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9
Apêndices

9.1. Apêndice A

Identificação do ínfimo e supremo

Seguindo uma notação usual:

O supremo e o ínfimo de dois números reais a e b, indicados por $a \vee b$ e $a \wedge b$, onde pode-se verificar que:

$$a \vee b = \frac{1}{2}(a + b + |a - b|)$$

$$a \wedge b = \frac{1}{2}(a + b - |a - b|)$$

Se a e b são números reais, teremos sempre:

$|a + b| \leq |a| + |b|$ e $\big||a| - |b|\big| \leq |a - b|$

Se f e g são funções reais, define-se a função máximo (supremo) de

f e g, anote $f \vee g$; e mínimo (ínfimo) de f e g, anote $f \wedge g$, peças fórmulas:

$\sup x_n = (f \vee g)(x) = f(x) \vee g(x)$

$\inf x_n = (f \wedge g)(x) = f(x) \wedge g(x)$

Caso $g = 0$, escrevemos f^+ no lugar de $f \vee g$, e f^- no lugar de $f \wedge g$. Então:

$$|f| = f^+ + f^-$$

e $$f = f^+ - f^-$$

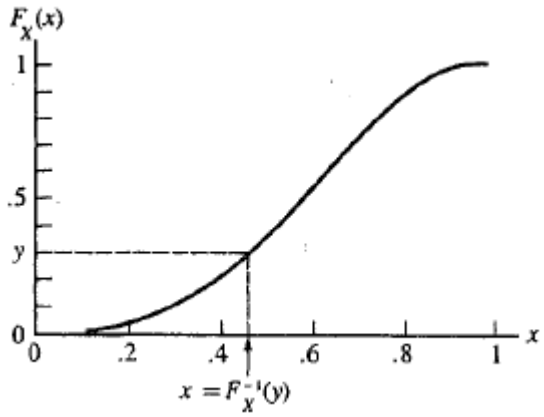
Temos: $$\sup\{f, g\} = \frac{1}{2}(f + g + |f - g|)$$

$$\inf\{f, g\} = \frac{1}{2}(f + g - |f - g|)$$

Sobre uma CDF sabe-se que:

$$\hat{F}_X^{-1}(y) = x \Leftrightarrow F_X(x) = y\}$$

$$\hat{F}_X^{-1}(y) = \inf\{x : F_X(x) \geq y\}$$



9.2.Apêndice B

Três passos para transformações de variáveis continuas

Seja $W = r(X, Y)$ a transformação desejada, os passos para obter f_W são:

1. Para cada w, obter um conjunto A_w = { (x, y) : $r(x, y) \leq w$ }
2. Ache a fdc:

$$F_W(w) = \mathrm{P}(W \leq w) = \mathrm{P}(r(X, Y) \leq w)$$

$$= \mathrm{P}(W \leq w) = \mathrm{P}(\{(x, y); r(x, y) \leq w\}) = \int \int_{A_w} f_{X,Y}(x, y)dxdy$$

3. Então $f_W(w) = F'_W(w)$ em todos os pontos de x nos quais a F_W seja diferenciável.

9.3. Apêndice C

Código R

```
######
###### Funções para B doador e as adicionais quando A doador
################################################################


################################################
######  Separa A e B de XYZ

 cria_A <-function(x,a){
  {
    a  <- x [seq(1, nrow(x ), by = 2), ]
              ###### registros     Impares ordenados pelos Py

  a  <- data.frame(a[order(a[,4]),])

  }
    return(a)

 }
```

```
 cria_B <-function(x,b){
  {
    b  <- x [seq(2, nrow(x ), by = 2), ]
                    ###### registros Pares ordenados pelos Pz
    b  <- data.frame(b[order(b[,5]),])

  }
    return(b)
 }



    ################################################
    ########## Ordenados os Pz de B,para buscar o Pz mais perto
do PY + residuo_aleatorio (de A).

    Intervalo <- function (a,b)
    {
          nrowA   =    nrow(a)
          nrowB   =    nrow(b)
          b_order  <- data.frame(b[order(b[,3]),])
          Ind <- array(NA,dim=c(nrowA , 4 ))
          Ind[ ,1] <-  a[,4]
          Ind[ ,2] <-  b_order[,3]

    cont<-0
    for(i in 1:nrowA)
    {
      for(j in 1:nrowB)
      {
        if(Ind[i,1]>=Ind[j,2]){
         cont<-cont+1
      }
        Ind[i,3]<- cont
        Ind[i,4]<- cont+1
     }
        cont<-0
    }

    for(i in 1:nrowA){
```

```
      if(Ind[i,1]<=0){
        Ind[i,3] <- 1
        Ind[i,4] <- 1
      } else{
            if (Ind[i,1]>=1){
               Ind[i,3] <- nrowA
               Ind[i,4] <- nrowA
             }
      }

    }
    for(i in 1:nrowA){
      if (a [i , 4] < b_order[ 1 ,3 ]){
          Ind[i,3] <- 1
          Ind[i,4] <- 1
              }
      }
    for(i in 1:nrowA){
      if (Ind[i,3] == nrowA){
            Ind[i,4] <- nrowA
              }
      }
     Ind
     }




    ################################################
    ######  calcula-se  o  Z_estimado  (invertendo  o  cálculo  dos
"percentis" - Pz_estimados).

     Inverte_Interpolacao <- function (a, b, ind) {
       nrowI   =    nrow(ind)
       nrowA   =    nrow(a)
       nrowb   =    nrow(b)
       intervalo <-  array(NA,dim=c(nrowA  ,2))
       intervalo [ ,1] <-  ind[,3]
       intervalo [ ,2] <-  ind[,4]

       x <-  array(NA,dim=c(nrowA  ,2))
```

```
        k = 0
        b_order  <- data.frame(b[order(b[,3]),])

      for(i in 1: nrowA ) {

                      k = intervalo[ i, 1]
                      x [i ,1 ] = k
                      inf <- b_order[intervalo[ i, 1], 2]
                      sup <- b_order[intervalo[ i, 2], 2]
                      ampZ <- sup - inf

                      p_inf  <-  b_order[intervalo[  i,  1],3  ]
### valores do Pz inferior e superior
                      p_sup <- b_order[intervalo[ i, 2],3 ]
                      ampPz  <- p_sup - p_inf

                      w <- a[i , 4]  - p_inf

       {if (ampPz != 0)
                      {
                       x [i ,2 ] <- inf + (( ampZ * w)/ ampPz )
                      }
        else {  x [i ,2 ] <- b_order[intervalo[ i, 1] ,2 ]
          }
      }

     if (( a [i , 4] <= 0) | (a [i , 4] < b_order[ 1 ,3 ])) {  x
[i ,2 ] <- b_order[ 1 ,2 ]}


     }
      x
       }
```

```
     ###########  calcula-se o Pz_estimado
     ############  e verificando quem é o observado mais proximo
no intervalo onde está Pz_estimado).

     Inverte_Intervalar <- function (a,b,ind) {
        nrowI   =    nrow(ind)
        nrowA   =    nrow(a)
        nrowb   =    nrow(b)
        intervalo <-  array(NA,dim=c(nrowA  ,2))
        intervalo [ ,1] <-  ind[,3]
        intervalo [ ,2] <-  ind[,4]
        nrow_IND  =    nrow(intervalo)

        x <-  array(NA,dim=c(nrowA  ,2))
        b_order  <- data.frame(b[order(b[,3]),])

      for(i in 1: nrowA ) {

        anterior = intervalo[ i, 1]
     if (intervalo[ i, 1]<nrowA) { posterior = intervalo [ i, 2] }
           x [i ,1 ] = anterior

         if ( (i < nrowb) )
           {
             if  ( (abs(a  [i  ,  4]  -  b_order[anterior,  3 ])) <=
(abs(a [i , 4] - b_order[posterior,3 ])) )
              { x [i ,2 ] <- b_order[anterior , 2 ] }

            else { x [i ,2 ] <- b_order[posterior, 2 ] }
           }
       else
            {  x [i ,2 ] <- b_order[anterior ,2 ]}
         }
         x
       }
```

```
    ##############################################################
#####
    Soma_residuo_e_percentil <- function (a,xyz,residuo )
    {
       nrowA <- nrow(a)
       ind_res_aleat                                              <-
data.frame(trunc(runif(nrow(a))*(nrow(xyz)- 1)) + 1)
       res_aleat <- data.frame(residuo[ind_res_aleat[ ,1], ])

    C <-  array(NA,dim=c(nrowA ,3 ))
    C[,1] <-  a[,3]                              ### Py
    C[,2] <-  res_aleat[,2]                  ### Residuo


    for(i in 1:nrowA)  {

    Flag <- 0
    if ( (a[i,3]== 0)  )
         { C[i,3] <-  a[i,3] + C[i,2]
           Flag <- 1  }

    while (Flag == 0){
    if  (((a[i,3]>=  0)  &  (a[i,3]<=  0.2)  &  (C[i,2]  >=  (-
0.75*a[i,3])) & (C[i,2] <= (3*a[i,3])))  |
       ((a[i,3]>=  0.2)  &  (a[i,3]<=  0.8)  &  (C[i,2]  >=  (-
0.75*a[i,3])) & (C[i,2] <= (0.75 - 0.75*a[i,3]))) |
       ((a[i,3]>=  0.8)  &  (a[i,3]<=  1)  &  (C[i,2]  >=  (-3  +
3*a[i,3])) & (C[i,2] <= (0.75 - 0.75*a[i,3]))) )
      { C[i,3] <-  a[i,3] + C[i,2]
        Flag <- 1
      }
       else { ind_res_aleat <- trunc((runif(1,0,1)*(nrow(xyz)- 1))
+ 1)
              C[i,2] <- residuo[ind_res_aleat, 2 ]


        }
      }
    }
    for(i in 1:nrowA)  {
```

```
if ( (C[i,3] < 0)  )
     { C[i,3] <-  0 }

if ( (C[i,3] > 1)  )
     { C[i,3] <-  1 }
}
C
}


###########
############  Interpolação com os arqquivos B e A doadores


   Sintese_BA_AB_Interpolacao <- function (A, B, XYZ, Residuo
)
{
    nrowA <-  nrow(A)
    nrowXYZ <-  nrow(XYZ)
    nrowB <-  nrow(B)
    nrowR <-  nrow(Residuo)

                      ### 1. Gera número ALEAT e residuo ALEAT

   C  <-  Soma_residuo_e_percentil(A, XYZ,Residuo)

  A <- data.frame(cbind(A,C[,3]))
  colnames(A )<- c( "X","Y","Py","Py + res_aleat")


 ###########
 ### Intervalo P_anterior e P_posterior)

   Intervalo <- Intervalo(A, B)
                                      ### - Interpolação
   P_est_obs_A  <- Inverte_Interpolacao(A,B, Intervalo)
   Sintese <- data.frame(cbind(A[ ,1:2],P_est_obs_A [ ,2]))

 Sintese
}
```

```
#####################


     Sintese_BA_AB_Intervalo <- function (A, B, XYZ, Residuo
)
{

    nrowA <-  nrow(A)
    nrowA <-  nrow(XYZ)
    nrowB <-  nrow(B)
    nrowR <-  nrow(Residuo)

     ### 1. Gera número ALEAT e residuo ALEAT

     C  <-  Soma_residuo_e_percentil(A, XYZ,Residuo)

  A <- data.frame(cbind(A,C[,3]))
  colnames(A )<- c( "X","Y","Py","Py + res_aleat")


                      ### Intervalo P_anterior e P_posterior)

   Intervalo <- Intervalo(A, B)
                               ### - Intervalar
   P_est_obs_A  <- Inverte_Intervalar(A,B, Intervalo)
   Sintese <- data.frame(cbind(A[ ,1:2],P_est_obs_A [ ,2]))

 Sintese
}
```

9.4.Apêndice D

As distribuições marginais são preservadas conforme mostradas nas tabelas 13 e 14, onde B e A , são os respectivos receptores.

***B* doador - Transformação não-paramétrica relacional**							
		TNRIr			***TNRIo***		
Valores originais			***Viés***	**EQM**		**Viés**	**EQM**
cor(X,Y)	**0,580047**	**0,580736**	0,000690	0,000000	**0,580736**	0,000690	0,000000
cor(X,Z)	**0,489605**	0,405740	0,083865	0,007033	0,403536	0,086070	0,007408
cor(Y,Z)	**0,735542**	0,743708	0,008167	0,000067	0,743833	0,008291	0,000069

Tabela 13 - Estimativas das correlações do emparelhamento estatístico *B* doador.

***A* doador - Transformação não-paramétrica relacional**							
		TNRIr			***TNRIo***		
Valores originais			***Viés***	**EQM**		***Viés***	**EQM**
cor(X,Y)	**0,580047**	0,470259	0,109788	0,012053	0,469120	0,110927	0,012305
cor(X,Z)	**0,489605**	**0,484469**	0,005136	0,000026	**0,484469**	0,005136	0,000026
cor(Y,Z)	**0,735542**	0,775334	0,039792	0,001583	0,776041	0,040499	0,001640

Tabela 14 - Estimativas das correlações do emparelhamento estatístico *A* doador.