##===========================================================================

## TOXOCARA MODEL [8]

## last update: 21/01/2013

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##== LIFE FUNCTIONS =========================================================

create <-

function(number){

individuals <- data.frame(

age = rep(0, number), # age of inds in months

ageCat = rep(0, number), # age category

ab = rep(FALSE, number), # antibody status

monthsExp = rep(0, number), # months post exposure

expStatus = rep(0, number) # number of exposures

)

return(individuals)

}

subsetAlive <-

function(x){

x <- subset(x, x$ageCat != 3)

return(x)

}

births <-

function(x, nBirths){

x <- rbind(x, create(nBirths))

return(x)

}

ageing <- # + categorize: [0,9), [9,60) & [60,180) & [180,Inf)

function(x){

x$age <- x$age + 1

x$ageCat <- cut(x$age,

c(0, 9, 5\*12, 15\*12, Inf),

labels = c(0:3),

right = FALSE)

return(x)

}

##== DISEASE FUNCTIONS ======================================================

seroConversion <- # no seroconversion for [0,9)

function(x, envcP, youngP, oldP, monthWiseP){

youngInds <- x$ageCat == 1 # select individuals [9,60)

oldInds <- x$ageCat == 2 # select individuals [60,180)

seroConvYng <- rbinom(sum(youngInds), 1, youngP \* monthWiseP \* envcP)

seroConvOld <- rbinom(sum(oldInds), 1, oldP \* monthWiseP \* envcP)

x$ab[youngInds] <- x$ab[youngInds] + seroConvYng

x$ab[oldInds] <- x$ab[oldInds] + seroConvOld

x$ab <- x$ab > 0 # re-convert to logical: pos OR neg

x$expStatus[youngInds] <- x$expStatus[youngInds] + seroConvYng

x$expStatus[oldInds] <- x$expStatus[oldInds] + seroConvOld

return(x)

}

seroReversion <-

function(x, startReversion, endReversion){

x$monthsExp[x$ab] <- x$monthsExp[x$ab] + 1

test <- runif(nrow(x)) < .5

x$ab[x$expStatus == 1 &

x$monthsExp >= rpois(1, startReversion[1]) & test] <- FALSE

x$ab[x$expStatus == 2 &

x$monthsExp >= rpois(1, startReversion[2]) & test] <- FALSE

x$ab[x$expStatus >= 3 &

x$monthsExp >= rpois(1, startReversion[3]) & test] <- FALSE

x$ab[x$expStatus == 1 &

x$monthsExp >= startReversion[1] + endReversion] <- FALSE

x$ab[x$expStatus == 2 &

x$monthsExp >= startReversion[2] + endReversion] <- FALSE

x$ab[x$expStatus >= 3 &

x$monthsExp >= startReversion[3] + endReversion] <- FALSE

x$monthsExp[!x$ab] <- 0

return(x)

}

##== REPORTER FUNCTION ======================================================

census <-

function(x, y, i){

y$n1[i] <- sum(x$ab[x$ageCat == 1])

y$n2[i] <- sum(x$ab[x$ageCat == 2])

y$n[i] <- y$n1[i] + y$n2[i]

y$pop[i] <- nrow(x)

y$prev[i] <- y$n[i] / y$pop[i]

y$prev1[i] <- y$n1[i] / sum(x$ageCat == 1)

y$prev2[i] <- y$n2[i] / sum(x$ageCat == 2)

return(y)

}

##== RUN LIFE CYCLES ========================================================

model <-

function(nStart, nCycles,

envcP, youngP, oldP, monthWiseP,

startReversion, endReversion){

ENVC <- rbeta(nCycles, envcP[1], envcP[2]) # random envcP

MONTH <- matrix(ncol = 12, nrow = nCycles/12) # random monthWiseP

for (i in 1:12)

MONTH[,i] <- rbeta(nCycles/12, monthWiseP[1,i], monthWiseP[2,i]) \*

(monthWiseP[4,i] - monthWiseP[3,i]) + monthWiseP[3,i]

YOUNG <- runif(nCycles, youngP[1], youngP[2]) # random youngP

OLD <- runif(nCycles, oldP[1], oldP[2]) # random oldP

inds <- create(nStart)

data <- data.frame(

n = numeric(nCycles),

n1 = numeric(nCycles),

n2 = numeric(nCycles),

pop = numeric(nCycles),

prev = numeric(nCycles),

prev1 = numeric(nCycles),

prev2 = numeric(nCycles)

)

for (i in 1:nCycles){

thisMonth <- 1 + (i-1)%%12

nBirths <- rpois(1, 5)

envcP <- ENVC[i]

monthWiseP <- MONTH[nCycles/12, thisMonth]

youngP <- YOUNG[i]

oldP <- OLD[i]

inds <- seroReversion(inds, startReversion, endReversion)

inds <- ageing(inds)

inds <- births(inds, nBirths)

inds <- subsetAlive(inds)

inds <- seroConversion(inds, envcP, youngP, oldP, monthWiseP)

data <- census(inds, data, i)

}

out <- list(inds = inds, data = data,

ENVC = ENVC, OLD = OLD, YOUNG = YOUNG, MONTH = MONTH)

class(out) <- "run"

return(out)

}

##== RUN CHAINS =============================================================

Model <-

function(nChains, nStart, nCycles,

envcP, youngP, oldP, monthWiseP,

startReversion, endReversion){

## Define seed and RNG kind

set.seed(123, kind = "default", normal.kind = "default")

## Run chains

out <- vector("list", nChains)

for (i in seq\_len(nChains)){

out[[i]] <- model(nStart, nCycles,

envcP, youngP, oldP, monthWiseP,

startReversion, endReversion)

}

class(out) <- "run"

return(out)

}