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**CRELES-2: Costa Rican Longevity
and Healthy Aging Study - Wave 2,
2006-2008 (Costa Rica Estudio de
Longevidad y Envejecimiento
Saludable, Ronda 2)**

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Recoded Variables

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Additional Information on the Recoded Variables Wave 2 data file

This document includes details of some variables that were constructed by the project staff on the basis of other variables originally in the data files. In the first section is a short description of the variables and in the second section the exact programming that was used to generate the variable using STATA software.

1. Short description of variables in the recoded variables data file (recodedvariables.dta)

Created variable	Variable label	Description
age	Correct age at date of the interview	Missing values were replaced with the correct age according to their national ID, using their birth date.
gam	Living in the Great Metropolitan Area	Living in the capital city of San José and surrounding metropolitan's area. Includes an area of 406km ²
urban	Living in the Urban area	Census tracts defined as urban areas by the National Institute of Census and Statistics of Costa Rica
mudanzalarga	Long-distance change in address	The participant changed address. Variable constructed with administrative records.
ingc	Income of Spouse(Thousand colones)	Income of the spouse of the Interviewee
ingtotal	Total Income of interviewee(Thousand colones)	Total Income of the interviewee
tenebienes	Household assets 0-10	Index adding the number of assets between 0-10
rsangre	Has Blood sample	If blood sample was collected for the interviewee
ranthro	Has anthropometry measures	If anthropometry measures were taken from the participant
rdieta	Has diet information	If diet information was taken from the participant
proxy	If a proxy was used	If the interviewee needed another person to help them answer the questionnaire

imc2	BMI	Weight divided by height squared, with missing values of height and weight imputed
discfun	Scale of functional disability 0-100	Based on the capacity to walk several blocks, use the stairs, push objects and raise arms
discbas	Scale of basic disability 0-100	ADL scale based on the capacity to walk across the room, bathe, eat, go to bed, use toilet and cut nails
discinst	Scale of instrumental disability 0-100	IADL scale based on the capacity to cook, manage money, shop and take medicines
disctot	Scale of general disability 0-100	Takes into account the functional, basic and instrumental disability
riskadl	cannot 5+ of 14 ADL IADL	A categorical variable, where 1 is if the person cannot perform 5 or more out of 14 ADLs and IADLs
indicog	Correct answers on the cognitive impairment scale	Based on the questions made to measure cognitive impairment
cogniscale	Scale of cognitive impairment Mean(standardized items)0-100	The cognitive impairment scale standardized so the score is between 0 and 100.
cognidis	Severe cognition disability (<75% scale or <12 items)	A categorical variable, where 1 states that the person has severe cognitive impairment.
depressed	8+ items out 15 depression scale	Categorical variable, where 1 states 8 or more symptoms of depression out of 15.
deprescale	Scale of depression Mean(standardized items)0-100	A scale of depression standardized so the score is located between 0 and 100.
htaclasif	Hypertension Measure	A categorical variable stating the status of the person's blood pressure
diabglucontrol	Diabetes measured by level of glucose	A categorical variable stating the status of the person's level of glucose
diabhemo	Diabetes measured by level of hemoglobin	A categorical variable stating the status of the person's level of hemoglobin
msnum	number of metabolic syndrome 4 components except waist	Including as components: HDL, tryglicerides, hypertension and diabetes

mesynd	metabolic syndrome	A dummy variable stating if the person has metabolic syndrome or not.
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Nutrientes (Details on calculating the nutrients is found in the "Sampling and Methods" document)

hatcalor	Total energy, kcal/d
hatprot	Protein, g/d
hatcarbo	Carbohydrate, g/d
hatxgibd	Glycemic index
hatxglb	Glycemic load, g/d
hattfat	Total fat, g/d
hatxsatf	Saturated fat, g/d
hatxmonf	Monounsaturated fat, g/d
hatxpolf	Polyunsaturated fat, g/d
hatxome6_wo	Omega-6 fatty acids, g/d
hatxpfn3_wo	Omega-3 fatty acids, g/d
hatxttfa	Trans fat, g/d
hatchol	Cholesterol, mg/d
hataofib	Dietary fiber, g/d
hatxatoc	Alpha-Tocopherol, mg/d
hatxgtoc	Gamma-Tocopherol, mg/d
hatcalc	Calcium, mg/d
hatxfe03	Iron, mg/d
hatalco	Alcohol intake, g/d
hicalorias	consumes more than 3000 calories perday
localorias	consumes less than 1500 calories perday
carbs	consumes more than 400g of carbs perday

II. Exact programming for generating new variables

```
****USING elderlypeople.dta**.
```

```
***Generating variables for income**
```

```
gen ing=hn4  
replace ing=. if hn4==9999
```

```
*Ingp: pension income***
```

```
gen ingp=hn5  
replace ingp=. if hn5==9999  
gen pensionado=aml2  
recode pensionado 2=0  
recode pensionado 9=.
```

```
*Generating income for the spouse***
```

```
*9999 is substitute for 0.01  
*Final income is ignored if all the incomes were ignore.
```

```
foreach var of varlist hn13-hn16 {  
  recode `var' 9999=0.01  
}  
gen ingc=int(hn13)+int(hn14)+int(hn15)+int(hn16)  
foreach var of varlist hn13-hn16 {  
  recode `var' 0.01=9999  
}
```

```
**Generating total income for the interviewee: ingtotal**
```

```
gen ingt=g2  
replace ingt=0 if g2==. & (g1m==2 | g1m==4)
```

```
replace ingt=7.5 if g2==9999 & g4==2  
replace ingt=27.5 if g2==9999 & g4==1  
replace ingt=50 if g2==9999 & g5==2  
replace ingt=60 if g2==9999 & g5==1  
replace ingt=. if ingt==9999
```

```
foreach var of varlist hn6 hn7 {  
  recode `var' 9999=0.01  
}  
gen ingotro=int(hn6)+int(hn7)  
foreach var of varlist hn6 hn7 {  
  recode `var' 0.01=9999  
}
```

```
replace ingotro=. if hn6==9999 & hn7==9999
```

```
foreach var of varlist ing ingp ingt ingotro {  
  recode `var' .=0.01  
}
```

```
gen ingtotal=int(ing)+int(ingp)+int(ingt)+int(ingotro)
```

*****Variable:tenebienes**.**

```
recode j32 9=.
recode j31 9=.
recode j30 9=.
```

```
gen indiviv=j30+j31+j32
gen vivind = indiviv
recode vivind 1/5 =1 6/8=2 9=3 .=9
```

```
lab var vivind "Condicion de la vivienda"
lab def vivind 1"Mal estado" 2"Regular" 3"Buenas condiciones" 9"No
valorado", modify
lab val vivind vivind
tab vivind
```

****Generating the index of household asets (tenebienes)**.**

*We are using values of tenen from wavel as starting point

```
replace tenen1=0 if vivind <3
replace tenen1=1 if vivind==3
```

```
replace tenen2=1 if j18==1
replace tenen2=0 if j18==2
```

```
replace tenen3=1 if j19==1 | j19==3
replace tenen3=0 if j19==2 | j19==4
```

```
replace tenen4=1 if j26==1
replace tenen4=0 if j26==2
```

```
replace tenen5=1 if j27==1
replace tenen5=0 if j27==. |j27==9
```

```
replace tenen6=1 if j20==1
replace tenen6=0 if j20==0
```

```
replace tenen7=1 if j28>=1 & j28<=3
replace tenen7=0 if j28==0
```

```
replace tenen8=1 if j21==1 | j22==1
replace tenen8=0 if j21==2 & j22==2
```

```
replace tenen9=1 if j23==1
replace tenen9=0 if j23==2
```

```
replace tenen10=1 if j29>=1 & j29<=3
replace tenen10=0 if j29==0
```

```
gen tenebienes =tenen1+tenen2+tenen3+tenen4+tenen5+ tenen6 + tenen7 +
tenen8 + tenen9+tenen10
```

*****Body Mass index imc2****

calculating the body mass index.
using anthropometry complete data, without adjusting for Missing values.

```
gen pesokg= ((k3b*10 + k3c)/10)/2.2
gen tallacm=((k4b *10 + k4c)/10)
gen tallam=tallacm/100
*gen imc=round(pesokg /(tallam* tallam))
```

```
*replacing 180 missings of weight and height
reg tallam k5b age sex
predict pta
replace tallam=pta if tallam==.
label var tallam "Talla en metros"
```

```
gen perpeso=ev16
recode perpeso 0=5
reg pesokg perpeso k8b k9b age sex tallam
predict ppe
replace pesokg=ppe if pesokg==.
label var pesokg "Peso en Kg"
```

```
gen imc2=round(pesokg /(tallam* tallam))
```

****Generating the index of cognitive impairment ****

```
gen
indicog=b1a+b1b+b1c+b1d+b2a+b2b+b2c+orden+b4a+b4b+b4c+b5a+b5b+b5c+b6
*(replacing with 0 pts for the ones who was a proxy)*.
recode indicog .= 0 if indicog==. & am3==2
```

```
*****
*Definition of hypertension (paper ACOSAP)*.
*****
```

```
*Se agrega medicinas
```

```
*categories according to diastolic *.
**pre-hypertensives are consider normal in hypertension*.
```

```
*hypertensive on the first measure if diastolic>=90*.
```

```
gen c138br=.
replace c138br=0 if (c138b<=89)
replace c138br=1 if (c138b>=90 & c138b~=. )
replace c138br=. if c138b==.
tab c138br, miss
tabulate c138br, summarize(c138b)
```

```
*hypertensive on the second measure if diastolic >=90*.
```

```
gen h28br=.
replace h28br=0 if (h28b<=89)
replace h28br=1 if (h28b>=90 & h28b~=. )
replace h28br=. if (h28b==. )
tab h28br, miss
```



```

tabulate h28br, summarize(h28b)

*adding both of the variables*.
gen cantdia=.
replace cantdia=c138br + h28br
replace cantdia=c138br if h28br==.
replace cantdia=h28br if c138br==.
replace cantdia=. if c138br==. & h28br==.
tab cantdia, miss
tabulate cantdia, summarize(diastolica)
lab def cantdia 0 "No HTA diast" 1 "HTA with one measure" 2 "HTA with
both measure", modify
lab val cantdia cantdia

* hypertensive on the first measure if systolic>=140*.
gen c138ar=.
replace c138ar=0 if (c138a<=139)
replace c138ar=1 if (c138a>=140 & c138a~=. )
replace c138ar=. if (c138a==.)
tab c138ar, miss
tabulate c138ar, summarize(c138a)

* hypertensive on the second measure if systolic>=140*.
gen h28ar=.
replace h28ar=0 if (h28a<=139)
replace h28ar=1 if (h28a>=140 & h28a~=. )
replace h28ar=. if (h28a==.)
tab h28ar, miss
tabulate h28ar, summarize(h28a)

*Adding the two variables*.
gen cantsis=.
replace cantsis=c138ar + h28ar
replace cantsis=c138ar if h28ar==.
replace cantsis=h28ar if c138ar==.
replace cantsis=. if c138ar==. & h28ar==.
tab cantsis, miss
tabulate cantsis, summarize(sistolica)
lab def cantsis 0 "No HTA sist" 1 "HTA with one measure" 2 "HTA for
both measures", modify
lab val cantsis cantsis

***Hypertensive at cutoff point**.

gen cantHTA= cantdia + cantsis
replace cantHTA= . if cantdia==. & cantsis==.
tab cantHTA

gen HTA3de4=.
replace HTA3de4= 0 if cantHTA<=2
replace HTA3de4= 1 if cantHTA>=3 & cantHTA~=.

*****Self reported High pressure*.
gen c4r=1 if c4==1
replace c4r=0 if c4==2
replace c4r=. if c4>=8

```

```

*****Hypertensive controlled with medications *****.
gen htacont=1 if antihta==1

**People who state NOT to have hipertensi3n and are taking the meds*.
*replace htacont=0 if c4r==0 & antihta==1

***Hypertensive for general prevalence taking into account the
medication and the measurements **.
gen hiperten= HTA3de4
replace hiperten= 1 if HTA3de4==0 & antihta==1
replace hiperten= 1 if HTA3de4==. & antihta==1

tab hiperten

lab var antihta "Taking anti-hypertensive drugs"

***Categories for hypertension***.
gen htaclasif= hiperten
replace htaclasif=1 if (HTA3de4==0 & antihta==1)
replace htaclasif=2 if HTA3de4==1 & (antihta==1 | c4r==1)
replace htaclasif=3 if (HTA3de4==1 & antihta==0) & hiperten~=.
lab def htaclasif 0 "Normal(No hblood pressure)" 1 "Controlled HTA " 2
"Uncontrolled HTA " 3 "Hidden HTA", modify
lab val htaclasif htaclasif

**DEFINITON ACCORDING TO GLYCOSIDE HEMOGLOBIN**.

**Using the variables: riskemog y diab**

gen riskemog=1 if hbac1>=6.5
replace riskemog= 0 if hbac1<6.5
replace riskemog=. if hbac1==.

*diabetes*.
gen diab=1 if c10==1
replace diab=0 if c10>=2
*replace diab=. if c10>=8

**diabetesemog calculates the prevalence using the biomarkers**
**self-report and medicines**

gen diabetesemog=diab
replace diabetesemog=1 if riskemogr==1
replace diabetesemog=. if riskemogr==.

**Including people without self-reported diabetes but that is taking
meds for diabetes **

replace diabetesemog=1 if diab==0 & antidiab==1

***clasificacion of diabetes with glycated hemoglobina***.

gen diabemogclasif= diabetesemog

```

```
replace diabemogclasif=1 if ((diab==1 | antidiab==1) & riskemogr==0)
replace diabemogclasif=2 if ((diab==1 | antidiab==1) & riskemogr==1)
replace diabemogclasif=3 if (diab==0 & riskemogr==1)
```

```
lab def diabemogclasif 0 "Not diabetic" 1 "Controlled diab" 2
"Uncontrolled diab" 3 "hidden diab", modify
```

```
lab val diabemogclasif htaclasif
```

```
**using the same labels of hypertension, because they have the same
categories***
```

```
**Dummy variables of control and no diagnosis (or hidden diagnosis)**
```

```
**Controlled diabetes is done only for the ones that have a diagnosis
of diabetes**
```

```
**or are taking meds: 1 controlled y 0 not controlled**
```

```
gen diabemogcontrol=diabemogclasif
recode diabemogcontrol 0=. 1=1 2=0 3=.
```

```
**Not diagnosed diabetes or hidden: is only generated for the ones who
have diabetes**
```

```
**With any of the criteria: self-reported, meds or biomarkers**
```

```
gen diabemogescondida=diabemogclasif
recode diabemogescondida 0=. 1/2=0 3=1
```

****DEFINITION ACCORDING TO GLUCOSE**.**

Using the variables that were already created: riskemog y diab

**diabetesgluc is the variable to calculate the prevalence with biomarkers, self report and medicines **

```
gen diabetesgluc=diab
replace diabetesgluc=1 if riskglucr==1
replace diabetesgluc=. if riskglucr==.
```

**Including people without self-reported diabetes but that is taking meds for diabetes **

```
replace diabetesgluc=1 if diab==0 & antidiab==1
```

***Clasificacions of diabetes with fasting glucose ***.

```
gen diabglucclasif= diabetesgluc
replace diabglucclasif=1 if ((diab==1 | antidiab==1) & riskglucr==0)
replace diabglucclasif=2 if ((diab==1 | antidiab==1) & riskglucr==1)
replace diabglucclasif=3 if (diab==0 & riskglucr==1)
```

```
lab def diabglucclasif 0 "Not diabetic" 1 "Controlled diab" 2
"Uncontrolled diab" 3 "hidden diab", modify
lab val diabglucclasif htaclasif
```

using the same labels of hypertension, because they have the same categories*

Dummy variables of control and no diagnosis (or hidden diagnosis)

Controlled diabetes is done only for the ones that have a diagnosis of diabetes

or are taking meds: 1 controlled y 0 not controlled

```
gen diabglucontrol=diabglucclasif
recode diabglucclasif 0=. 1=1 2=0 3=.
```

Not diagnosed diabetes or hidden: is only generated for the ones who have diabetes

With any of the criteria: self-reported, meds, or biomarkers

```
gen diabglucescondida=diabemogclasif
recode diabglucescondida 0=. 1/2=0 3=1
```

```
gen diabhemo=diabemogclasif
```

****GENERATES METABOLIC SYNDROME ***.**

Using risktgsr, riskhdlr from biomarkers.dta

```
gen msnum=0
replace msnum=msnum+1 if risktgsr==1
replace msnum=msnum+1 if riskhdlr==1
replace msnum=msnum+1 if htaclasif>=1 & htaclasif<=3
replace msnum=msnum+1 if diabemogclasif >=1 & diabemogclasif <=3
replace msnum=. if htaclasif == . | diabemogclas==.

gen mesynd=0
replace mesynd=1 if waist==1 & msnum >=2
replace mesynd =. if waist==. | msnum==.
```