

# Regional frequency analysis of the annual flows in Piemonte and Valle d'Aosta

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## Abstract

TO BE WRITTEN

## Introduction

Many practical hydrological problems require reliable models for estimation of mean annual runoff in a region. Runoff cannot be interpolated like purely distributed variables, as precipitation or temperature, because runoff in a cross section is representative of the whole contributing basin. Therefore, usual spatial interpolation methods cannot be used for estimation in ungauged basins. As regards the statistical approach, one of the firsts and more popular methods in regional frequency analysis is the “index-flood” technique (Dalrymple, 1960). Many Regional Flood estimation projects (see e.g. Rossi and Villani, 1995; Robson and Reed, 1999) are based on Dalrymple’s methodology, but also flow duration curves can be referred to the index flow method (Claps and Fiorentino, 1997; Castellarin et al., 2004a,b).

In this work we are interested in the annual flow, that is the amount of water crossing a river section in one year. If compared with hydrological extremes, applications of regional analysis to average variables, like the annual flow, are much less frequent in literature. Vogel and Wilson (1996) present some applications related to the US, while in Italy some previous works can be traced back to Ferraresi et al. (1988), Claps and Mancino (2002) and Brath et al. (2004). The purpose of the Regional frequency analysis of the annual flow is the estimation of its probability distribution in basins with few or no data.

The fundamental hypothesis of Dalrymple’s method is that the distribution of a variable in different sites belonging to a “homogeneous region” is identical, with the exception of the scale parameter, the index-flow. In this document we show how the `nsRFA` package can be used to:

1. regionalize the index-flow;
2. regionalize the growth curve, i.e. the rescaled distribution function.

The methodology has been applied to Piemonte and Valle d’Aosta, two contiguous regions in the North-West of Italy. This territory is characterized by a marked heterogeneity. In this relatively small region, very different orographic and climatic conditions coexist: in few hundreds kilometres the climate changes from the appenninic-mediterranean one in the south-eastern hills to the alpine-continental one in the mountainous Valle d’Aosta, passing from all the intermediate conditions. For this reason, a regional frequency analysis in this territory is both complex and interesting.

The following results are documented in Viglione et al. (2006) and Viglione (2007).

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## Data

In `nsRFA` data referred to 47 basins in Piemonte and Valle d’Aosta are in:

```
> data(hydroSIMN)
```

To have some information on these data

```
> ls()
```

```
> help(hydroSIMN)
```

The object used in this work are `annualflows`, a data.frame containing the annual flows of 47 hydrometric stations in Piemonte and Valle d'Aosta, measured by the SIMN (Servizio Idrografico e Mareografico Nazionale), and `parameters`, a data.frame containing morphometric and climatic descriptors that have been derived for all these river basins.

## Regionalization of the index-flow

The “index-flow” parameter can be either the sample mean (e.g. Hosking and Wallis, 1997) or the sample median (e.g. Robson and Reed, 1999). Viglione et al. (2007) show that, for variables characterized by low skewness coefficients, the estimation of the mean is less biased than that of the median. For this reason in this work the sample mean is used as the index-flow. Due to its simplicity, the most frequently used method to estimate the index-flow is the multiregressive approach (see e.g. Kottegoda and Rosso, 1997), that relates the index-flow to catchment characteristics, such as climatic indices, geologic and morphologic parameters, land cover type, etc., through linear (used here) or non-linear equations.

The choice of the best linear regressions between the mean annual flow and the catchment attributes is performed using the function `bestlm()`. Different types of linear models are investigated. The candidate dependent variable is selected between 4 possibilities:

```
> Dm <- parameters[, "Dm"]
> logDm <- log(Dm)
> sqrtDm <- sqrt(Dm)
> sqrt3Dm <- Dm^(1/3)
```

The candidate regressors are:

```
> attributes <- parameters[,-c(1,2)]
> logattributes <- log(attributes[,-c(7:9)])
> mixedattributes <- cbind(attributes, logattributes[,1])
> names(mixedattributes) <- c(names(attributes), "lnAm")
```

The best regressions with the non transformed mean annual flows are:

```
> nontrasfregr <- bestlm(Dm, mixedattributes, kmax=3, nbest=4); nontrasfregr
```

	model	R2adj
1	Am + S2000 + IT	0.8851092
2	S2000 + IT + lnAm	0.8845462
3	Am + S2000 + IB	0.8793968
4	Am + S2000 + lnAm	0.8789050
5	S2000 + lnAm	0.8773823
6	Am + S2000	0.8761521
7	Hm + lnAm	0.8648352
8	Am + Hm	0.8588129
9	IT	0.8467383
10	IB	0.6094562
11	lnAm	0.5440745
12	Am	0.5323001

Other diagnostics of these regressions can be obtained using the functions in REGRDIAGNOSTICS. Here we calculate the Root Mean Squared Error (RMSE), and the Root Mean Squared Error of the cross validation (RMSEjk)

```
> nregr <- dim(nontrasfregregr$subselect)[1]
> diagn <- data.frame(matrix(NA, nrow=nregr, ncol=2)); names(diagn) <- c("RMSE","RMSEjk")
> for (i in 1:nregr){
+ f <- paste("Dm ~", paste(colnames(nontrasfregregr$subselect)[nontrasfregregr$subselect[i,]], coll
+ regr <- lm(f, mixedattributes)
+ diagn[i,1] <- RMSE.lm(regr)
+ diagn[i,2] <- RMSEjk.lm(regr)
+ }
> diagn
```

	RMSE	RMSEjk
1	104.0258	113.4305
2	104.2804	114.1658
3	106.5805	116.2866
4	106.7976	116.3828
5	108.7094	116.6226
6	109.2534	116.9209
7	114.1359	122.2157
8	116.6509	124.9485
9	122.9100	127.3007
10	196.2029	203.4998
11	211.9910	219.7052
12	214.7109	222.3708

The best multiplicative regressions (linearized with the logarithms) are:

```
> multregr <- bestlm(logDm, logattributes, kmax=3, nbest=4); multregr
```

	model	R2adj
1	Hm + LLDP + IB	0.8468383
2	S + Hm + IB	0.8467204
3	Am + Hm + LLDP	0.8458270
4	Am + S + Hm	0.8447653
5	Am + Hm	0.8330193
6	Hm + IB	0.8245532
7	IT + IB	0.8069278
8	Am + IT	0.8015272
9	IT	0.7787654
10	IB	0.5571305
11	Am	0.5172267
12	Pm	0.3590828

whose RMSE and RMSEjk are:

```
> nregr <- dim(multregr$subselect)[1]
> diagn <- data.frame(matrix(NA, nrow=nregr, ncol=2)); names(diagn) <- c("RMSE","RMSEjk")
> for (i in 1:nregr){
+ f <- paste("logDm ~", paste(colnames(multregr$subselect)[multregr$subselect[i,]],
```

```

+                                     collapse=" + ")
+ regr <- lm(f, logattributes)
+ fitt <- regr$fitted.values
+ crossval <- jackknife1.lm(regr)
+ diagn[i,1] <- RMSE(Dm, exp(fitt))
+ diagn[i,2] <- RMSE(Dm, exp(crossval))
+ }
> diagn

```

	RMSE	RMSEjk
1	129.3508	141.2024
2	128.9386	141.0293
3	127.9561	139.3443
4	127.5461	139.2905
5	130.8245	139.3654
6	135.7904	145.6343
7	140.2605	148.5320
8	141.6007	150.6099
9	149.1973	156.0839
10	214.6567	224.6109
11	217.2887	225.2206
12	266.0818	275.1440

The best regressions with the transformed mean annual flows are:

```
> trasfregr_log <- bestlm(logDm, mixedattributes, kmax=3, nbest=4); trasfregr_log
```

	model	R2adj
1	Hm + NORD + IB	0.9001788
2	Hm + NORD + lnAm	0.8922544
3	Hm + EST + lnAm	0.8893036
4	Hm + S2000 + lnAm	0.8885439
5	S2000 + lnAm	0.8838486
6	Hm + lnAm	0.8828080
7	Hm + IB	0.8823572
8	S2000 + IB	0.8723769
9	IT	0.8382124
10	IB	0.5944382
11	lnAm	0.5172267
12	Am	0.4877632

```

> nregr <- dim(trasfregr_log$subselect)[1]
> diagn <- data.frame(matrix(NA, nrow=nregr, ncol=2)); names(diagn) <- c("RMSE", "RMSEjk")
> for (i in 1:nregr){
+   f <- paste("logDm ~", paste(colnames(trasfregr_log$subselect)[trasfregr_log$subselect[i,]],
+                                     collapse=" + "))
+   regr <- lm(f, mixedattributes)
+   fitt <- regr$fitted.values
+   crossval <- jackknife1.lm(regr)
+   diagn[i,1] <- RMSE(Dm, exp(fitt))
+   diagn[i,2] <- RMSE(Dm, exp(crossval))

```

```

+ }
> diagn

      RMSE  RMSEjk
1  101.7852 110.5497
2  103.2933 112.9716
3  101.7492 111.8125
4  103.0333 112.0052
5  106.2369 113.4683
6  108.6799 116.1945
7  111.3227 118.5316
8  117.3381 125.3689
9  136.1306 144.1668
10 202.3507 210.0492
11 217.2887 225.2206
12 226.6542 236.5474

> trasfregr_sqrt <- bestlm(sqrtDm, mixedattributes, kmax=3, nbest=4); trasfregr_sqrt

      model      R2adj
1  S2000 + IT + lnAm 0.8936962
2  Hm + S2000 + lnAm 0.8893312
3  Hm + NORD + IB 0.8893250
4  S2000 + lnAm 0.8877719
5  S2000 + NORD + lnAm 0.8876825
6  Hm + lnAm 0.8801759
7  Hm + IB 0.8747952
8  Am + S2000 0.8738923
9  IT 0.8490673
10 IB 0.6065118
11 lnAm 0.5348015
12 Am 0.5137850

> nregr <- dim(trasfregr_sqrt$subselect)[1]
> diagn <- data.frame(matrix(NA, nrow=nregr, ncol=2)); names(diagn) <- c("RMSE", "RMSEjk")
> for (i in 1:nregr){
+ f <- paste("sqrtDm ~", paste(colnames(trasfregr_sqrt$subselect)[trasfregr_sqrt$subselect[i,],
+ collapse=" + "))
+ regr <- lm(f, mixedattributes)
+ fitt <- regr$fitted.values
+ crossval <- jackknife1.lm(regr)
+ diagn[i,1] <- RMSE(Dm, fitt^2)
+ diagn[i,2] <- RMSE(Dm, crossval^2)
+ }
> diagn

      RMSE  RMSEjk
1  100.5960 109.7789
2  103.8121 113.0390
3  105.1730 114.7534
4  105.9916 113.4752

```

```

5 105.2430 115.6963
6 109.2252 116.6429
7 112.8295 120.2861
8 110.4650 118.5180
9 124.9163 129.9945
10 197.6366 204.9570
11 213.2123 220.8817
12 218.5031 226.6602

```

```
> trasfregr_sqrt3 <- bestlm(sqrt3Dm, mixedattributes, kmax=3, nbest=4); trasfregr_sqrt3
```

```

          model      R2adj
1      Hm + NORD + IB 0.8944924
2 S2000 + IT + lnAm 0.8936365
3 Hm + S2000 + lnAm 0.8906543
4      Hm + NORD + lnAm 0.8906427
5          S2000 + lnAm 0.8881545
6          Hm + lnAm 0.8825746
7          Hm + IB 0.8788041
8          S2000 + IB 0.8725909
9              IT 0.8469916
10             IB 0.6035465
11             lnAm 0.5298848
12             Am 0.5059347

```

```

> nregr <- dim(trasfregr_sqrt3$subselect)[1]
> diagn <- data.frame(matrix(NA, nrow=nregr, ncol=2)); names(diagn) <- c("RMSE", "RMSEjk")
> for (i in 1:nregr){
+   f <- paste("sqrt3Dm ~", paste(colnames(trasfregr_sqrt3$subselect)[trasfregr_sqrt3$subselect
+                                     collapse=" + "]))
+   regr <- lm(f, mixedattributes)
+   fitt <- regr$fitted.values
+   crossval <- jackknife1.lm(regr)
+   diagn[i,1] <- RMSE(Dm, fitt^3)
+   diagn[i,2] <- RMSE(Dm, crossval^3)
+ }
> diagn

```

```

          RMSE  RMSEjk
1 103.6245 112.8929
2 100.1596 109.2270
3 103.1318 112.2067
4 103.9504 113.9002
5 105.7137 113.0890
6 108.4943 115.8495
7 111.8762 119.2041
8 116.0246 124.1258
9 127.2240 132.8930
10 198.7465 206.1318
11 214.1709 221.8712
12 220.5780 229.0946

```

The choice of the best regression is based on the RMSE of the cross-validation (function `RMSEjk.lm` or `jackknife1.lm` plus `RMSE`). So the best regression is:

```
> bestregr <- lm(sqrt3Dm ~ S2000 + IT + lnAm, mixedattributes); bestregr
```

Call:

```
lm(formula = sqrt3Dm ~ S2000 + IT + lnAm, data = mixedattributes)
```

Coefficients:

(Intercept)	S2000	IT	lnAm
-14.86525	0.01601	0.71038	3.32829

```
> summary(bestregr)
```

Call:

```
lm(formula = sqrt3Dm ~ S2000 + IT + lnAm, data = mixedattributes)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.84607	-0.16793	-0.01297	0.14732	0.80262

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-14.86525	5.72525	-2.596	0.012840 *
S2000	0.01601	0.00344	4.655	3.11e-05 ***
IT	0.71038	0.39298	1.808	0.077653 .
lnAm	3.32829	0.83259	3.998	0.000247 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3457 on 43 degrees of freedom

Multiple R-squared: 0.9006, Adjusted R-squared: 0.8936

F-statistic: 129.8 on 3 and 43 DF, p-value: < 2.2e-16

that we check with the following tests: the Variance inflation factors (if  $VIF > 5$  there is a problem of multicollinearity) and correlation between the regressors:

```
> vif.lm(bestregr)
```

S2000	IT	lnAm
4.692027	11.211280	13.021852

```
> cor(bestregr$model[-1])
```

	S2000	IT	lnAm
S2000	1.000000	0.150096	-0.398042
IT	0.150096	1.000000	0.804859
lnAm	-0.398042	0.804859	1.000000

the Student t test of significance of the coefficients (probability  $Pr(> |t|)$  of the significance test, the smallest-the best):

```
> prt.lm(bestregr)
```

```

          S2000          IT          lnAm
3.105746e-05 7.765271e-02 2.469395e-04

```

So there is a correlation problem between IT and lnAm, that can cause collinearity, and that causes the non-significance of the coefficient of IT in the model.

Therefore we choose:

```

> bestregr <- lm(logDm ~ Hm + NORD + IB, mixedattributes)
> bestregr

```

Call:

```
lm(formula = logDm ~ Hm + NORD + IB, data = mixedattributes)
```

Coefficients:

```

(Intercept)          Hm          NORD          IB
  7.857719      0.000291      0.072216     -1.695636

```

```
> summary(bestregr)
```

Call:

```
lm(formula = logDm ~ Hm + NORD + IB, data = mixedattributes)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-0.273533 -0.059161  0.007672  0.041782  0.244361

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.858e+00  7.849e-02 100.117 < 2e-16 ***
Hm           2.910e-04  2.465e-05  11.807 4.42e-15 ***
NORD         7.222e-02  2.427e-02   2.976 0.00478 **
IB          -1.696e+00  9.503e-02 -17.843 < 2e-16 ***
---

```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 0.1018 on 43 degrees of freedom

Multiple R-squared: 0.9067, Adjusted R-squared: 0.9002

F-statistic: 139.3 on 3 and 43 DF, p-value: < 2.2e-16

```
> prt.lm(bestregr)
```

```

          Hm          NORD          IB
4.420213e-15 4.780480e-03 1.707744e-21

```

```
> vif.lm(bestregr)
```

```

          Hm          NORD          IB
1.148364 1.330344 1.336530

```

```
> cor(bestregr$model[-1])
```



	Hm	NORD	IB
Hm	1.0000000	-0.1887886	0.2002600
NORD	-0.1887886	1.0000000	0.4140169
IB	0.2002600	0.4140169	1.0000000

We also check the normality of the residuals (using a goodness-of-fit test):

```
> p_norm <- A2_GOFlaio(bestregr$residuals, dist="NORM"); p_norm

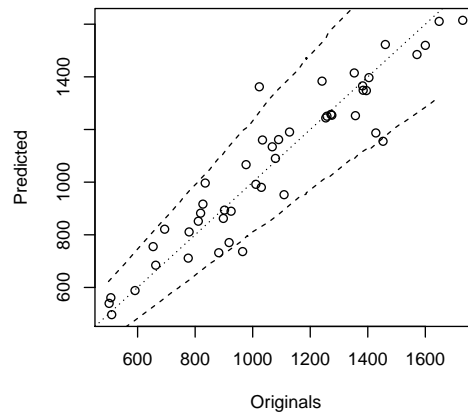
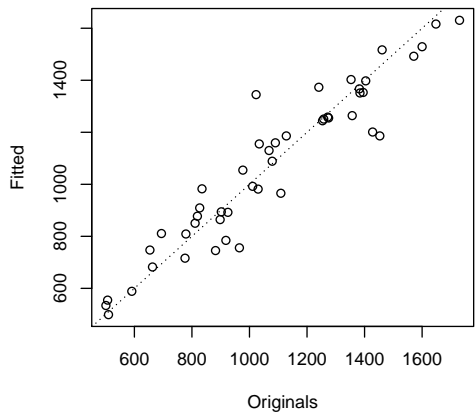
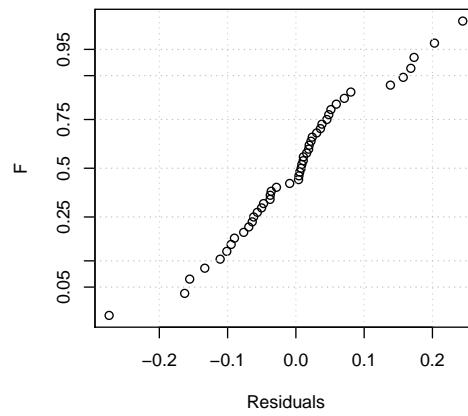
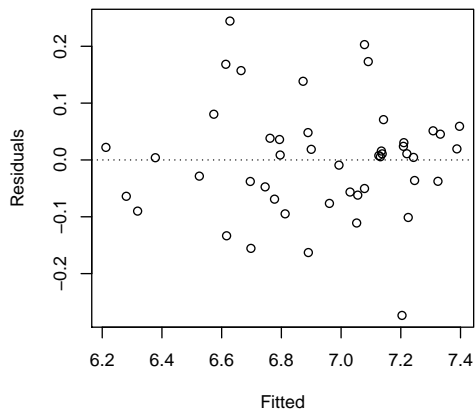
      A2      p(A2)
0.5963062 0.8765066
```

and calculate the root mean square errors:

```
> rmse <- RMSE(Dm, exp(bestregr$fitted.values))
> predicted <- jackknife1.lm(bestregr)
> rmse_jk <- RMSE(Dm, exp(predicted))
```

Some diagnostics can be plotted as:

```
> op <- par(mfrow=c(2,2))
> plot(bestregr$fitted.values, bestregr$residuals, xlab="Fitted", ylab="Residuals")
> abline(0,0,lty=3)
> normplot(bestregr$residuals, xlab="Residuals")
> plot(parameters[,c("Dm")], exp(bestregr$fitted.values), xlab="Originals", ylab="Fitted")
> abline(0,1,lty=3)
> intervals <- predinterval.lm(bestregr)
> intervals <- intervals[order(intervals[,1]),]
> plot(parameters[,c("Dm")], exp(predicted), xlab="Originals", ylab="Predicted")
> abline(0,1,lty=3)
> lines(exp(intervals[,c(1,2)]),lty=2)
> lines(exp(intervals[,c(1,3)]),lty=2)
> par(op)
```



Diagnostic plots of the best regression model. Counterclockwise from upper left: residuals as a function of the estimated values; originals against the fitted values; result of cross-validation and normal plot of residuals.

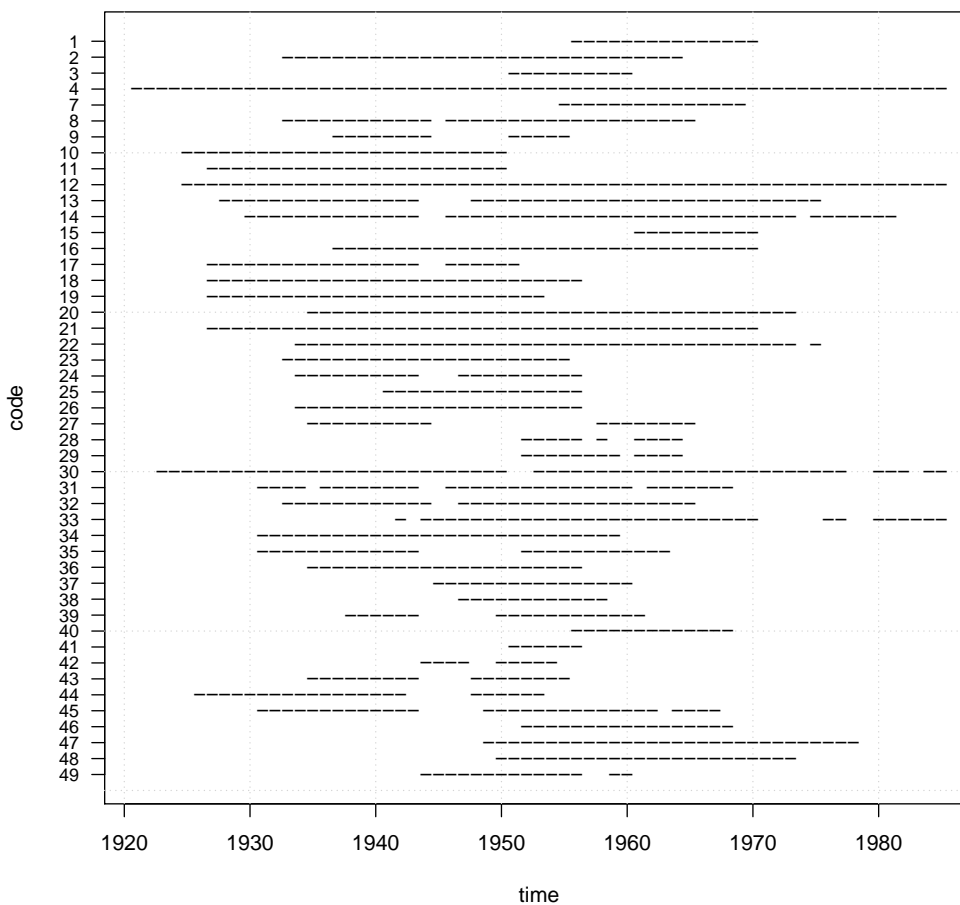
## Regionalization of the growth-curve

TO BE COMPLETED...

```
> D <- annualflows["dato"][,]  
> y <- annualflows["anno"][,]  
> cod <- annualflows["cod"][,]
```

Plot consistency of data series:

```
> consistencyplot(y, cod)
```



Data consistency.

Choice of sites with more than 15 records:

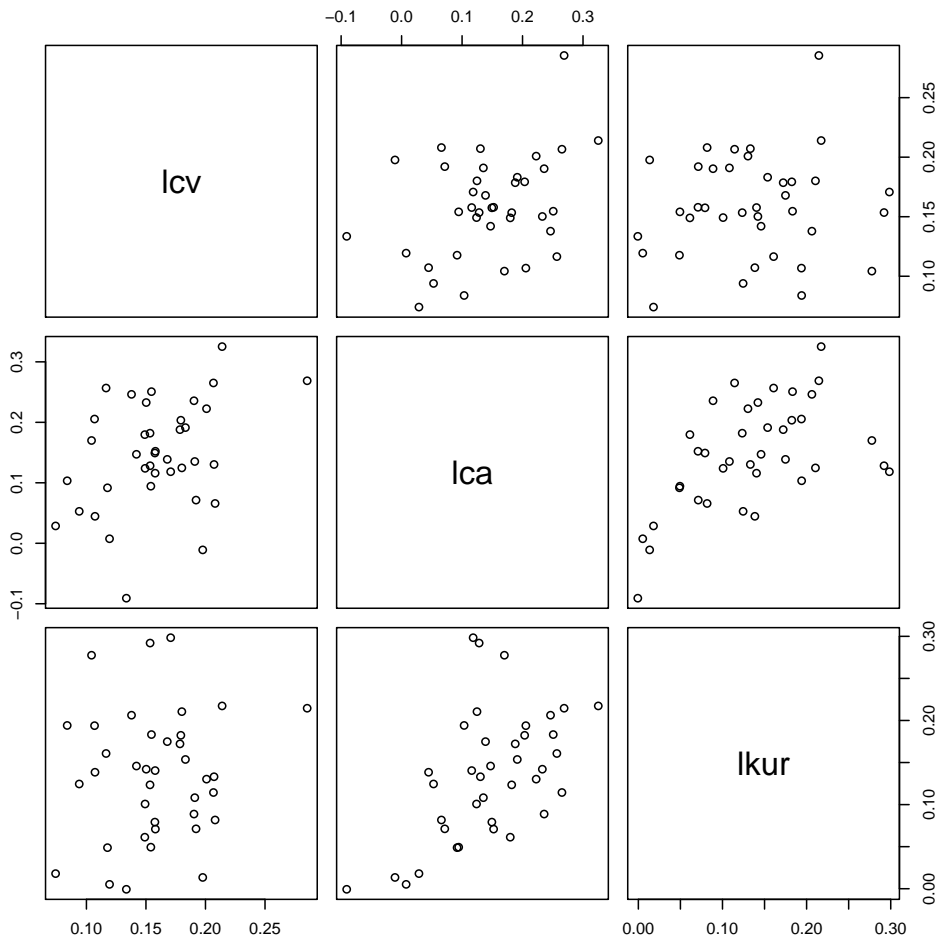
```
> ni <- tapply(D, cod, length)  
> annualflows15 <- annualflows[unsplit(ni, cod)>=15,]  
> parameters15 <- parameters[ni>=15,]  
> D15 <- annualflows15["dato"][,]  
> cod15 <- annualflows15["cod"][,]
```

L-moments of the series:

```
> LM15 <- data.frame(t(sapply(split(D15, cod15), Lmoments)))
```

L-moment ratios plot:

```
> plot(LM15[3:5])
```

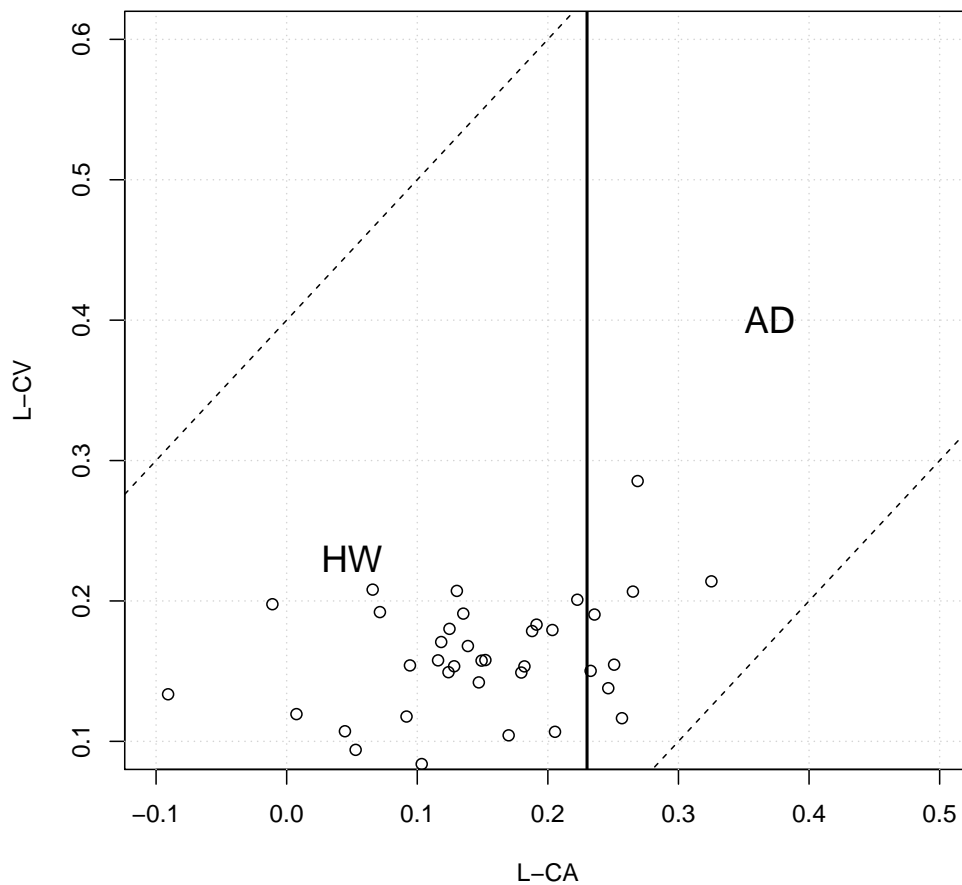


L-moment ratios plot.

Which homogeneity test do I use:

```
> Lspace.HWvsAD()
```

```
> points(LM15[,4:3])
```



L-moment ratios plot.

Homogeneity test on the entire region:

```
> D15adim <- D15/unsplit(tapply(D15, cod15, mean), cod15)
> Hws <- HW.tests(D15adim, cod15)[1]; Hws
```

H1  
7.776372

Choice of the classification variables through multi-regression approach:

```
> bestlm(LM15[, "lcv"], parameters15[, 3:16], kmax=3)
```

	model	R2adj
1	S2000 + Rc + IB	0.6780821
2	Am + S2000 + Rc	0.6767409
3	Am + LLDP + S2000	0.6762082
4	S2000 + Ybar	0.6595223
5	Hm + Ybar	0.6435752
6	Am + S2000	0.6306392
7	S2000	0.5394290
8	Hm	0.5321995
9	Ybar	0.3584742

or reasoning with distance matrices:

```
> bestlm(as.numeric(AD.dist(D15,cod15)), data.frame(apply(parameters15[,3:16], 2, dist)),  
+       kmax=3)
```

	model	R2adj
1	Am + S2000 + Ybar	0.16116558
2	S2000 + EST + Ybar	0.15822746
3	Pm + S2000 + Ybar	0.15718520
4	S2000 + Ybar	0.14887002
5	Hm + Ybar	0.14154585
6	S2000 + EST	0.11684503
7	S2000	0.10917391
8	Hm	0.09862238
9	Ybar	0.05313668

We choose Hm and Ybar as classification variables. Mantel test:

```
> Y <- AD.dist(D15,cod15)  
> X <- data.frame(apply(parameters15[,c("Hm","Ybar")],2,dist))  
> datamantel <- cbind(as.numeric(Y),X)  
> regrmantel <- lm(Y ~ Hm + Ybar, datamantel)  
> #summary(regrmantel)  
> mantel.lm(regrmantel, Nperm=100)
```

P.Hm	P.Ybar
1	1

Cluster formation:

```
> param <- parameters15[c("Hm","Ybar")]  
> n <- dim(param)[1]; k <- dim(param)[2]  
> param.norm <- (param - matrix(sapply(param, mean), nrow=n, ncol=k, byrow=TRUE))/  
+       matrix(sapply(param, sd), nrow=n, ncol=k, byrow=TRUE)  
  
> nclusters=1  
> while (max(HWs) > 2.1) {  
+   nclusters <- nclusters+1  
+   clusters <- traceWminim(param.norm, nclusters)  
+   indclusters <- unsplit(clusters, cod15)  
+   HWs <- rep(NA, nclusters)  
+   for (i in unique(clusters)) {  
+     HWs[i] <- HW.tests(D15adim[indclusters==i], cod15[indclusters==i])[1]  
+   }  
+   print(HWs)  
+ }  
  
[1] 4.426389 1.617630  
[1] 4.7201696 -0.1214777 0.4974403  
[1] 1.7858483 1.9609622 -0.2935966 0.4070506
```

So the number of regions is 4.

Regional L-moments: My regional L-moment ratios are not calculated as in Hosking and Wallis, but using the pooled growth-curves.

```
> regLM15 <- t(sapply(split(D15adim, indclusters), Lmoments))[,3:5]
> regLM15
```

```
      lcv      lca      lkur
1 0.1143714 0.1506529 0.1543626
2 0.1544286 0.1005249 0.1224144
3 0.1648291 0.1361256 0.1197992
4 0.1999977 0.1872976 0.1400214
```

If I calculate them with the method of Hosking and Wallis:

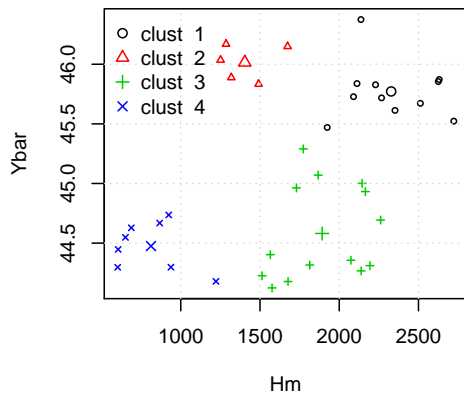
```
> for (i in 1:nclusters) {
+   print(regionalLmoments(D15adim[indclusters==i], cod15[indclusters==i])[3:5])
+ }
```

```
      lcvR      lcaR      lkurR
0.1156601 0.1550459 0.1489688
      lcvR      lcaR      lkurR
0.1557402 0.1021739 0.1096460
      lcvR      lcaR      lkurR
0.1680399 0.1406213 0.1180470
      lcvR      lcaR      lkurR
0.2032194 0.1938267 0.1438153
```

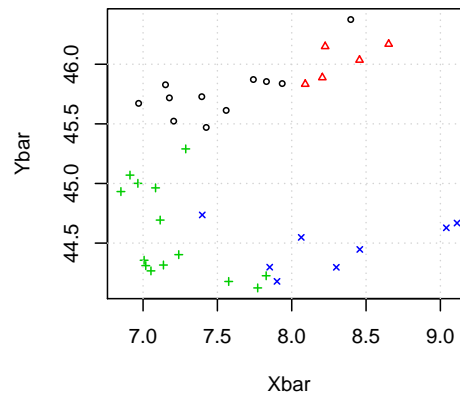
Plot of clusters:

```
> op <- par(mfrow=c(2,2))
> plot(parameters15[c("Hm","Ybar")], col=clusters, pch=clusters, cex=0.6,
+       main="Clusters in the space of classification variables", cex.main=1, font.main=1)
> grid()
> points(tapply(parameters15["Hm"], clusters, mean),
+        tapply(parameters15["Ybar"], clusters, mean),
+        col=c(1:nclusters), pch=c(1:nclusters))
> legend("topleft", paste("clust ",c(1:nclusters)),
+        col=c(1:nclusters), pch=c(1:nclusters), bty="n")
> plot(parameters15[c("Xbar","Ybar")], col=clusters, pch=clusters, cex=0.6,
+       main="Clusters in geographical space", cex.main=1, font.main=1)
> grid()
> plot(LM15[,4:3], pch=clusters, col=clusters, cex=0.6,
+       main="Clusters in L-moments space", cex.main=1, font.main=1)
> points(regLM15[,2:1], col=c(1:nclusters), pch=c(1:nclusters))
> grid()
> plot(LM15[,4:5], pch=clusters, col=clusters, cex=0.6,
+       main="Clusters in L-moments space", cex.main=1, font.main=1)
> points(regLM15[,2:3], col=c(1:nclusters), pch=c(1:nclusters))
> grid()
> par(op)
```

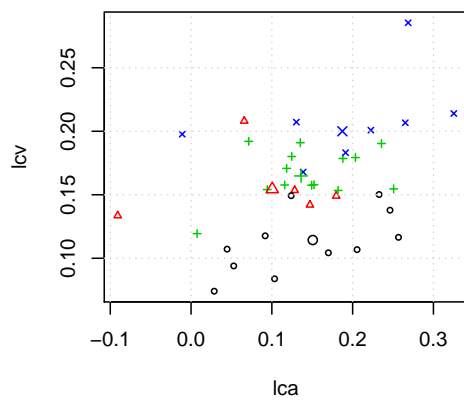
Clusters in the space of classification variables



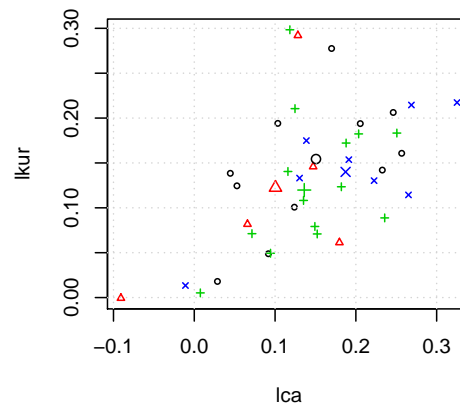
Clusters in geographical space



Clusters in L-moments space



Clusters in L-moments space

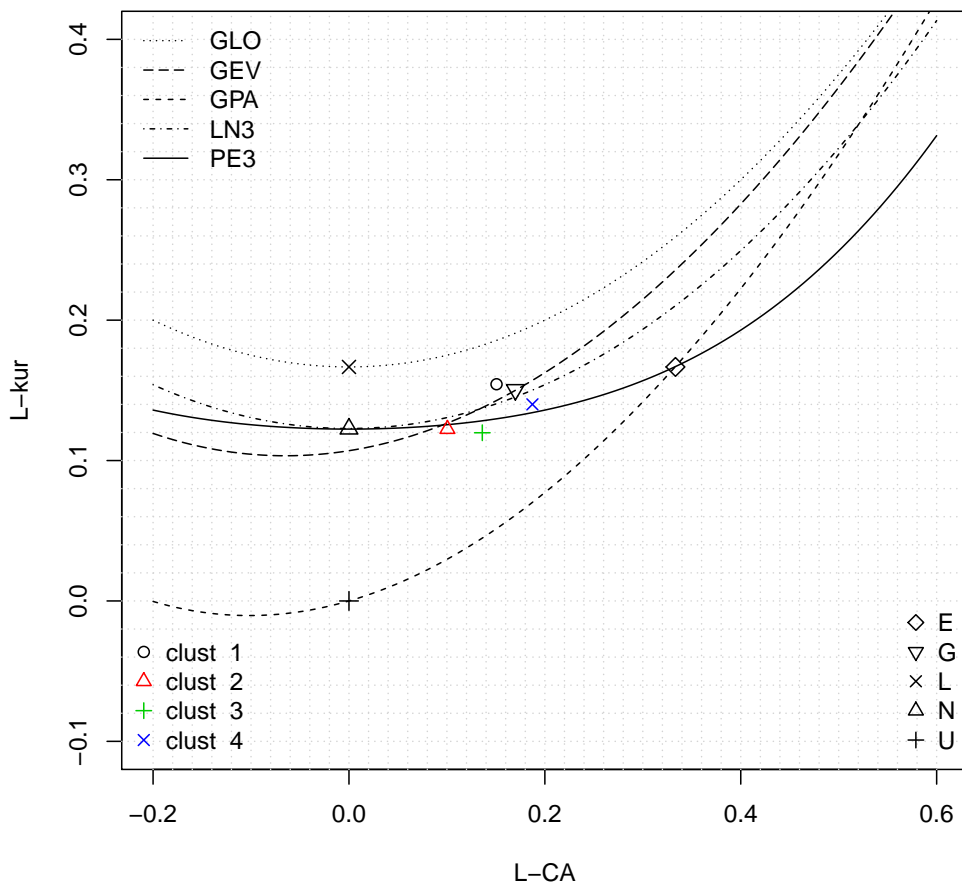


Clusters.

Model selection (L-moments ratio diagram):

```
> Lmoment.ratio.diagram()
> points(regLM15[,2:3], col=c(1:nclusters), pch=c(1:nclusters))
> legend("bottomleft",paste("clust ", c(1:nclusters)),
+       col=c(1:nclusters), pch=c(1:nclusters), bty="n")
```





L-moments ratio diagram.

The points are around the Pearson type III distribution. If we apply the Anderson-Darling goodness-of-fit test, we obtain:

```
> for (i in 1:nclusters) {
+   GOFA2_P3 <- A2_GOFIaio(D15adim[indclusters==i], dist="P3")
+   cat(paste("\np(A2) for Cluster ", i, ":\n", sep=""))
+   print(GOFA2_P3)
+ }
```

```
p(A2) for Cluster 1:
      A2      p(A2)
0.3152134 0.5608133
```

```
p(A2) for Cluster 2:
      A2      p(A2)
0.2531199 0.3859892
```

```
p(A2) for Cluster 3:
      A2      p(A2)
0.5713187 0.9220134
```

p(A2) for Cluster 4:  
 A2      p(A2)  
 0.6638851 0.9532153

For the 4-th cluster, the goodness of fit test is not passed with a 5% significance level.  
 Parameters of the Pearson type III distributions using the method of L-moments:

```
> paramgamma=NULL
> for (i in 1:nclusters) {
+   paramgamma[[i]] <- par.gamma(1, regLM15[i,1], regLM15[i,2])
+   cat(paste("\nCluster",i,"\n"))
+   print(format(paramgamma[[i]][1:3]))
+ }
```

Cluster 1 :  
           xi           beta           alfa  
 "0.5457898" "0.09534035" "4.764092"

Cluster 2 :  
           xi           beta           alfa  
 "0.09842929" "0.08508402" "10.59624"

Cluster 3 :  
           xi           beta           alfa  
 "0.2800572" "0.1237543" "5.817518"

Cluster 4 :  
           xi           beta           alfa  
 "0.3496308" "0.2093341" "3.106847"

Expressed in the other way:

```
> for (i in 1:nclusters) {
+   cat(paste("\nCluster",i,"\n"))
+   print(format(par2mom.gamma(paramgamma[[i]]$xi,
+     paramgamma[[i]]$beta, paramgamma[[i]]$alfa)))
+ }
```

Cluster 1 :  
           mu           sigma           gamm  
 "4.816127" "0.07043515" "2.707181"

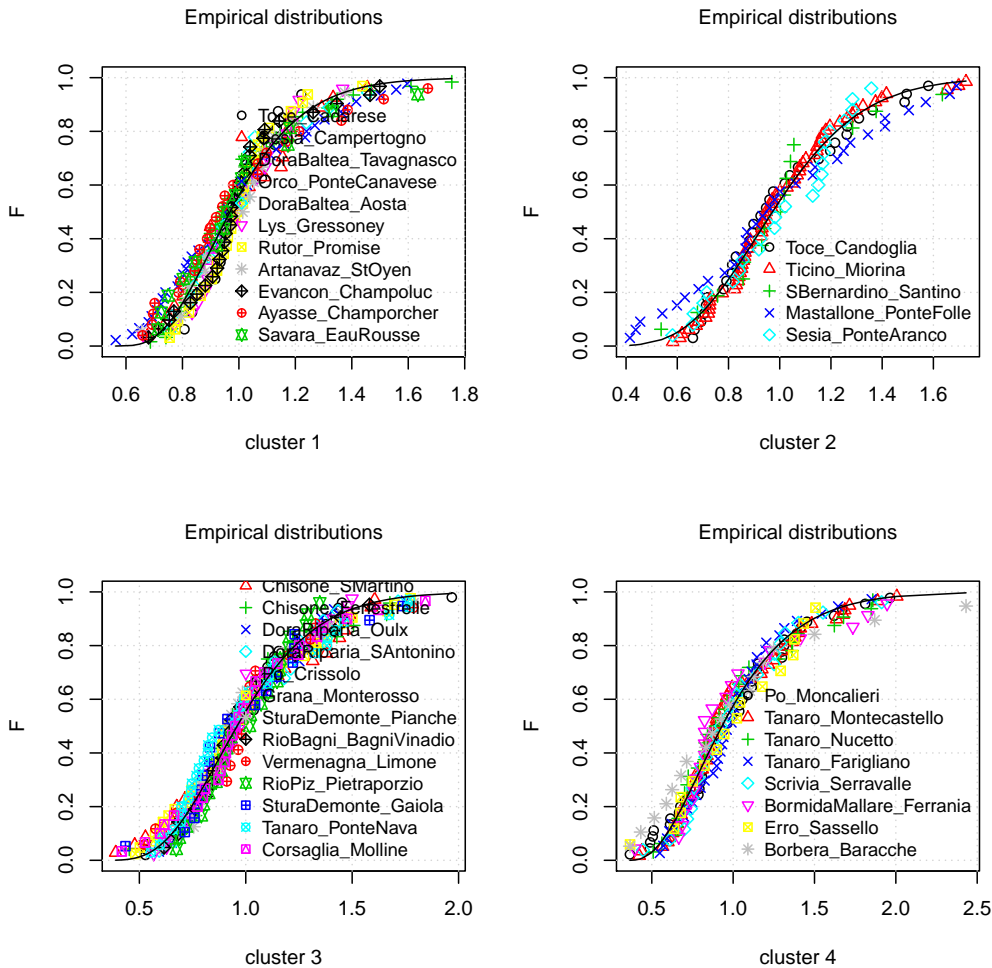
Cluster 2 :  
           mu           sigma           gamm  
 "10.60462" "0.02669378" "6.374819"

Cluster 3 :  
           mu           sigma           gamm  
 "5.852176" "0.06549131" "3.779259"

Cluster 4 :  
           mu           sigma           gamm  
 "3.180037" "0.1237784" "3.382401"

Regional growth-curves:

```
> op <- par(mfrow=c(2,2))
> for (i in 1:nclusters) {
+   FF <- F.gamma(D15adim[indclusters==i], paramgamma[[i]]$xi,
+               paramgamma[[i]]$beta, paramgamma[[i]]$alfa)
+   regionalplotpos(D15adim[indclusters==i], cod15[indclusters==i],
+                 xlab=paste("cluster", i),
+                 main="Empirical distributions", cex.main=1, font.main=1)
+   lines(sort(D15adim[indclusters==i]), sort(FF))
+   nomi <- names(clusters)[clusters==i]
+   legend("bottomright", legend=nomi, pch=c(1:length(nomi)),
+         col=c(1:length(nomi)), bty="n", cex=.9)
+ }
> par(op)
```



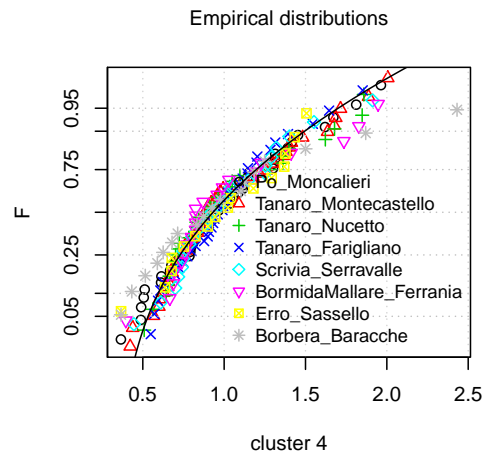
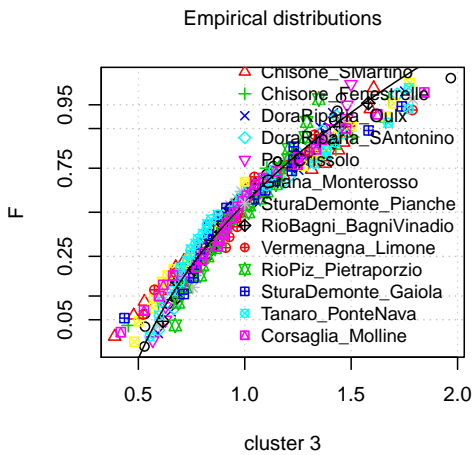
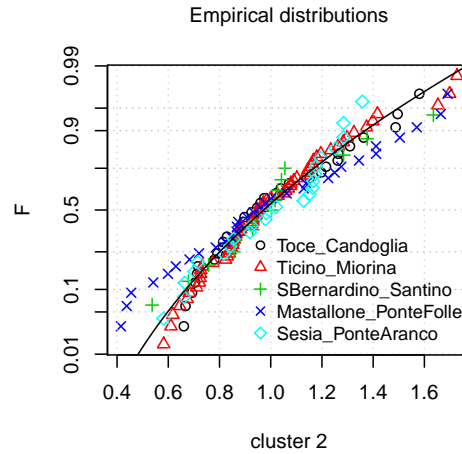
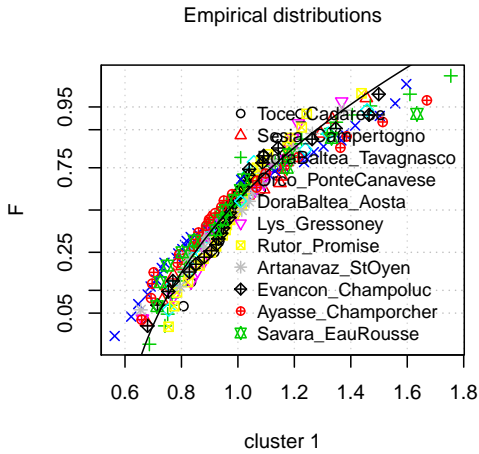
Regional growth-curves:

```
> op <- par(mfrow=c(2,2))
> for (i in 1:nclusters) {
+   Fs <- seq(0.001,0.999,by=.001)
+   regionalnormplot(D15adim[indclusters==i], cod15[indclusters==i],
+                   xlab=paste("cluster", i),
```

```

+           main="Empirical distributions", cex.main=1, font.main=1)
+ normpoints(invF.gamma(Fs, paramgamma[[i]]$xi, paramgamma[[i]]$beta,
+           paramgamma[[i]]$alfa), type="l")
+ nomi <- names(clusters)[clusters==i]
+ legend("bottomright", legend=nomi, pch=c(1:length(nomi)),
+       col=c(1:length(nomi)), bty="n", cex=.9)
+ }
> par(op)

```

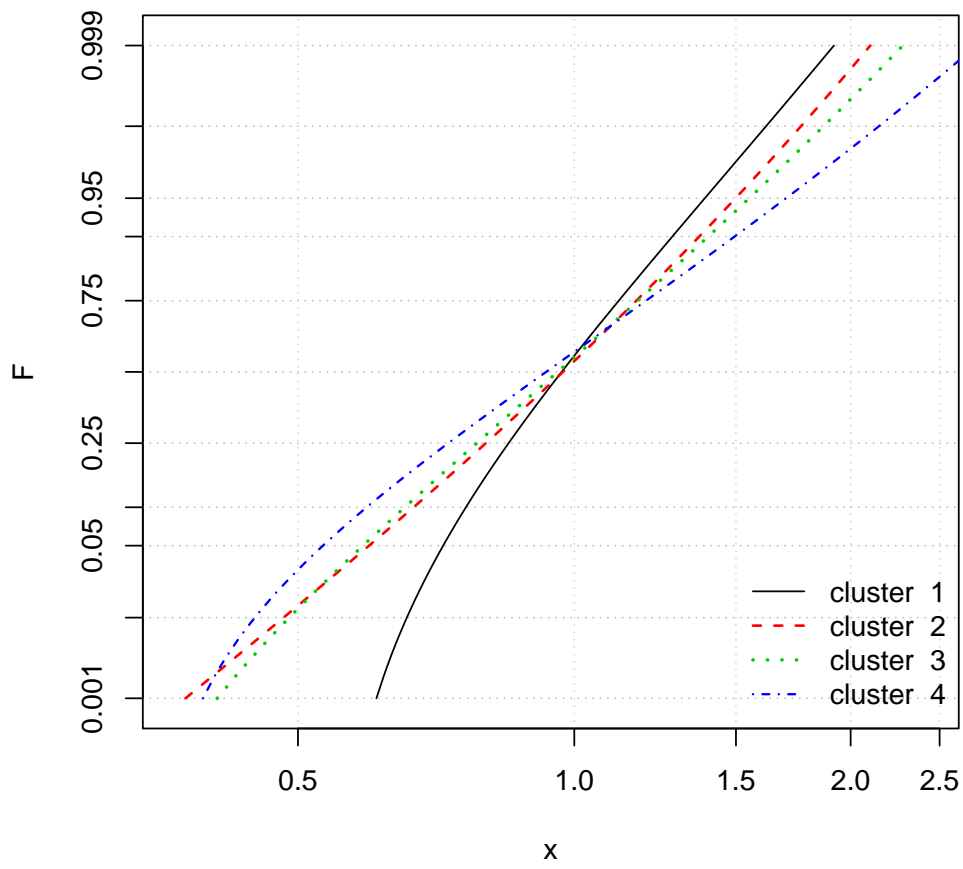


Comparison between regional growth-curves:

```

> spess=c(1, 1.5, 2, 1.3)
> Fs <- seq(0.001,0.999,by=.001)
> lognormplot(D15adim, line=FALSE, type="n", )
> for (i in 1:nclusters) {
+ qq <- invF.gamma(Fs, paramgamma[[i]]$xi, paramgamma[[i]]$beta,
+           paramgamma[[i]]$alfa)
+ normpoints(qq, type="l", lty=i, col=i, lwd=spess[i])
+ }
> legend("bottomright", paste("cluster ", c(1:nclusters)),
+       col=c(1:nclusters), lty=c(1:nclusters), lwd=spess, bty="n")

```



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