# WHO Child Growth Standards
# R igrowup  package

The package igrowup_R contains:

1. The source codes of two functions: *igrowup.standard* ("igrowup_standard.r") and *igrowup.restricted* ("igrowup_restricted.r");

2. Nine tab-limited txt reference tables containing the WHO Child Growths Standards: weianthro.txt, lenanthro.txt, wflanthro.txt, wfhanthro.txt and bmianthro.txt, hcanthro.txt, acanthro.txt, tsanthro.txt, ssanthro.txt;

3. The file Readme.pdf;

4. And output files related to an example survey data (survey.csv): MySurvey_prev_rc.csv, MySurvey_z_rc.csv, MySurvey_prev_st.csv and MySurvey_z_st.csv.

**Note:** The two functions *igrowup.standard* and *igrowup.restricted* concern to the following analyses, respectively:

1) standard analysis: takes into account all nine indicators and for which all available (non-missing and non-flagged) z-score values are used for each indicator-specific prevalence estimation;

2) restricted analysis: takes into account only the indicators length/height-for-age, weight-for-age, weight-for-length, weight-for-height and body mass index (BMI)-for-age and records with at least one flagged z-score (flagged, true missing or with oedema) are excluded to compute the prevalences.

**Supported versions:** The functions in this package were developed and tested using R version 3.0.1 (2013-10-07) only. Some adaptations might be necessary to run them in older versions.

**Contact for reporting bugs/comments:**
Should you encounter any problem with these functions, please send an e-mail with a clear description of the identified problem to anthro2005@who.int, specifying in the subject line that it concerns the igrowup_R package. Thank you.

**SETUP and RUN**

1. Download the file **"igrowup_R.zip"** to a basic directory [dir] where you want to include the package.

2. Restore reference data sets using the following commands:
weianthro<-read.table("[dir]\\weianthro.txt",header=T,sep="",skip=0)
lenanthro<-read.table("[dir]\\lenanthro.txt",header=T,sep="",skip=0)
bmianthro<-read.table("[dir]\\bmianthro.txt",header=T,sep="",skip=0)
hcanthro<-read.table("[dir]\\hcanthro.txt",header=T,sep="",skip=0)
acanthro<-read.table("[dir]\\acanthro.txt",header=T,sep="",skip=0)
ssanthro<-read.table("[dir]\\ssanthro.txt",header=T,sep="",skip=0)
tsanthro<-read.table("[dir]\\tsanthro.txt",header=T,sep="",skip=0)
wflanthro<-read.table("[dir]\\wflanthro.txt",header=T,sep="",skip=0)
wfhanthro<-read.table("[dir]\\wfhanthro.txt",header=T,sep="",skip=0)

Source the igrowup_standard.r and igrowup_restricted.r files in the package directory [dir], using the command
> source("[dir]\\igrowup_standard.r")
> source("[dir]\\igrowup_restricted.r")

**REFERENCES:**

WHO Multicentre Growth Reference Study Group (2006). WHO Child Growth Standards: Length/height-for-age, weight-for-age, weight-for-length, weight-for-height and body mass index-for-age: Methods and development. Geneva: World Health Organization; pp 312. (web site: http://www.who.int/childgrowth/publications/en/ )

WHO Multicentre Growth Reference Study Group (2007). WHO Child Growth Standards: Head circumference-for-age, arm circumference-for-age, triceps skinfold-for-age and subscapular skinfold-for-age: Methods and development. Geneva: World Health Organization; pp 217. (web site: http://www.who.int/childgrowth/publications/en/ )

## Function igrowup.standard

**DESCRIPTION**

- This function calculates z-scores for the *eight* anthropometric indicators, weight-for-age, length/height-for-age, weight-for-length/height, body mass index (BMI)-for-age, head circumference-for-age, arm circumference-for-age, triceps skinfold-for-age and subscapular skinfold-for-age based on the WHO Child Growth Standards. In this function, all available (non-missing and non-flagged) z-score values are used for each indicator-specific prevalence estimation (standard analysis).

- Extreme (i.e. biological implausible) z-scores for each indicator are flagged according to the following system:

| | |
|---|---|
| Weight-for-age z-score (ZWEI) | ZWEI<-6 or ZWEI >5 |
| Length/height-for-age z-score (ZLEN) | ZLEN<-6 or ZLEN >6 |
| Weight-for-length/height z-score (ZWFL) | ZWFL<-5 or ZWFL>5 |
| BMI-for-age z-score (ZBMI) | ZBMI <-5 or ZBMI >5 |
| Head circumference-for-age z-score (ZHC) | ZHC  <-5 or ZHC  >5 |
| Arm circumference-for-age z-score (ZAC) | ZAC  <-5 or ZAC  >5 |
| Triceps skinfold-for-age z-score (ZTS) | ZTS  <-5 or ZTS  >5 |
| Subscapular skinfold-for-age z-score (ZSS) | ZSS  <-5 or ZSS  >5 |

- The function also provides sex- and age-specific estimates for the prevalence of under/over nutrition and summary statistics (mean and SD) of the z-scores for each indicator.

**USAGE**

igrowup.standard(FileLab="Temp",FilePath="C:\\Documents and Settings\\", mydf=, sex=, age=, age.month=F, weight=,lenhei=,measure=,headc=,armc=, triskin=,subskin=, oedema=rep("n",dim(mydf)[1]), sw=rep(1,dim(mydf)[1]))

**REQUIRED ARGUMENTS:**

- mydf: the data frame containing the variables to be used.

- sex: the name of the variable containing gender information; if it is numeric, its values must be: 1 for males and 2 for females. If it is character, it must be "m" or "M" for males and "f" or "F" for females. No z-scores will be calculated if sex is missing.

**OPTIONAL ARGUMENTS**

The following parameters can be left unspecified, and a default analysis will be performed. Note: If none of the measurement variables (weight, lenhei, headc, armc, triskin, subskin) is provided, the analysis output will be empty. If the variable age is not available, results will be provided only for weight-for-length/height.

- FileLab: a label chosen to be used as part of the output files names. It is specified in double quotes. If unspecified, the default label "Temp" will be used.

- FilePath: the directory where the user requires the output Excel files to be stored. If unspecified, the default directory "C:\\Documents and Settings\\" will be used.

- age: to specify the name of a numeric variable containing age information; age can be in either days or months (if optional argument age.month is set to TRUE). An exact age in days is expected and should not be rounded if age is in months. Age-related z-scores will NOT be calculated if age is missing.

- age.month: a logical flag; if TRUE, variable age unit will be treated as months. Function converts it to days by dividing age by 30.4375 and rounding it to integer so that reference tables can be used. When unspecified, the default value FALSE is used and age unit is treated as days.

- weight: the name of the numeric variable containing body weight information, which must be in kilograms. Weight-related z-scores are not calculated if body weight is missing.

- lenhei: the name of a numeric variable containing length (recumbent length) or height (standing height) information, which must be in centimeters. Length/height-related z-scores will not be calculated if lenhei is missing. For children with age below 24 months (i.e. below 731 days) and standing height measured, the function converts it to recumbent length by adding 0.7 cm; and for children with age equal and above 24 months and measured in recumbent length, the macro converts it to standing height by subtracting 0.7 cm. This way all the z-scores calculated by this function are length-based for children below 24 months, and height-based otherwise. This converted length/height according to age is assigned to the variable clenhei in the exported Excel file.

- headc: the name of the numeric variable containing head circumference information, which must be in centimeters. Head circumference-for-age z-scores are not calculated if head circumference is missing.

- armc: the name of the numeric variable containing arm circumference information, which must be in centimeters. Arm circumference-for-age z-scores are not calculated if arm circumference is missing.

- triskin: the name of the numeric variable containing triceps skinfold information, which must be in millimeters. Triceps skinfold-for-age z-scores are not calculated if triceps skinfold is missing.

- subskin: the name of the numeric variable containing subscapular skinfold information, which must be in millimeters. Subscapular skinfold-for-age z-scores are not calculated if subscapular skinfold is missing.

- measure: the name of a character variable indicating whether recumbent length or standing height was measured for each observation. The values of this variable must be "L" or "l" for recumbent length, and "H" or "h" for standing height. Although it is highly recommended that this variable is provided according to the measurements taken in the survey, it is possible to run the analysis without specifying this variable. If unspecified, the default vector rep(NA,dim(mydf)[1]) with all missing values is used. The function imputes the missing values according to the following algorithm:

    a. If age is not missing, then it is recumbent length if age below 24 months (731 days), and standing height if age equal and above 24 months.

    b. If age is missing, then it is recumbent length if measurement<87 cm and standing height if measurement≥87 cm.

- oedema: the name of the character variable containing oedema information. The values of this variable must be "n" or "N" for non-oedema, and "y" or "Y" for oedema. Although it is highly recommended that this variable is provided by the survey, it is possible to run the analysis without specifying this variable. If unspecified, the default vector rep("n",dim(mydf)[1]) with values considered as non-oedema is used. Missing values will be treated as non-oedema. For oedema, weight related z-scores (zwei, zwfl and zbmi) are NOT calculated (set to missing), BUT they are treated as being < -3 SD in the weight-related indicator prevalence estimation.

- sw: the name of a numeric variable containing the sampling weights. If unspecified, the rep(1,dim(mydf)[1]) vector is used, i.e. where all records have equal sampling weights, and un-weighted analysis is performed. Negative values are not allowed.

**Note:** It is possible to miss one or more optional arguments. The corresponding default values will be used whenever an argument is unspecified.

**EXPORTED FILES**

This function does not provide any value; instead it creates, in the directory FilePath, two Excel files: one containing z-score variables and the other relevant created variables ("FileLab_z_st.csv"); another displaying sex- and age-specific estimates for the prevalence (and their corresponding 95% confidence intervals) of under/over nutrition and summary statistics (mean and SD) of the z-scores for each indicator ("FileLab_prev_st.csv").

The file FileLab_z_st.csv contains all variables in the input data frame mydf plus the following 19 variables:

| Variable | Description |
|---|---|
| agedays | age in days for deriving z-score |
| clenhei | converted length/height for deriving z-score |

| | |
|---|---|
| cbmi | BMI value based on length/height given by clenhei |
| zwei | Weight-for-age z-score |
| zlen | Length/Height-for-age z-score |
| zwfl | Weight-for-length/height z-score |
| zbmi | BMI-for-age z-score |
| zhc | Head circumference-for-age z-score |
| zac | Arm circumference-for-age z-score |
| zts | Triceps skinfold-for-age z-score |
| zss | Subscapular skinfold-for-age z-score |
| fwei | Flag for zwei<-6 or zwei>5 |
| flen | Flag for zlen<-6 or zlen>6 |
| fwfl | Flag for zwfl<-5 or zwfl>5 |
| fbmi | Flag for zbmi<-5 or zbmi>5 |
| fhc | Flag for zhc<-5 or zhc>5 |
| fac | Flag for zac<-5 or zac>5 |
| fts | Flag for zts<-5 or zts>5 |
| fss | Flag for zss<-5 or zss>5 |

For the file "FileLab_prev_st.csv," only children aged below 61 months are included in the analysis. The age groups are: Total (0-60), 0-5, 6-11, 12-23, 24-35, 36-47 and 48-60 completed months. The youngest age group is 3-5 months for the arm circumference, triceps and subscapular skinfolds indicators. Where age is missing, only weight-for-length/height z-scores can be derived and these cases are included in the Total (0-60) age group.

**EXAMPLE**

**Step 1: Before using the igrowup.standard function for the first time, remember to follow the 3 steps in the SETUP and RUN given above.**

**Step 2:** Import your data file into R. The following example is using the data set survey.csv contained in the package igrowup_R.

```
#Example: dataframe=survey
> survey<-read.csv("[dir]\\survey.csv",header=T,sep=",",skip=0,na.strings="")
```

**Step 3:**
```
#Standard analysis
> igrowup.standard(FilePath="D:\\R igrowup example",
   FileLab="MySurvey",mydf=survey,sex=GENDER,age=agemons,age.month=T,weight=WEIGH
   T,lenhei=HEIGHT,measure=measure,oedema=oedema,headc=HEAD,armc=MUAC,
   triskin=TRI,subskin=SUB,sw=SW)
```

**Output: The files MySurvey_z_st.csv and MySurvey_prev_st.csv are created in the directory "D:/R igrowup example".**

## Function igrowup.restricted

**DESCRIPTION**

- This function calculates z-scores for the *four* anthropometric indicators, weight-for-age, length/height-for-age, weight-for-length/height and body mass index (BMI)-for-age, based on the WHO Child Growth Standards. In this function, records with at least one flagged z-score (flagged, true missing or with oedema) are excluded to computate the prevalences (restricted analysis).

- Extreme (i.e. biological implausible) z-scores for each indicator are flagged according to the following system:

| | |
|---|---|
| Weight-for-age z-score (ZWEI) | ZWEI<-6 or ZWEI >5 |
| Length/height-for-age z-score (ZLEN) | ZLEN<-6 or ZLEN >6 |
| Weight-for-length/height z-score (ZWFL) | ZWFL<-5 or ZWFL>5 |
| BMI-for-age z-score (ZBMI) | ZBMI <-5 or ZBMI >5 |

- The function also provides sex- and age-specific estimates for the prevalence of under/over nutrition and summary statistics (mean and SD) of the z-scores for each indicator.

**USAGE**

igrowup.restricted(FileLab="Temp",FilePath="C:\\Documents and Settings\\", mydf=, sex=, age=, age.month=F, weight=, lenhei=,measure=, oedema=rep("n",dim(mydf)[1]), sw=rep(1,dim(mydf)[1]))

**REQUIRED ARGUMENTS:**

- mydf: the data frame containing the variables to be used.

- sex: the name of the variable containing gender information; if it is numeric, its values must be: 1 for males and 2 for females. If it is character, it must be "m" or "M" for males and "f" or "F" for females. No z-scores will be calculated if sex observation is missing.

**OPTIONAL ARGUMENTS**

The following parameters can be left unspecified, and a default analysis will be performed. Note: If none of the measurement variables (weight, lenhei) is provided, the analysis output will be empty. If the variable age is not available, results will be provided only for weight-for-length/height.

- FileLab: a label chosen to be used as part of the output files names. It is specified in double quotes. If unspecified, the default label "Temp" will be used.

- FilePath: the directory where the user require the output Excel files to be stored. If unspecified, the default directory "C:\\Documents and Settings\\" will be used.

- age: to specify the name of a numeric variable containing age information; age can be in either days or months (if optional argument age.month is set to TRUE). An exact age in days is expected and should not be rounded if age is in months. Age-related z-scores will NOT be calculated if age is missing.

- age.month: a logical flag; if TRUE, variable age unit will be treated as months. Function converts it to days by dividing age by 30.4375 and rounding it to integer so that reference tables can be used. When unspecified, the default value FALSE is used and age unit is treated as days.

- weight: the name of the numeric variable containing body weight information, which must be in kilograms. Weight-related z-scores are not calculated if body weight is missing.

- lenhei: the name of a numeric variable containing length (recumbent length) or height (standing height) information, which must be in centimeters. Length/height-related z-scores will not be calculated if lenhei is missing. For children with age below 24 months (i.e. below 731 days) and standing height measured, the function converts it to recumbent length by adding 0.7 cm; and for children with age equal and above 24 months and measured in recumbent length, the macro converts it to standing height by subtracting 0.7 cm. This way all the z-scores calculated by this function are length-based for children below 24 months, and height-based otherwise. This converted length/height according to age is assigned to the variable clenhei in the exported Excel file.

- measure: the name of a character variable indicating whether recumbent length or standing height was measured for each observation. The values of this variable must be "L" or "l" for recumbent length, and "H" or "h"  for standing height. Although it is highly recommended that this variable is provided according to the measurements taken in the survey, it is possible to run the analysis without specifying this variable. If unspecified, the default vector rep(NA,dim(mydf)[1]) with all missing values is used. The function imputes the missing values according to the following algorithm:

    a. If age is not missing, then it is recumbent length if age below 24 months (731 days), and standing height if age equal and above 24 months.

    b. If age is missing, then it is recumbent length if measurement<87 cm and standing height if measurement≥87 cm.

- oedema: the name of the character variable containing oedema information. The values of this variable must be "n" or "N" for non-oedema, and "y" or "Y" for oedema. Although it is highly recommended that this variable is provided by the survey, it is possible to run the analysis without specifying this variable. If unspecified, the default vector rep("n",dim(mydf)[1]) with values considered as non-oedema is used. Missing values will be treated as

non-oedema. For oedema, weight related z-scores (zwei, zwfl and zbmi) are NOT calculated (set to missing), BUT they are treated as being < -3 SD in the weight-related indicator prevalence estimation.

- sw: the name of a numeric variable containing the sampling weights. If unspecified, the rep(1,dim(mydf)[1]) vector is used, i.e. where all records have equal sampling weights, and un-weighted analysis is performed. Negative values are not allowed.

**Note:** It is possible to miss one or more optional arguments. The corresponding default values will be used whenever an argument is unspecified.

## EXPORTED FILES

This function does not provide any value; instead it creates, in the directory FilePath, two Excel files: one containing z-score variables and the other relevant created variables ("FileLab_z_rc.csv"); another displaying sex- and age-specific estimates for the prevalence (and their corresponding 95% confidence intervals) of under/over nutrition and summary statistics (mean and SD) of the z-scores for each indicator ("FileLab_prev_rc.csv").

The file FileLab_z_rc.csv contains all variables in the input data frame mydf plus the following 11 variables:

| Variable | Description |
|----------|-------------|
| agedays | age in days for deriving z-score |
| clenhei | converted length/height for deriving z-score |
| cbmi | BMI value based on length/height given by clenhei |
| zwei | Weight-for-age z-score |
| zlen | Length/Height-for-age z-score |
| zwfl | Weight-for-length/height z-score |
| zbmi | BMI-for-age z-score |
| fwei | Flag for zwei<-6 or zwei>5 |
| flen | Flag for zlen<-6 or zlen>6 |
| fwfl | Flag for zwfl<-5 or zwfl>5 |
| fbmi | Flag for zbmi<-5 or zbmi>5 |

For the file "FileLab_prev_rc.csv," only children aged below 61 months are included in the analysis. The age groups are: Total (0-60), 0-5, 6-11, 12-23, 24-35, 36-47 and 48-60 completed months. Where age is missing, only weight-for-length/height z-scores can be derived and these cases are included in the Total (0-60) age group.

**EXAMPLE**

**Step 1: Before using the igrowup.restricted function for the first time, remember to follow the 3 steps in the SETUP and RUN given above.**

**Step 2:** Import your data file into R. The following example is using data set survey.csv contained in the package igrowup_R.

```
#Example: dataframe=survey
> survey<-read.csv("[dir]\\survey.csv",header=T,sep=",",skip=0,na.strings="")
```

**Step 3:**

```
>#Example: dataframe=survey
>#Restricted analysis
>igrowup.restricted(FilePath=" D:\\R igrowup example",
    FileLab="MySurvey",mydf=survey,sex=GENDER,age=agemons,age.month=T,
    weight=WEIGHT, lenhei=HEIGHT,measure=measure,oedema=oedema,sw=SW)
```

**Output: The files MySurvey_z_rc.csv and MySurvey_prev_rc.csv are created in the directory "D:/R igrowup example".**