Clamix – Clustering Symbolic Objects Described by Discrete Distributions

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Outline

Symbolic objects

In this paper we present an approach to clustering of (very) large data sets of mixed units – units measured in different scales.
The approach is based on representation of units by *symbolic objects* (SOs) [Billard, L., Diday, E. (2006)]. The SOs can describe either single units or groups of initial units condensed into SOs in a pre-processing step.
For clustering of SOs we adapted two classical clustering methods:

- *leaders method* (a generalization of k-means method [Hartigan, J. A. (1975)], dynamic clouds [Diday, E. (1979)]).
- Ward's *hierarchical clustering method* [Ward, J. H. (1963)].

Symbolic objects described with distributions

An SO X is described by a list $X = [\mathbf{x}_i]$ of descriptions of variables V_i. In our model, each variable is described with frequency distribution (*bar chart*) of its values

$$\mathbf{f}_{xi} = [f_{xi1}, f_{xi2}, \ldots, f_{xik_i}].$$

With

$$\mathbf{x}_i = [p_{xi1}, p_{xi2}, \ldots, p_{xik_i}]$$

we denote the corresponding probability distribution.

$$\sum_{j=1}^{k_i} p_{xij} = 1, \quad i = 1, \ldots, m$$

Clustering and optimization

We approach the clustering problem as an optimization problem over the set of *feasible* clusterings Φ_k – partitions of units into k clusters. The *criterion function* has the following form

$$P(\mathbf{C}) = \sum_{C \in \mathbf{C}} p(C). \tag{1}$$

The *total error* $P(\mathbf{C})$ of the clustering $\mathbf{C}$ is a sum of *cluster errors* $p(C)$. We assume a model in which the error of a cluster is a sum of differences of its units from the cluster's *representative* T

$$p(C, T) = \sum_{X \in C} d(X, T). \tag{2}$$

Representatives

The best representative is called a *leader*

$$T_C = \underset{T}{\operatorname{argmin}}\, p(C, T). \tag{3}$$

Then we define

$$p(C) = p(C, T_C) = \min_T \sum_{X \in C} d(X, T). \tag{4}$$

The SO X is described by a list $X = [\mathbf{x}_i]$. Assume that also representatives are described in the same way $T = [\mathbf{t}_i]$, $\mathbf{t}_i = [t_{i1}, t_{i2}, \ldots, t_{ik_i}]$.

Dissimilarity between SOs

We introduce a dissimilarity measure between SOs with

$$d(X,T) = \sum_i \alpha_i d(\mathbf{x}_i, \mathbf{t}_i), \quad \alpha_i \geq 0, \quad \sum_i \alpha_i = 1, \qquad (5)$$

where

$$d(\mathbf{x}_i, \mathbf{t}_i) = \sum_{j=1}^{k_i} w_{xij}\delta(p_{xij}, t_{ij}), \quad w_{xij} \geq 0. \qquad (6)$$

The weight w_{xij} can be for the same unit X different for each variable V_i (needed in descriptions of ego-centric networks, population pyramids, etc.).

Leaders method

Leaders method is a generalization of a popular nonhierarchical clustering k-means method.
The idea is to get "optimal" clustering into a pre-specified number of clusters with the following iterative procedure:

determine an initial clustering
repeat
  determine leaders of the clusters in the current clustering;
  assign each unit to the nearest new leader – producing a new clustering
until the leaders stabilize.

Selection of the new leaders

Given a cluster C, the corresponding leader T_C is the solution of the problem

$$T_C = \operatorname{argmin}_T \sum_{X \in C} d(X, T) = \operatorname{argmin}_T \sum_{X \in C} \sum_i \alpha_i d(\mathbf{x}_i, \mathbf{t}_i)$$

$$= \operatorname{argmin}_T \sum_i \alpha_i \sum_{X \in C} d(\mathbf{x}_i, \mathbf{t}_i) = \left[\operatorname{argmin}_{\mathbf{t}_i} \sum_{X \in C} d(\mathbf{x}_i, \mathbf{t}_i) \right]_{i=1}^{m}$$

Therefore $T_C = [\mathbf{t}_i^*]$ and $\mathbf{t}_i^* = \operatorname{argmin}_{\mathbf{t}_i} \sum_{X \in C} d(\mathbf{x}_i, \mathbf{t}_i)$

Leaders

To simplify the notation we omit the index i.

$$\mathbf{t}^* = \underset{\mathbf{t}}{\operatorname{argmin}} \sum_{X \in C} d(\mathbf{x}, \mathbf{t}) = \underset{\mathbf{t}}{\operatorname{argmin}} \sum_{X \in C} \sum_{j=1}^{k} w_{xj} \delta(p_{xj}, t_j)$$

$$= \underset{\mathbf{t}}{\operatorname{argmin}} \sum_{j=1}^{k} \sum_{X \in C} w_{xj} \delta(p_{xj}, t_j)$$

$$= \Big[\underset{t_j \in \mathbb{R}}{\operatorname{argmin}} \sum_{X \in C} w_{xj} \delta(p_{xj}, t_j) \Big]_{j=1}^{k}$$

Leaders

Again we omit the index j

$$t^* = \underset{t \in \mathbb{R}}{\operatorname{argmin}} \sum_{x \in C} w_x \delta(p_x, t)$$

This is a standard optimization problem with one real variable. The solution has to satisfy the condition

$$\frac{\partial}{\partial t} \sum_{x \in C} w_x \delta(p_x, t) = 0$$

or

$$\sum_{x \in C} w_x \frac{\partial \delta(p_x, t)}{\partial t} = 0 \tag{7}$$

Dissimilarities δ

	$\delta(x,t)$	t^*_{ij}
1	$(p_x - t)^2$	$\frac{P_{ij}}{A_{ij}}$
2	$(\frac{p_x - t}{t})^2$	$\frac{Q_{ij}}{P_{ij}}$
3	$\frac{(p_x - t)^2}{t}$	$\sqrt{\frac{Q_{ij}}{A_{ij}}}$
4	$(\frac{p_x - t}{p_x})^2$	$\frac{H_{ij}}{F_{ij}}$
5	$\frac{(p_x - t)^2}{p_x}$	$\frac{A_{ij}}{H_{ij}}$
6	$\frac{(p_x - t)^2}{p_x t}$	$\sqrt{\frac{P_{ij}}{H_{ij}}}$

$$A_{ij} = \sum_{X \in C} w_{Xij} \qquad P_{ij} = \sum_{X \in C} w_{Xij} p_{Xij} \qquad Q_{ij} = \sum_{X \in C} w_{Xij} p^2_{Xij}$$

$$H_{ij} = \sum_{X \in C} \frac{w_{Xij}}{p_{Xij}} \qquad F_{ij} = \sum_{X \in C} \frac{w_{Xij}}{p^2_{Xij}}$$

Leaders

For $\delta_1(p_x, t) = (p_x - t)^2$ we get from (8)

$$0 = \sum_{x \in C} w_x \frac{\partial}{\partial t}(p_x - t)^2 = -2 \sum_{x \in C} w_x (p_x - t)$$

Therefore

$$t^* = \frac{\sum_{x \in C} w_x p_x}{\sum_{x \in C} w_x} = \frac{P}{A}$$

Leaders for δ_1

Let $w_{xij} = w_{xi}$ then for each $i = 1, \ldots, m$:

$$\sum_{j=1}^{k_i} t^*_{ij} = \frac{1}{A_i} \sum_{j=1}^{k_i} \sum_{X \in C} w_{xi} p_{xij} = \frac{1}{A_i} \sum_{X \in C} w_{xi} \sum_{j=1}^{k_i} p_{xij} = 1$$

The leaders' components are *distributions*.
Let further $w_{xij} = n_{xi}$ then for each $i = 1, \ldots, m$:

$$t^*_{Cij} = \frac{\sum_{X \in C} n_{xi} p_{xij}}{\sum_{X \in C} n_{xi}} = \frac{\sum_{X \in C} f_{xij}}{\sum_{X \in C} n_{xi}} = \frac{f_{Cij}}{n_{Ci}} = p_{Cij}$$

The leader of a union of clusters is again its distribution!

Determining the new clustering

Given leaders $\mathbf{T}$ the corresponding optimal clustering $\mathbf{C}^*$ is determined from

$$P(\mathbf{C}^*) = \sum_{X \in \mathcal{U}} \min_{T \in \mathbf{T}} d(X, T) = \sum_{X \in \mathcal{U}} d(X, T_{c^*(X)}) \qquad (8)$$

where

$$c^*(X) = \operatorname*{argmin}_k d(X, T_k)$$

We assign each unit X to the closest leader $T_k \in \mathbf{T}$.

Hierarchical agglomerative clustering

The hierarchical agglomerative clustering procedure is based on a step-by-step merging of the two closest clusters.

each unit forms a cluster: $\mathbf{C}_n = \{\{X\}: X \in \mathcal{U}\}$;
they are at level 0: $h(\{X\}) = 0,\ X \in \mathcal{U}$;
for $k = n-1$ **to** 1 **do**
  determine the closest pair of clusters
    $(u, v) = \text{argmin}_{i,j:\ i \neq j}\{D(C_i, C_j): C_i, C_j \in \mathbf{C}_{k+1}\}$;
  join the closest pair of clusters $C_{(uv)} = C_u \cup C_v$
    $\mathbf{C}_k = (\mathbf{C}_{k+1} \setminus \{C_u, C_v\}) \cup \{C_{(uv)}\}$;
    $h(C_{(uv)}) = D(C_u, C_v)$
    determine the dissimilarities $D(C_{(uv)}, C_s), C_s \in \mathbf{C}_k$
endfor

$\mathbf{C}_k$ is a partition of the finite set of units $\mathcal{U}$ into k clusters. The level $h(C)$ of the cluster $C_{(uv)} = C_u \cup C_v$.

Generalized Ward's relation

To obtain the compatibility with the adapted leaders method, we define the dissimilarity between clusters C_u and C_v, $C_u \cap C_v = \emptyset$, as

$$D(C_u, C_v) = p(C_u \cup C_v) - p(C_u) - p(C_v).$$

$\mathbf{u}_i$ and $\mathbf{v}_i$ are components of the leaders of clusters C_u and C_v, and $\mathbf{z}_i$ is a component of the leader of the cluster $C_u \cup C_v$. After some computation we get for δ_1:

$$z = \frac{A_u u + A_v v}{A_u + A_v}.$$

and

$$D(C_u, C_v) = \sum_i \alpha_i \sum_j \frac{A_{uij} \cdot A_{vij}}{A_{uij} + A_{vij}} (u_{ij} - v_{ij})^2 \qquad (9)$$

a *generalized Ward's relation*.

Other dissimilarities

Relations similar to Ward's can be derived for other dissimilarity measures $\delta(x,t)$ (see [Kejžar, N. et al. (2011)]).

δ	$D(C_u, C_v)$	z
δ_1	$\frac{A_u \cdot A_v}{A_u + A_v}(u-v)^2$	$\frac{A_u u + A_v v}{A_u + A_v}$
δ_2	$\frac{(u-z)^2}{uz^2}P_u + \frac{(v-z)^2}{vz^2}P_v$	$\frac{uP_u + vP_v}{P_u + P_v}$
δ_3	$2(zA_z - uA_u - vA_v)$	$\sqrt{\frac{u^2A_u + v^2A_v}{A_u + A_v}}$
δ_4	$(u-z)^2F_u + (v-z)^2F_v$	$\frac{H_u + H_v}{1/uH_u + 1/vH_v}$
δ_5	$\frac{(u-z)^2}{uz^2}A_u + \frac{(v-z)^2}{vz^2}A_v$	$\frac{A_u + A_v}{H_u + H_v}$
δ_6	$\frac{(u-z)^2}{u^2z}P_u + \frac{(v-z)^2}{v^2z}P_v$	$\frac{P_u + P_v}{H_u + H_v}$

The proposed approach is partially implemented in the R-packages `Clustddist` and `Clamix`.

Sheme of analysis

raw data

⇓

ENCODE

⇓

unified data

⇓

MAKE SOs

⇓

SOs - lists of distributions

⇓

`leaderSO`

⇓

clustering and cluster leaders

⇓

`hclustSO`

⇓

hierarchy and cluster leaders

⇓

ANALYSIS

⇓

dendrogram, reports

Encoding of numerical variables


```
# make "encWater" encoding

encWater <- list(
  "[0]"            = function(x) x<=0,
  "(0,5.65]"       = function(x) x<=5.65,
  "(5.65,29.5]"    = function(x) x<=29.5,
  "(29.5,53.9)"    = function(x) x< 53.9,
  "[53.9,62.4)"    = function(x) x< 62.4,
  "[62.4,70.75)"   = function(x) x< 70.75,
  "[70.75,78.05]"  = function(x) x<=78.05,
  "(78.05,88)"     = function(x) x< 88,
  "[88,100]"       = function(x) x<=100,
  "NA"             = function(x) TRUE )

encodeSO <- function(x,encoding,codeNA){
  if(is.na(x)) return(codeNA)
  for(i in 1:length(encoding)) if(encoding[i](x)) return(i)
}
```

SR22

Encoding of numerical variables


```
> source("C:\\...\\sr14\\encFood.R")
> b <- read.delim("./sr14/abbrev.txt",dec=",",row.names=2)
> colnames(b)
 [1] "NDB_No"      "Water"       "Energ_Kcal"  "Protein"     "Tot_Lipid"
 [6] "Carbohydrt"  "Fiber_TD"    "Ash"         "Calcium"     "Phosphorus"
[11] "Iron"        "Sodium"      "Potassium"   "Magnesium"   "Zinc"
[16] "Copper"      "Manganese"   "Selenium"    "Vit_A"       "Vit_E"
[21] "Thiamin"     "Ribolflavin" "Niacin"      "Panto_Acid"  "Vit_B6"
[26] "Folate"      "Vit_B12"     "Vit_C"       "FA_Sat"      "FA_Mono"
[31] "FA_Poly"     "Cholestrl"   "GmWt_1"      "GmWt_Desc1"  "GmWt_2"
[36] "GmWt_Desc2"  "Refuse_Pct"
> water <- b[[2]]
> water[1:10]
 [1] 15.87 15.87  0.24 42.41 41.11 48.42 51.80 39.28 36.75 37.65
> names(encWater)
 [1] "[0]"          "(0,5.65]"     "(5.65,29.5]"  "(29.5,53.9)"
 [5] "[53.9,62.4)"  "[62.4,70.75)" "[70.75,78.05]" "(78.05,88)"
 [9] "[88,100]"     "NA"
> wat <- sapply(water,function(x) encodeSO(x,encWater,10))
> wat[1:10]
 [1] 3 3 2 4 4 4 4 4 4 4
> varCats <- vector("list",31)
> varCats[[1]]  <- names(encWater)
  ...
> varCats[[31]] <- names(encCholestr)
> names(varCats) <- colnames(b)[2:32]
> foodSO <- vector("list",nVar)
> foodSO[[1]] <- wat
 ...
> foodSO[[31]] <- cho
```

Encoding of ordinal or nominal variables


```
cf <- read.table("./cars/cars.csv",header=TRUE,
  dec=".",row.names=1)
levType <- c("LI","KL","EN","KA","KB","RO","TE","KU")
typ <- factor(cf$type,levels=levType)
carsSO <- vector("list",26)
names(carsSO) <- colnames(cf)
carsSO$type <- as.integer(typ)
carsCats <- vector("list",26)
names(carsCats) <- colnames(cf)
carsCats$type <- c(levType,NA)
```

Data and metadata


```
setwd("C:/..../clamix.R")
source("C:\\....\\clamix.R\\clamix.R")
source("C:\\....\\clamix.R\\sr14\\encFood.R")
nVar <- 31
varCats <- vector("list",nVar)
varCats[[1]]  <- names(encWater)
varCats[[2]]  <- names(encEnergKC)
varCats[[3]]  <- names(encProtein)
varCats[[4]]  <- names(encTotLipi)
varCats[[5]]  <- names(encCarbohyd)
.......
varCats[[28]] <- names(encFaSat)
varCats[[29]] <- names(encFaMono)
varCats[[30]] <- names(encFaPoly)
varCats[[31]] <- names(encCholestr)
nVarP <- nVar+1
nCats <- sapply(varCats,length)
so <- emptySO(nCats)
b <- read.delim("./sr14/abbrev.txt",dec=",",row.names=2)
numSO <- nrow(b)
names(varCats) <- colnames(b)[2:32]
long <- rownames(b)
namedSO <- so; names(namedSO) <- c(names(varCats),"num")
for(i in 1:nVar) names(namedSO[[i]]) <- varCats[[i]]
save(nVar,nVarP,so,namedSO,numSO,long,varCats,file="./sr14/sr14.meta")
SOs <- vector("list",numSO)
for(i in 1:numSO){
  st <- so
  for(j in 1:nVar) st[[j]][foodSO[i,j]] <- 1
  st$num <- 1
  names(SOs)[[i]] <- rownames(foodSO)[[i]]
  SOs[[i]] <- st
}
save(nVar,nVarP,so,numSO,SOs,file="./sr14/sr14.so")
```

Transformation — classes

A `list` with a number of `data.frames` that consist of one variable described with distributions each can be transformed into a `symData` object. A *`symData object`* is an R class for description of histogram symbolic data. The class is represented as a list of:

`SOs`	a vector of symbolic objects (of *class `symObject`*); the transformed data set
`so`	an empty `symObject`
`namedSO`	an empty `symObject` with names for categories of each variable
`alpha`	a vector of weights α_j
`type`	a type of `symData`.

A `symObject` is an R class for description of a histogram symbolic object (one unit). It is represented as a list of variables. Each variable is represented as a vector. The last two components of the vector correspond to the number of `NA`s and the size (`num`) of the variable items.
The transformation of the data set is done via function `create.symData`.

Transformation — example


```
data(popul06f)
data(popul06m)
datalist <- list("M"=popul06f,"F"=popul06m)
dataset <- create.symData(datalist,"fDist")
summary(dataset) # description of the class

summary symData :

Dimension (units x variables): 224 x 2
Type of distributions: fDist
Outlook of symObject:
symObject :
Number of variables: 2
M
  0-4   5-9 10-14 15-19 20-24 25-29 30-34 35-39 40-44 45-49 50-54
    0     0     0     0     0     0     0     0     0     0     0
55-59 60-64 65-69 70-74 75-79   80+    NA   num
    0     0     0     0     0     0     0     0
F
  0-4   5-9 10-14 15-19 20-24 25-29 30-34 35-39 40-44 45-49 50-54
    0     0     0     0     0     0     0     0     0     0     0
55-59 60-64 65-69 70-74 75-79   80+    NA   num
    0     0     0     0     0     0     0     0
```

distSO


```
# computes weighted squared Euclidean dissimilarity between SOs

distSO <- function(X,Y,nVar,alpha){
  d <- numeric(nVar)
  for(i in 1:nVar) {
    ln <- length(X[[i]]);
    nX <- as.double(X[[i]][ln]); nY <- as.double(Y[[i]][ln])
    d[i] <- nX*sum((X[[i]][-ln]/nX-Y[[i]][-ln]/nY)**2)
  }
  dis <- as.numeric(d %*% alpha)/2
  if (is.na(dis)) dis <- Inf
  return(dis)
}
```

leaderSO


```
leaderSO <- function(dataset,maxL){
  #attach(dataset)
  so <- dataset$so; alpha <- dataset$alpha
  SOs <- dataset$SOs; nVar <- length(so)
  numSO <- length(SOs)
  L <- vector("list",maxL); Ro <- numeric(maxL)
# random partition into maxL clusters
  clust <- sample(1:maxL,numSO,replace=TRUE)
  tim <- 1; step <- 0
  repeat {
    step <- step+1
  # new leaders - determine the leaders of clusters in current partition
    for(k in 1:maxL){L[[k]] <- so; names(L)[[k]] <- paste("L",k,sep="")}
    for(i in 1:numSO){j <- clust[i];
      for(k in 1:nVar) L[[j]][[k]] <- L[[j]][[k]] + SOs[[i]][[k]] }
  # new partition - assign each unit to the nearest new leader
    clust <- integer(numSO)
    R <- numeric(maxL); p <- double(maxL)
    for(i in 1:numSO){d <- double(maxL)
      for(k in 1:maxL){d[k] <- distSO(SOs[[i]],L[[k]],nVar,alpha)}
      r <- min(d); j <- which(d==r)
      if(length(j)==0){
        cat("unit",i,"\n",d,"\n"); flush.console(); print(SOs[[i]]); flush.console()
        u <- which(is.na(d))[[1]]; cat("leader",u,"\n"); print(L[[u]])
        stop()}
      j <- which(d==r)[[1]];
      clust[i] <- j
      p[j] <- p[j] + r; if(R[j]<r) R[j]<- r
    }
```

leaderSO


```
  # report
    cat("\nStep",step,"\n")
    print(table(clust)); print(R); print(Ro-R); Ro <- R;
    print(p); print(sum(p)); flush.console()
    tim <- tim-1
    if(tim<1){
      ans <- readline("Times repeat = ")
      tim <- as.integer(ans); if (tim < 1)  break
    }
  # in the case of empty cluster put in the most distant SO
    repeat{
      t <- table(clust); em <- setdiff(1:maxL,as.integer(names(t)))
      if(length(em)==0) break
      j <- em[[1]]; rmax <- 0; imax <- 0
      for(i in 1:numSO){d <- double(maxL)
        for(k in 1:maxL){d[[k]] <- distSO(SOs[[i]],L[[k]],nVar,alpha)}
        r <- max(d);  if(rmax<r) {rmax <- r; imax <- i}
      }
      clust[[imax]] <- j; L[[j]] <- SOs[[imax]]
      cat("*** empty cluster",j,"- SO",imax,"transfered, rmax =",rmax,"\n")
      flush.console()
    }
  }
  #detach(dataset)
  leaders <- dataset
  leaders$SOs <- L
  return (list(clust=clust,leaders_symData=leaders,R=R,p=p))
}
```

hclustSO


```
hclustSO <- function(dataset){
# compute order of dendrogram
  orDendro <- function(i){if(i<0) return(-i)
    return(c(orDendro(m[i,1]),orDendro(m[i,2])))}
  #attach(dataset)
  so <- dataset$so; alpha <- dataset$alpha
  L <- dataset$SOs; nVar <- length(so)
  numL <- length(L); numLm <- numL-1
# each unit is a cluster; compute inter-cluster dissimilarity matrix
  D <- matrix(nrow=numL,ncol=numL); diag(D) <- Inf
  for(i in 1:numLm) for(j in (i+1):numL) {
      D[i,j] <- distCl(L[[i]],L[[j]],nVar,alpha); D[j,i] <- D[i,j]
  }
  active <- 1:numL; m <- matrix(nrow=numLm,ncol=2)
  node <- rep(0,numL); h <- numeric(numLm); LL <- vector("list",numLm)
  for(k in 1:numLm) LL[[k]] <- so
  for(k in 1:numLm){
  # determine the closest pair of clusters (p,q)
    ind <- active[sapply(active,function(i) which.min(D[i,active]))]
    dd <- sapply(active,function(i) min(D[i,active]))
    pq <- which.min(dd)
  # join the closest pair of clusters
    p<-active[pq]; q <- ind[pq]; h[k] <- D[p,q]
    if(node[p]==0){m[k,1] <- -p; Lp <- L[[p]]
      } else {m[k,1] <- node[p]; Lp <- LL[[node[p]]]}
    if(node[q]==0){m[k,2] <- -q; Lq <- L[[q]]
      } else {m[k,2] <- node[q]; Lq <- LL[[node[q]]]}
    for(t in 1:nVar) LL[[k]][[t]] <- Lp[[t]] + Lq[[t]]
    active <- setdiff(active,p)
    Lpq <- LL[[k]]
```

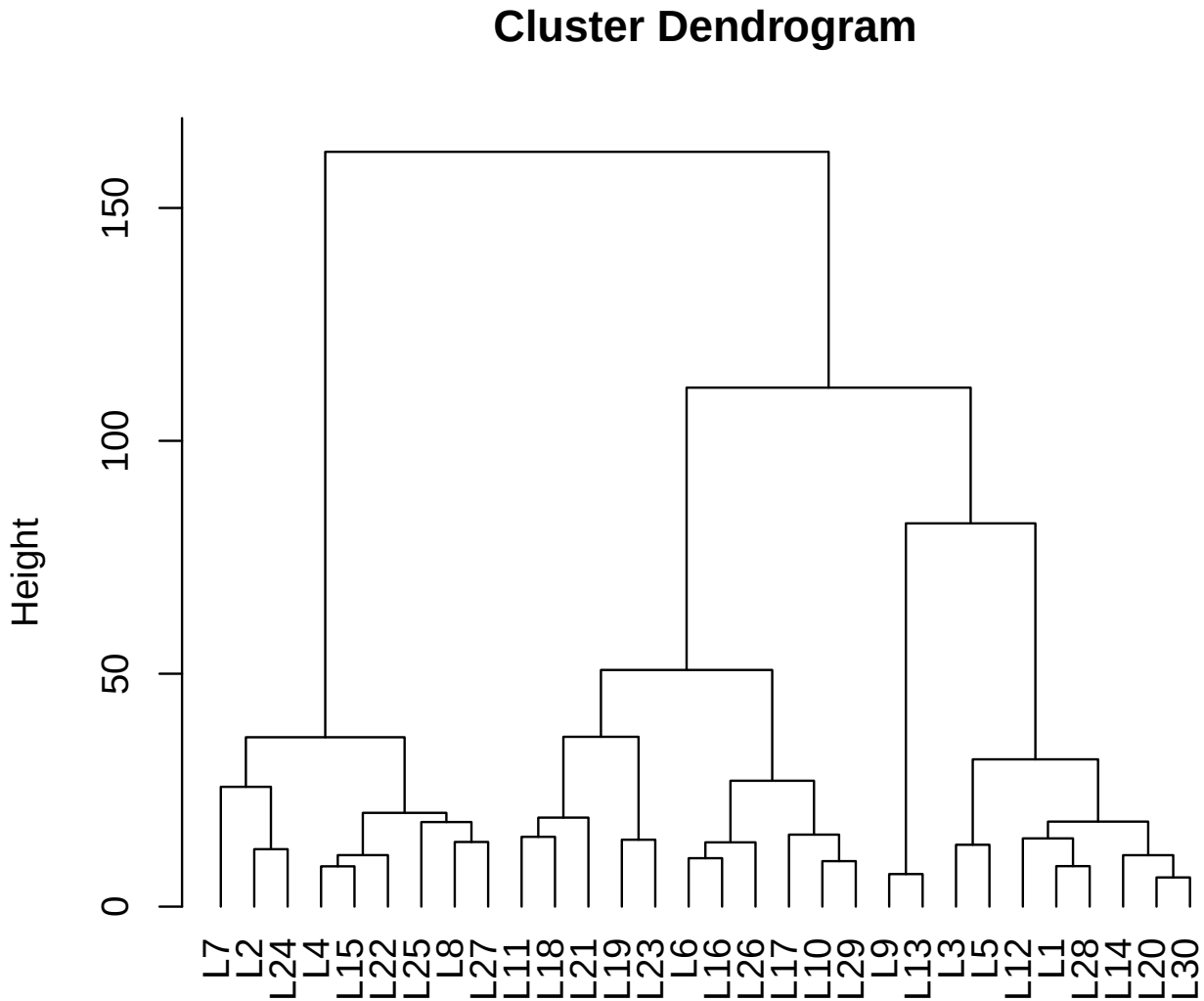
hclustSO


```
  # determine dissimilarities to the new cluster
    for(s in setdiff(active,q)){
      if(node[s]==0){Ls <- L[[s]]} else {Ls <- LL[[node[s]]]}
      D[q,s] <- distCl(Lpq,Ls,nVar,alpha); D[s,q] <- D[q,s]
    }
    node[q] <- k
  }
  hc <- list(merge=m,height=h,order=orDendro(numLm),labels=names(L),
    method="adapted ward",call=match.call(),dist.method="squared euclidean",leaders=LL)
  class(hc) <- "hclust"
  #detach(dataset)
  return(hc)
}
```

Application


```
> setwd("C:/.../clamix/clamix.R"); source("C:\\...\\clamix.R\\Clamix.R")
> load("./sr14/sr14.so"); objects()
[1] "dat"      "distSO"   "emptySO"  "encodeOS" "numSO"    "nVar"     "nVarP"
[8] "so"       "SOs"
> w <- rep(1/nVar,nVar)
> rez <- leaderSO(SOs,30,w,so)

Step 1
clust
  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24
132 244 232 263 249 589 752 193 273  57 220 235 139  80  81 530  32 201 357  36 185  74 124 205
 28  29  30
178  25 148
 [1] 0.4466406 0.4443925 0.4568250 0.4571872 0.4660656 0.4721637 0.4488782 0.4399954 0.4803863 0
.......
[21]  77.52889  31.03541  50.96077  80.89709  41.74524   8.06992  35.82662  73.81336  10.05692
[1] 2483.908
Times repeat = 3
........

Step 42
clust
  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24
116 179 367 215 299 186 275 122 324 255 179 165 165 168 206 276 221  57 308 105  73 161 290 126
 28  29  30
200 185  93
 [1] 0.3961897 0.4226399 0.4669776 0.4373342 0.4699742 0.4520931 0.4155581 0.3473073 0.4438606 0
[11] 0.4576676 0.4220990 0.3943517 0.4682425 0.4087065 0.4355381 0.4578319 0.3822814 0.4319199 0
[21] 0.2938638 0.4417081 0.4029236 0.2948455 0.4391676 0.4188643 0.4375495 0.4436210 0.4508061 0
 [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [1]  27.622636  37.895837 138.264393  64.037659 106.219657  61.910683  56.140880  28.080116  82
[10]  74.473877  47.658137  44.289150  41.319062  53.270737  67.129032  95.597943  71.012699   6
[19]  79.517072  27.804608   5.580203  55.304348  69.345717  19.494624  77.636606  37.387824 112
[28]  59.985484  59.407323  26.572320
[1] 1735.163
Times repeat = 0
> save(rez,file="sr14.rez")
> hc <- hclustSO(rez$leaders,w)
> plot(hc, hang = -1)
```

Dendrogram



Analysis of results

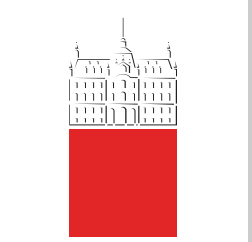

```
> long[rez$clust==7]
  [1] "LUNCHEON MEAT,BF,THIN SLICED"
  [2] "BEEF,COMP OF RTL CUTS,LN,1/4\"FAT,ALL GRDS,CKD"
  [3] "BEEF,COMP OF RTL CUTS,LN,1/4\"FAT,CHOIC,CKD"
  [4] "BEEF,COMP OF RTL CUTS,LN,1/4\"FAT,SEL,CKD"
  [5] "BEEF,COMP OF RTL CUTS,LN,1/4\"FAT,PRIME,CKD"
  [6] "BEEF,BRISKET,WHL,LN,1/4\"FAT,ALL GRDS,CKD,BRSD"
  [7] "BEEF,BRISKET,FLAT HALF,LN,1/4\"FAT,ALL GRDS,CKD,BRSD"
  [8] "BEEF,BRISKET,POINT HALF,LN,1/4\"FAT,ALL GRDS,CKD,BRSD"
  [9] "BEEF,CHUCK,ARM POT RST,LN,1/4\"FAT,ALL GRDS,CKD,BRSD"
 [10] "BEEF,CHUCK,ARM POT RST,LN,1/4\"FAT,CHOIC,CKD,BRSD"
  ....
 [43] "BEEF,RIB,SML END (RIBS 10-12),LN,1/4\"FAT,PRIME,CKD,RSTD"
 [44] "BEEF,RIB,SHORTRIBS,LN,CHOIC,CKD,BRSD"
 [45] "BEEF,RND,FULL CUT,LN&FAT,1/4\"FAT,CHOIC,CKD,BRLD"
 [46] "BEEF,RND,FULL CUT,LN&FAT,1/4\"FAT,SEL,CKD,BRLD"
  ..........
 [79] "BEEF,SHANK CROSSCUTS,LN,1/4\"FAT,CHOIC,CKD,SIMMRD"
 [80] "BEEF,SHRT LOIN,PRTRHS STEAK,LN,1/4\"FAT,CHOIC,CKD,BRLD"
 [81] "BEEF,SHRT LOIN,T-BONE STEAK,LN,1/4\"FAT,CHOIC,CKD,BRLD"
 [82] "BEEF,TENDERLOIN,LN&FAT,1/4\"FAT,CHOIC,CKD,RSTD"
 [83] "BEEF,TENDERLOIN,LN&FAT,1/4\"FAT,SEL,CKD,BRLD"
  .....
[102] "BEEF,TOP SIRLOIN,LN,1/4\"FAT,CHOIC,CKD,BRLD"
[103] "BEEF,TOP SIRLOIN,LN,1/4\"FAT,CHOIC,CKD,PAN-FRIED"
[104] "BEEF,TOP SIRLOIN,LN,1/4\"FAT,SEL,CKD,BRLD"
[105] "BEEF,GROUND,EX LN,CKD,BKD,WELL DONE"
[106] "BEEF,GROUND,EX LN,CKD,BRLD,MED"
[107] "BEEF,GROUND,EX LN,CKD,BRLD,WELL DONE"
  .........
[271] "BEEF,TOP SIRLOIN,LN&FAT,1/8\"FAT,CHOIC,CKD,PAN-FRIED"
[272] "BEEF,TOP SIRLOIN,LN&FAT,1/8\"FAT,SEL,CKD,BRLD"
[273] "LAMB,DOM,COMP OF RTL CUTS,LN,1/4\"FAT,CHOIC,CKD"
[274] "BEEF,SHRT LOIN,T-BONE STEAK,LN&FAT,1/8\"FAT,ALL GRDS,CKD,BRLD"
[275] "BEEF,SHRT LOIN,T-BONE STEAK,LN&FAT,1/8\"FAT,SEL,CKD,BRLD"
```

Analysis of results

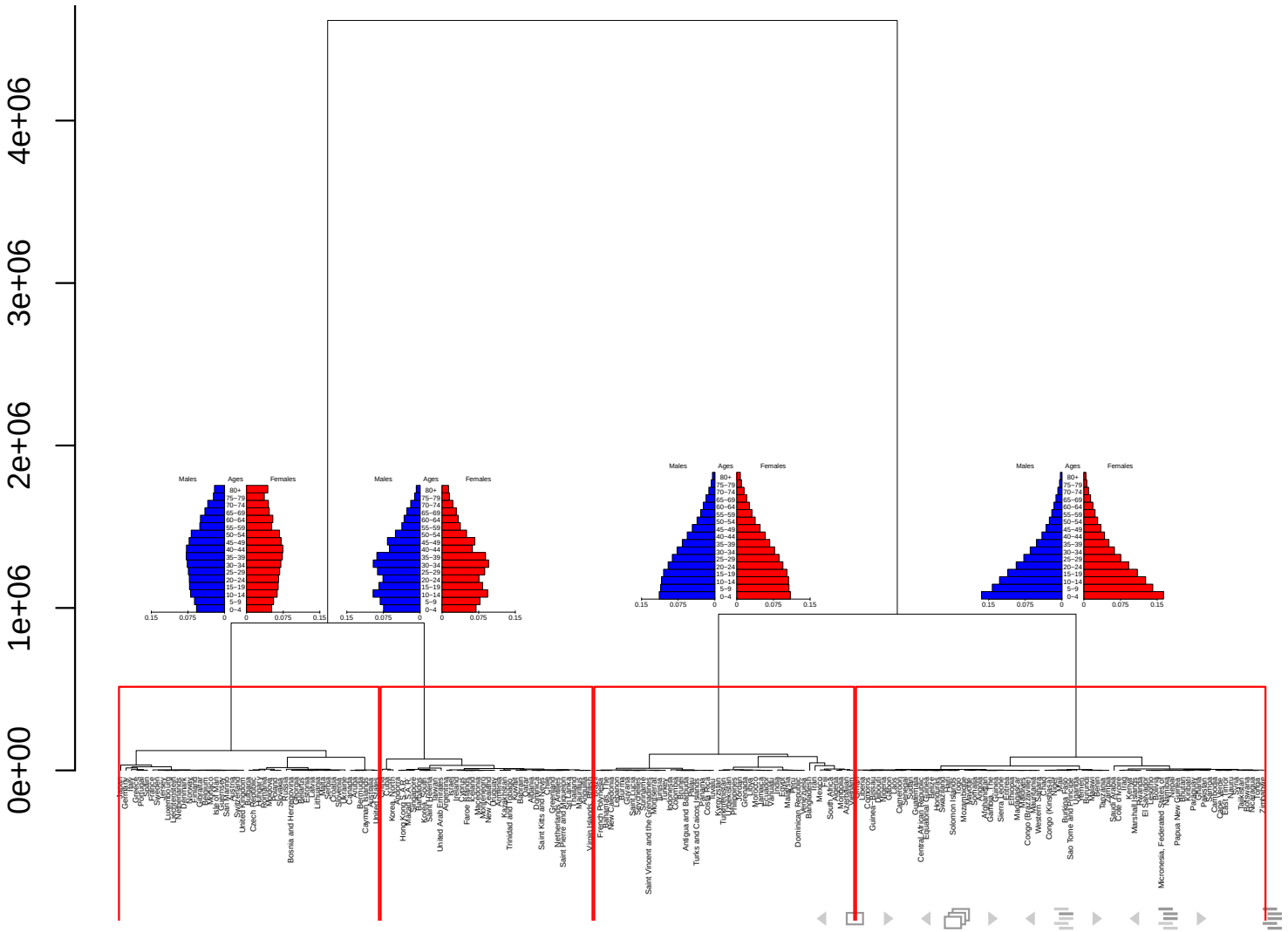

```
total <- namedSO
for(i in 1:numL) for(j in 1:nVarP) total[j] <- total[j] + L[[i]][[j]]


testSOvarP <- function(SO,var,total,a){
  pt <- total[var]/total$num
  pj <- SO[[var]]/SO$num
  te <- qnorm(1-a/2)*sqrt(pt*(1-pt)/SO$num)
  dif <- pj - pt; test <- abs(dif) > te
  for(k in 1:length(pt)) if(test[k]) {q <- pj[k]/pt[k]
    if(q > 1) cat(format(names(test)[k],width=15,justify="right"),
      format(c(pj[k],pt[k],q),
      width=12,justify="left",digits=5,nsmall=7),"\n")
  }
}
```

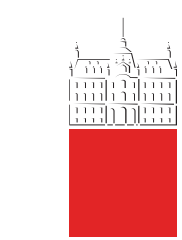
Analysis of results


```
> for(v in 1:nVar) {
+  cat("\n",v,". ",names(total)[[v]],"\n",sep="")
+  testSOvarP(L[[7]],v,total,0.001)}

1. Water
    [53.9,62.4)    0.7563636    0.1240272    6.0983712
2. Energ_Kcal
      (160,232]    0.5709091    0.1425733    4.0043206
      (232,312]    0.4036364    0.1400894    2.8812766
3. Protein
     [23.05,37]    1.0000000    0.1599603    6.2515528
4. Tot_Lipid
         [3.8,8)    0.2109091    0.1390959    1.5162857
        [8,13.7)    0.4654545    0.1394271    3.3383373
    [13.7,23.5)    0.3054545    0.1392615    2.1933888
5. Carbohydrt
             [0]    0.9890909    0.2702434    3.6600000
6. Fiber_TD
             [0]    1.0000000    0.3957609    2.5267782

  .........
30. FA_Poly
  (0.115,0.335]    0.3309091    0.1563173    2.1169068
  (0.335,0.685]    0.5854545    0.1549925    3.7773077
31. Cholestrl
        (66,80]    0.3018182    0.0816360    3.6971197
        (80,94]    0.4363636    0.0864382    5.0482759
       (94,550]    0.1818182    0.0796489    2.2827443
```

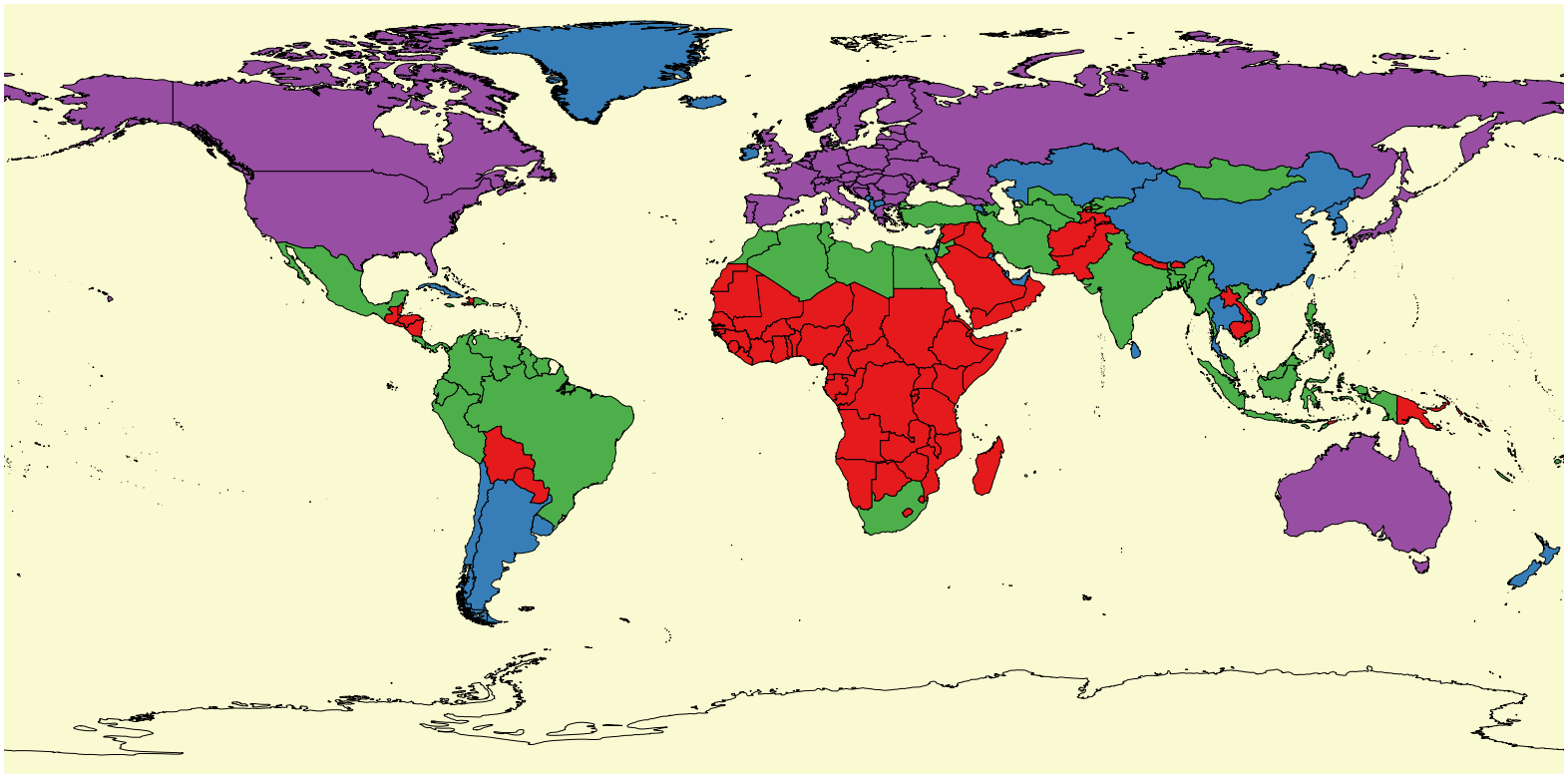


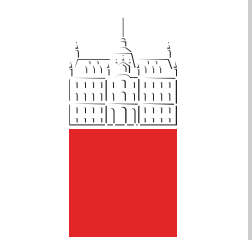
Population pyramids / World 2001



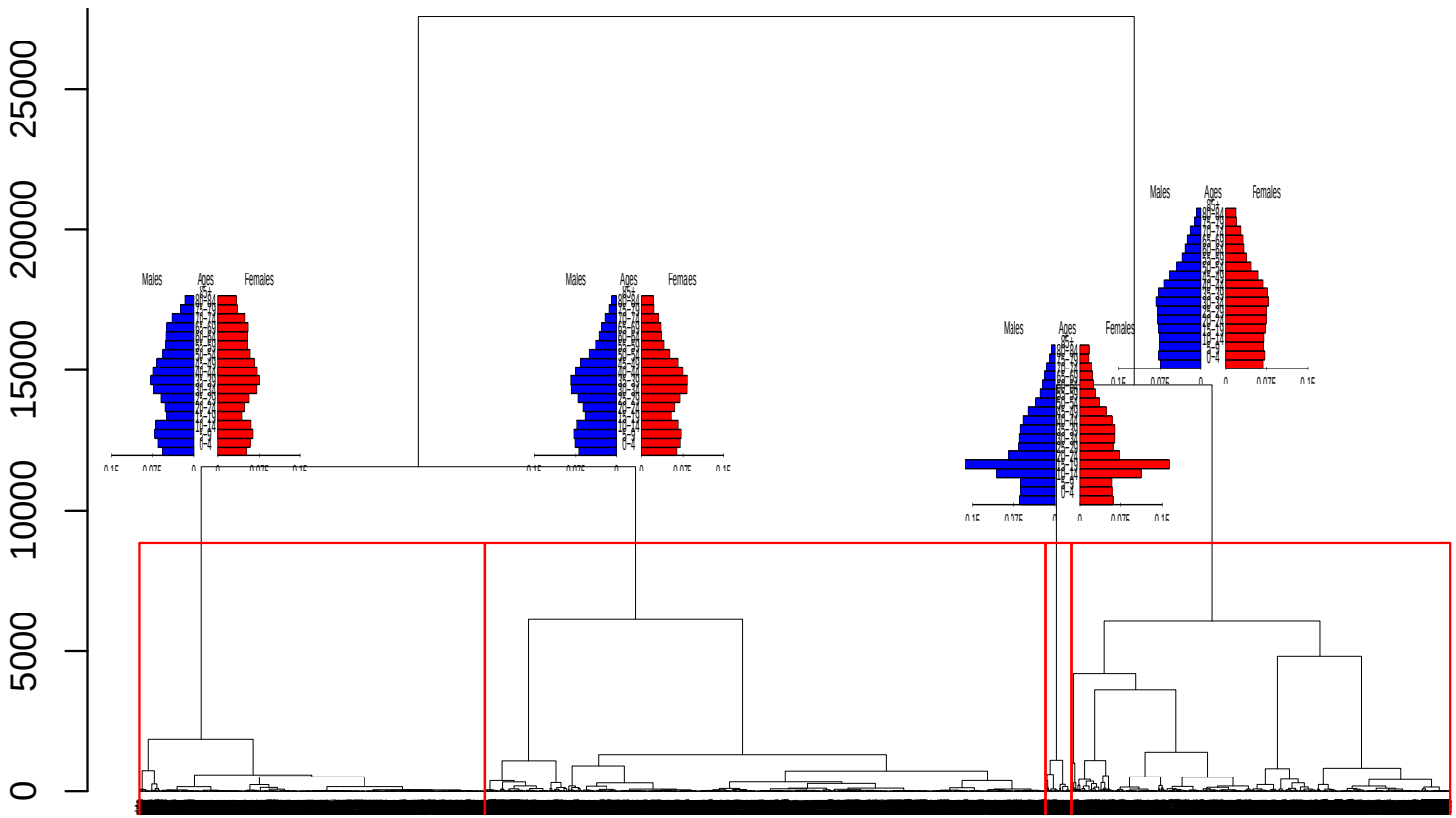


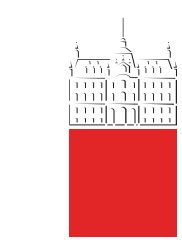
World 2001 / 4 clusters on the map



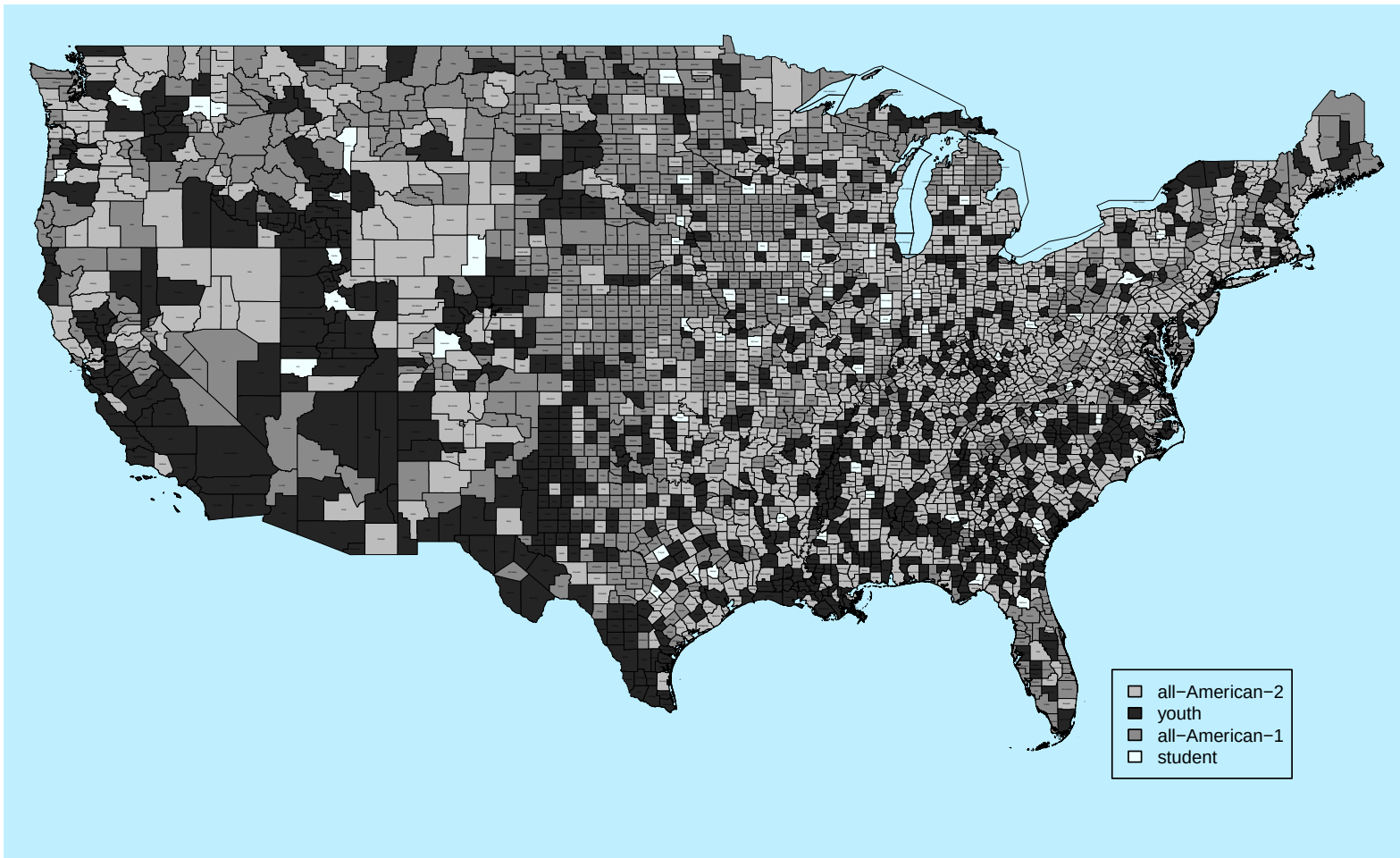


Population pyramids / US counties

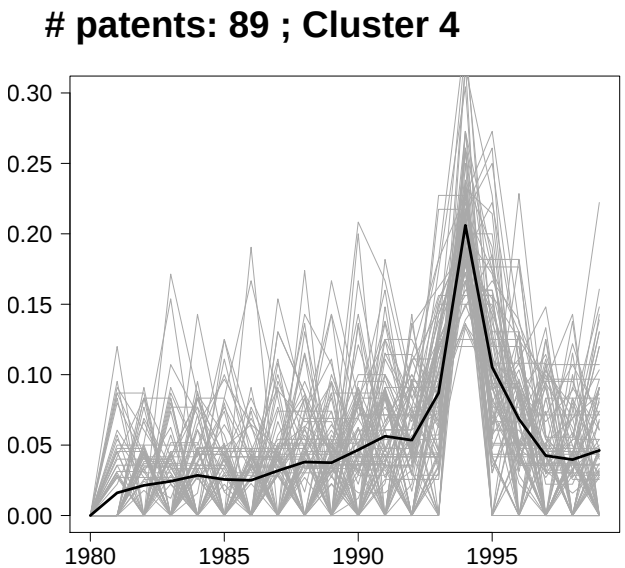


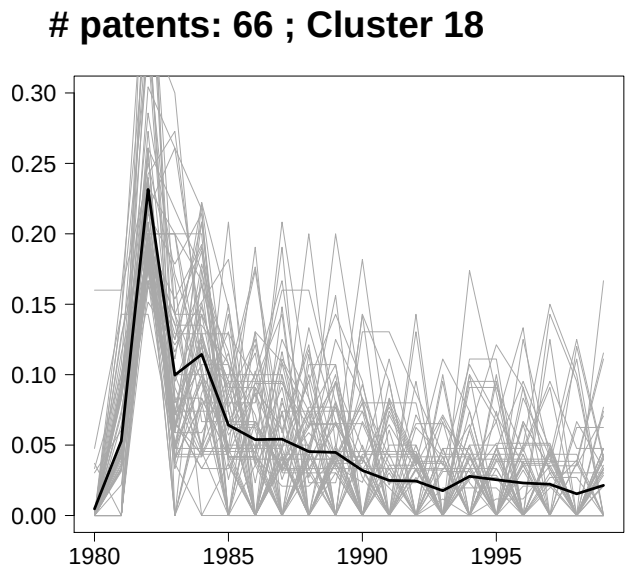


US counties map



k-means clusters of patents with patents' temporal distributions and cluster leaders





Patents clusters for δ_3

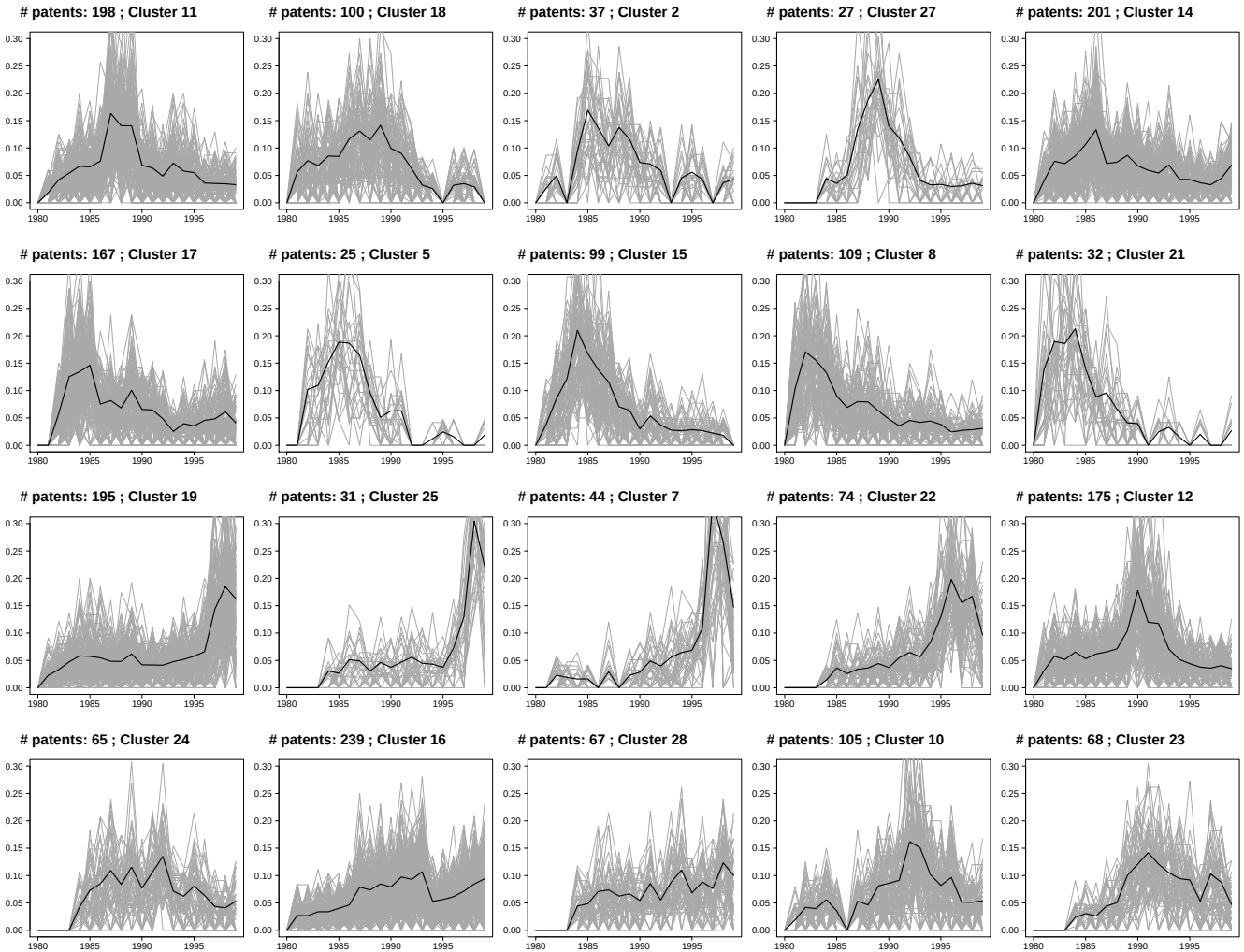
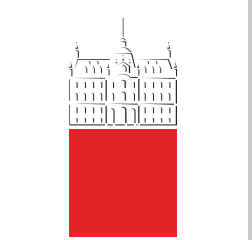
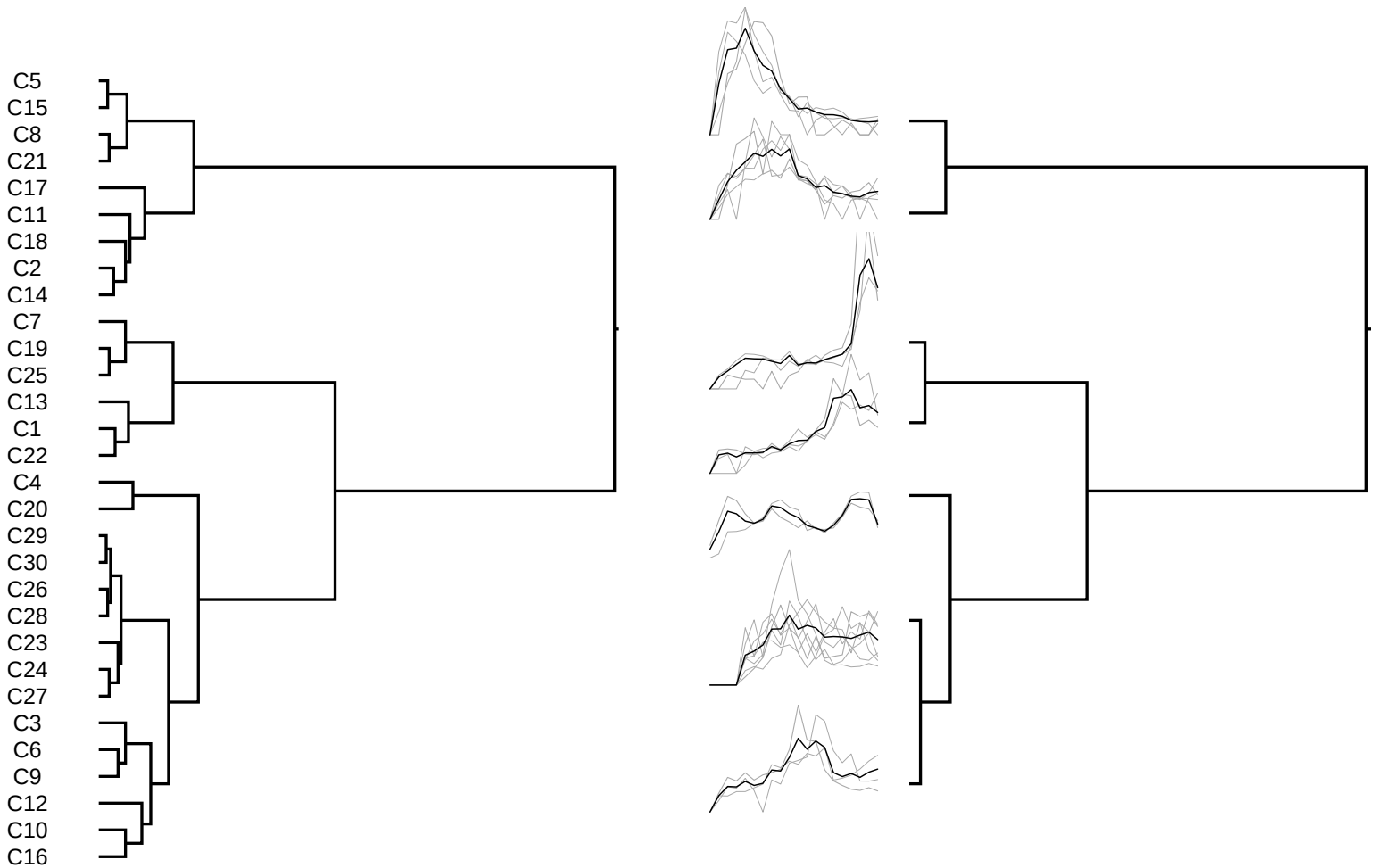


Fig. 2. Citations 20+, leaders for δ_4 - 1st part



Patents / clustering of leaders



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