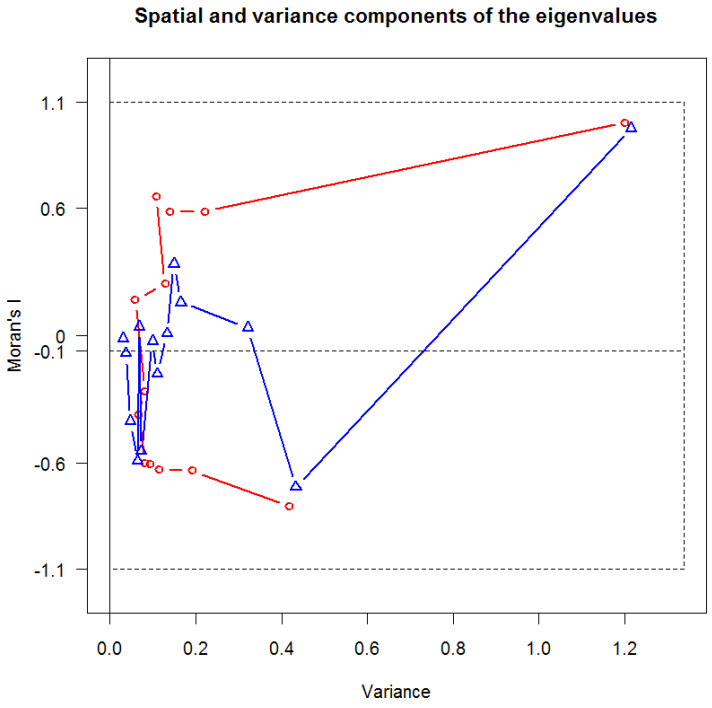
Figure 2. Neighboring graph.



 # perform the spca. Three positive and three negative eigenvalues are kept.
f.spca<-spca(Y,xy=coord[,2:3],cn=tt,plot.nb=F,scannf=F,nfposi=3,nfnega=3)

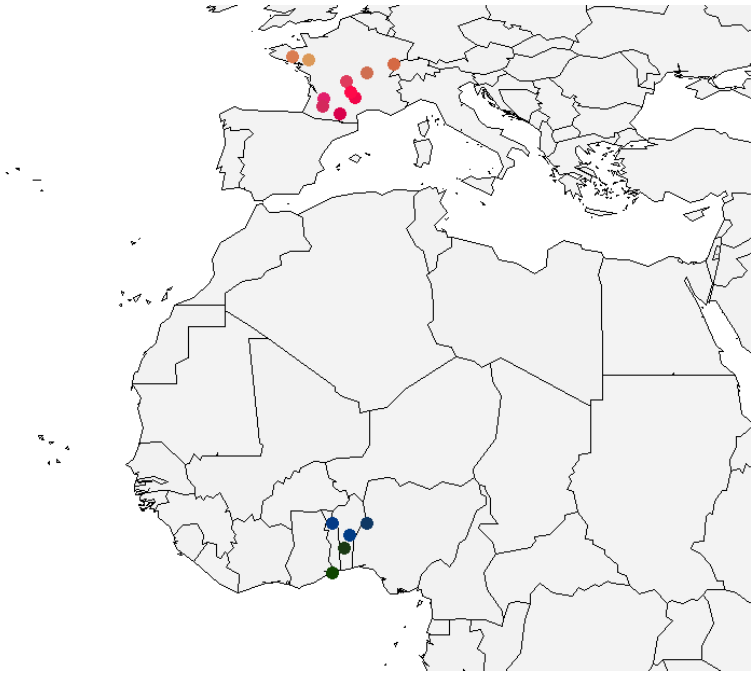
 # plot the screeplot of spca using a special function screeplot1.spca (in Appendix): Figure 3
source("screeplot1.spca.R")
screeplot1.spca(f.spca)

Figure 3. Screen plot of ordinary PCA (blue line) and spatial PCA (red line).



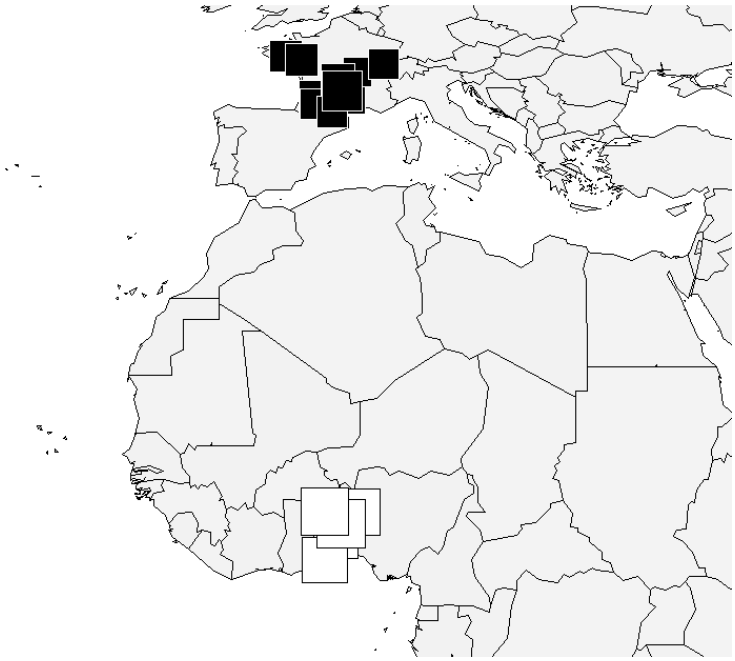
 # plot the colorplot corresponding to the first three axes.-> Figure 4
plot(wrld_simpl,xlim=c(-10,20),ylim=c(0,50),col=grey(950:951/1000))
colorplot(coord[,2:3],f.spca$li,axes=1:3,add.plot=T)

Figure 4. Color plot corresponding to the first three components.



```
# plot the bubbleplot corresponding to the first axis.-> Figure 5
plot(wrld_simpl,xlim=c(-10,20),ylim=c(0,50),col=grey(950:951/1000))
s.value(coord[,2:3],f.spca$li[,1],include.ori=F,add.p=T,cleg=0)
```

Figure 5. Projection of the breeds scores of the first sPC onto the geographical map. The areas of the squares are proportional to the absolute value of the score. The color of the square (black or white) corresponds to the sign of the score.



References

1. Jombart, T., adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics* 2008, *24*, 1403-1405.

2. Lalo ë D., Jombart T., Dufour A.-B. and Moazami-Goudarzi K. () Consensus genetic structuring and typological value of markers using Multiple Co-Inertia Analysis. *Genetics Selection Evolution*. **2007**, *39*, 545-567.

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Appendix: screeplot1.spca function. File “screeplot1.spca.R”

```
summary1.spca<-function (object, ..., printres = TRUE)
{
   if (!inherits(object, "spca"))
      stop("to be used with 'spca' object")
   if (!require(ade4, quietly = TRUE))
      stop("the library ade4 is required; please install this package")
   if (!require(spdep, quietly = TRUE))
      stop("the library spdep is required; please install this package")
   norm.w <- function(X, w) {
      f2 <- function(v) sum(v * v * w)/sum(w)
      norm <- apply(X, 2, f2)
      return(norm)
   }
   resfin <- list()
   if (printres) {
      cat("\nSpatial principal component analysis\n")
      cat("\nCall: ")
      print(object$call)
   }
   appel <- as.list(object$call)
   obj <- eval(appel$obj)
   if (is.null(appel$truenames))
      truenames <- FALSE
   f1 <- function(vec) {
      m <- mean(vec, na.rm = TRUE)
      vec[is.na(vec)] <- m
      return(vec)
   }
   if (is.genind(obj)) {
      X <- obj@tab
   }
   if (is.genpop(obj)) {
      X <- makefreq(obj, quiet = TRUE)$tab
   }
   X <- apply(X, 2, f1)
   if (truenames) {
      rownames(X) <- rownames(truenames(obj))
      colnames(X) <- colnames(truenames(obj))
   }
   nfposi <- object$nfposi
   nfnega <- object$nfnega
```

```
dudi <- dudi.pca(X, center = TRUE, scale = FALSE, scannf = FALSE,
   nf = qr(X)$rank)
lw <- object$lw
n <- nrow(X)
I0 <- -1/(n - 1)
L <- listw2mat(lw)
eigL <- eigen(0.5 * (L + t(L)))$values
Imin <- min(eigL)
Imax <- max(eigL)
Ival <- data.frame(I0 = I0, Imin = Imin, Imax = Imax)
row.names(Ival) <- ""
if (printres) {
   cat("\nConnection network statistics:\n")
   print(Ival)
}
Istat <- c(I0, Imin, Imax)
names(Istat) <- c("I0", "Imin", "Imax")
resfin$Istat <- Istat
nf <- dudi$nf
eig <- dudi$eig[1:nf]
cum <- cumsum(dudi$eig)[1:nf]
ratio <- cum/sum(dudi$eig)
w <- apply(dudi$l1, 2, lag.listw, x = lw)
moran <- apply(w * as.matrix(dudi$l1) * dudi$lw, 2, sum)
res <- data.frame(var = eig, cum = cum, ratio = ratio, moran = moran)
row.names(res) <- paste("Axis", 1:nf)
if (printres) {
   cat("\nScores from the centred PCA\n")
   print(res)
}
resfin$pca <- res
eig <- object$eig
nfposimax <- sum(eig > 0)
nfnegamax <- sum(eig < 0)
ms <- multispati(dudi = dudi, listw = lw, scannf = FALSE,
   nfposi = nfposimax, nfnega = nfnegamax)
ndim <- dudi$rank
nf <- nfposi + nfnega
agarder <- c(1:nfposi, if (nfnega > 0) (ndim - nfnega + 1):ndim)
varspa <- norm.w(ms$li, dudi$lw)
moran <- apply(as.matrix(ms$li) * as.matrix(ms$ls) * dudi$lw,
   2, sum)
res <- data.frame(eig = eig, var = varspa, moran = moran/varspa)
```

```
    row.names(res) <- paste("Axis", 1:length(eig))
    if (printres) {
        cat("\nsPCA eigenvalues decomposition:\n")
        print(res[agarder, ])
    }
    resfin$spca <- res
    return(invisible(resfin))
}

screeplot1.spca<-function (x,cex=1, ..., main = NULL)
{
    opar <- par("las")
    on.exit(par(las = opar))
    sumry <- summary1.spca(x, printres = FALSE)
    labels <- lapply(1:length(x$eig), function(i) bquote(lambda[.(i)]))
    par(las = 1)
    xmax <- sumry$pca[1, 1] * 1.1
    I0 <- sumry$Istat[1]
    Imin <- sumry$Istat[2]
    Imax <- sumry$Istat[3]
    plot(x = sumry$spca[, 2], y = sumry$spca[, 3], type = "b",
        col="red",pch=1,cex=cex,lwd=2,
        xlab = "Variance", ylab = "Moran's I",
        xlim = c(0, xmax), ylim = c(Imin * 1.1, Imax * 1.1),
        yaxt = "n", ...)
    ytick <- c(I0, round(seq(Imin, Imax, le = 5), 1))
    ytlab <- as.character(round(seq(Imin, Imax, le = 5), 1))
    ytlab <- c(as.character(round(I0, 1)), as.character(round(Imin,
        1)), ytlab[2:4], as.character(round(Imax, 1)))
    axis(side = 2, at = ytick, labels = ytlab)
    rect(0, Imin, xmax, Imax, lty = 2)
    segments(0, I0, xmax, I0, lty = 2)
    abline(v = 0)
    if (is.null(main))
        main <- ("Spatial and variance components of the eigenvalues")
    title(main)
    lines ( x = sumry$pca[, 1], y = sumry$pca[, 4],type="b",cex=cex,
        col="blue",pch=2,lwd=2)
    return(invisible(match.call()))
}
```