**“Skeletal Age” for mapping the impact of fracture on mortality**

**Supplementary File 4. R codes used to construct skeletal age for individual fracture sites associated with increased mortality risk**

**# (1) Skeletal age for the high-risk fracture sites in men**

***## Analysis macro***

func\_Skel\_Age <- function(sk.age, gender, fracture, thres\_age){

 qx = c( 2.059, 0.175, 0.204, 0.033, 0.064, 0.032, 0.096, 0.094, 0.000, 0.000, 0.000, 0.000, 0.060, 0.151, 0.153, 0.185, 0.369, 0.437, 0.589, 0.445, 0.577, 0.579, 0.317, 0.476, 0.441, 0.713, 0.895, 0.477, 0.543, 0.611, 0.507, 0.638, 0.572, 0.740, 0.849, 0.620, 0.840, 0.729, 0.960, 0.771, 0.906, 1.306, 1.020, 1.419, 1.055, 1.160, 1.448, 1.782, 1.712, 2.112, 1.873, 2.174, 2.949, 2.198, 2.617, 3.138, 4.276, 4.323, 4.333, 5.031, 5.880, 5.611, 6.368, 7.896, 7.888, 8.288, 11.187, 12.640, 12.769, 13.729, 15.648, 16.632, 18.592, 20.907, 24.536, 27.730, 28.554, 30.961, 36.073, 41.158, 47.602, 51.960, 61.761, 66.589, 78.630, 92.359, 100.496, 112.117, 128.829, 151.725, 162.987, 179.113, 204.320, 222.943, 235.269, 245.015, 294.884, 340.168, 345.695, 350.626, 364.807, 350.383, 338.862, 283.469, 550.671, 435.282, 1000.000)

 age = 0:106

 fx\_hr = sk.age$est[sk.age$sex == gender & sk.age$fx == fracture]

 Lx1 = qx

 lx1 = qx

 Tx1 = qx

 Ex1 = qx

 Lx2 = qx

 lx2 = qx

 Tx2 = qx

 Ex2 = qx

 length = length(qx)-1

 Lx1[1] = 100000

 Lx1[length+1] = NA

 Tx1[length+1] = NA

 Ex1[length+1] = NA

 Lx2[1] = 100000

 Lx2[length+1] = NA

 Tx2[length+1] = NA

 Ex2[length+1] = NA

 for (x in 2:length) {

 Lx1[x] = Lx1[x-1]\*(1-(qx[x-1]\*1.00)/1000)

 Lx2[x] = Lx2[x-1]\*(1-(qx[x-1]\*fx\_hr)/1000)

 }

 lx1 = (Lx1 + lead(Lx1))/2

 lx1[length] = 0

 lx1[length+1] = NA

 lx2 = (Lx2 + lead(Lx2))/2

 lx2[length] = 0

 lx2[length+1] = NA

 for (x in 1:length) {

 Tx1[x] = sum(lx1[x:length])

 Tx2[x] = sum(lx2[x:length])

 }

 Ex1 = Tx1 / Lx1

 Ex2 = Tx2 / Lx2

 Lx1 = round(Lx1)

 lx1 = round(lx1)

 Tx1 = round(Tx1)

 Ex1 = round(Ex1,1)

 Lx2 = round(Lx2)

 lx2 = round(lx2)

 Tx2 = round(Tx2)

 Ex2 = round(Ex2,1)

 Diff = Ex1- Ex2

 Skel.Age = age+Diff

 print(Skel.Age)

 df = data.frame(age, qx, Ex1, Ex2, Diff, Skel.Age)

 df$fx = fracture

 skage = subset(df, age>thres\_age, select = c(age, fx, Skel.Age))

 skage

 }

***## Dataset***

sk.age = read.csv("C:\\Garvan\\Skeletal age\\Analysis\\Skeletal\_age.csv")

***## Analysis***

*### (1.1) Any fracture*

any\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Any fracture",49)

any\_fx\_men

*### (1.2) Hip fracture*

hip\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Hip", 49)

hip\_fx\_men

*### (1.3) Femur fracture*

femur\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Femur", 49)

femur\_fx\_men

*### (1.4) Pelvis fracture*

pelvis\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Pelvis", 49)

pelvis\_fx\_men

*### (1.5) Vertebral fracture*

vert\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Vertebrae", 49)

vert\_fx\_men

*### (1.6) Humerus fracture*

hum\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Humerus", 49)

hum\_fx\_men

*### (1.7) Rib fracture*

rib\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Rib", 49)

rib\_fx\_men

*### (1.8) Clavicle fracture*

clav\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Clavicle", 49)

clav\_fx\_men

*### (1.9) Lower leg fracture*

leg\_fx\_men = func\_Skel\_Age(sk.age, "Men", "Lower leg", 49)

leg\_fx\_men

*### Dataset - Skeletal age for high-risk fracture sites in men*

library(dplyr)

library(tidyverse)

df\_list = list(any\_fx\_men, hip\_fx\_men, femur\_fx\_men, pelvis\_fx\_men, vert\_fx\_men, hum\_fx\_men, rib\_fx\_men, clav\_fx\_men, leg\_fx\_men)

sa.men = df\_list %>% reduce(full\_join, by = "age")

head(sa.men)

**# (2) Skeletal age for the high-risk fracture sites in women**

***## Analysis macro***

func\_Skel\_Age <- function(sk.age, gender, fracture, thres\_age){

 qx = c(1.331, 0.148, 0.072, 0.035, 0.034, 0.034, 0.067, 0.131, 0.032, 0.063, 0.124, 0.124, 0.095, 0.191, 0.096, 0.162, 0.130, 0.294, 0.163, 0.063, 0.187, 0.218, 0.185, 0.210, 0.147, 0.320, 0.200, 0.251, 0.217, 0.370, 0.210, 0.317, 0.377, 0.304, 0.225, 0.398, 0.317, 0.433, 0.665, 0.523, 0.526, 0.709, 0.900, 0.630, 0.498, 0.705, 1.026, 1.067, 1.556, 1.456, 1.452, 1.313, 1.448, 2.205, 2.413, 2.365, 2.487, 2.633, 2.636, 2.993, 3.567, 3.901, 5.035, 5.070, 5.352, 6.482, 6.636, 7.310, 7.955, 9.231, 9.933, 12.446, 14.182, 15.618, 16.567, 16.675, 19.111, 23.939, 26.242, 27.700, 35.226, 34.403, 44.070, 50.708, 58.747, 66.721, 64.897, 81.356, 96.449, 114.857, 126.731, 137.871, 161.417, 180.891, 209.809, 229.592, 241.967, 282.213, 299.071, 322.506, 378.927, 330.566, 366.203, 400.171, 327.020, 329.680, 1000.000)

 age = 0:106

 fx\_hr = sk.age$est[sk.age$sex == gender & sk.age$fx == fracture]

 Lx1 = qx

 lx1 = qx

 Tx1 = qx

 Ex1 = qx

 Lx2 = qx

 lx2 = qx

 Tx2 = qx

 Ex2 = qx

 length = length(qx)-1

 Lx1[1] = 100000

 Lx1[length+1] = NA

 Tx1[length+1] = NA

 Ex1[length+1] = NA

 Lx2[1] = 100000

 Lx2[length+1] = NA

 Tx2[length+1] = NA

 Ex2[length+1] = NA

 for (x in 2:length) {

 Lx1[x] = Lx1[x-1]\*(1-(qx[x-1]\*1.00)/1000)

 Lx2[x] = Lx2[x-1]\*(1-(qx[x-1]\*fx\_hr)/1000)

 }

 lx1 = (Lx1 + lead(Lx1))/2

 lx1[length] = 0

 lx1[length+1] = NA

 lx2 = (Lx2 + lead(Lx2))/2

 lx2[length] = 0

 lx2[length+1] = NA

 for (x in 1:length) {

 Tx1[x] = sum(lx1[x:length])

 Tx2[x] = sum(lx2[x:length])

 }

 Ex1 = Tx1 / Lx1

 Ex2 = Tx2 / Lx2

 Lx1 = round(Lx1)

 lx1 = round(lx1)

 Tx1 = round(Tx1)

 Ex1 = round(Ex1,1)

 Lx2 = round(Lx2)

 lx2 = round(lx2)

 Tx2 = round(Tx2)

 Ex2 = round(Ex2,1)

 Diff = Ex1- Ex2

 Skel.Age = age+Diff

 print(Skel.Age)

 df = data.frame(age, qx, Ex1, Ex2, Diff, Skel.Age)

 df$fx = fracture

 skage = subset(df, age>thres\_age, select = c(age, fx, Skel.Age))

 skage

 }

***## Analysis***

*### (2.1) Any fracture*

any\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Any fracture",49)

any\_fx\_women

*### (2.2) Hip fracture*

hip\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Hip", 49)

hip\_fx\_women

*### (2.3) Femur fracture*

femur\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Femur", 49)

femur\_fx\_women

*### (2.4) Pelvis fracture*

pelvis\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Pelvis", 49)

pelvis\_fx\_women

*### (2.5) Vertebral fracture*

vert\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Vertebrae", 49)

vert\_fx\_women

*### (2.6) Humerus fracture*

hum\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Humerus", 49)

hum\_fx\_women

*### (2.7) Rib fracture*

rib\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Rib", 49)

rib\_fx\_women

*### (2.8) Clavicle fracture*

clav\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Clavicle", 49)

clav\_fx\_women

*### (2.9) Lower leg fracture*

leg\_fx\_women = func\_Skel\_Age(sk.age, "Women", "Lower leg", 49)

leg\_fx\_women

*### Dataset - Skeletal age for high-risk fracture sites in women*

df\_list = list(any\_fx\_women, hip\_fx\_women, femur\_fx\_women, pelvis\_fx\_women, vert\_fx\_women, hum\_fx\_women, rib\_fx\_women, clav\_fx\_women, leg\_fx\_women)

sa.women = df\_list %>% reduce(full\_join, by = "age")

head(sa.women)

***## Dataset for both men and women***

sa.both = rbind(sa.men, sa.women)

sa.both

write.csv(sa.both, "C:\\Garvan\\Skeletal age\\Analysis\\Skeletal\_age\_both.csv", row.names = FALSE)