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require(phydynR)

Warning: package 'ape' was built under R version 3.3.2
Warning: package 'expm' was built under R version 3.3.2
Warning: package 'phytools' was built under R version 3.3.2
Warning: package 'maps' was built under R version 3.3.2
Warning: package 'phangorn' was built under R version 3.3.2
Warning: package 'ggplot2' was built under R version 3.3.2
Warning: package 'BH' was built under R version 3.3.2
Warning: package 'Rcpp' was built under R version 3.3.2
Warning: package 'RcppArmadillo' was built under R version 3.3.2

source('model1.R')

MH <- 20
PID <- Sys.getpid()

# counterfactuals sim'ed separately, eg:
#~ nh_wtransm <- c(
#~   nh1 = 1
#~   ,nh2 = 1
#~   ,nh3 = 1
#~   ,nh4 = 1
#~   ,nh5 = 1
#~ )

#~ o <- ode(y=y0, times=times_day, func=dydt, parms=list() , method = 'adams')
o <- ode(y=y0, times=times_day, func=dydt, parms=list() , method = 'rk4')
tfgy <- .tfgy( o )

#####
#~ incidence and prevalence
yfin <- tfgy[[4]][[length(times_day)]]
ffin <- tfgy[[2]][[length(times_day)]]
newinf <- sum(ffin[1:120, 1:120] ) * 365
plwhiv <- sum( yfin[-length(yfin)] )

#~ sample time and states
sampleTimes <- scan( file = 'sampleTimes' )
ss <- matrix( scan( file = 'sampleStates' ) , byrow=TRUE, ncol = m)
colnames(ss) <- DEMES
# regularise
ss <- ss + 1e-4
ss = sampleStates <- ss / rowSums(ss)

# modify sample times so max corresponds to 2013

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sampleTimes <- sampleTimes + (years2days(2013) - max(sampleTimes) )

# test by downsampling
if (F)
{
n <- length( sampleTimes )
keep <- sample.int( n, size = 2e3, replace=F)
sampleTimes <- sampleTimes[keep]
sampleStates <- sampleStates[keep, ]
}

## sim tree

print('sim tree')

[1] "sim tree"

print(date())

[1] "Wed Jun 21 18:48:10 2017"

st.tree <- system.time( {
#~ daytree <- sim.co.tree.fgy(tfgy, sampleTimes, sampleStates)
  daytree <- rcolgem::sim.co.tree.fgy(tfgy, sampleTimes, sampleStates)
})

Warning in rcolgem::sim.co.tree.fgy(tfgy, sampleTimes, sampleStates):
Estimated number of extant lineages at earliest time on time axis is
20.3646096708416, and sampled lineages are not likely to have a single
common ancestor. Root of returned tree will have daughter clades corresponding
to simulated trees.

print(date())

[1] "Wed Jun 21 18:50:18 2017"

# rescale tree
tree <- daytree
sampleTimes <- days2years( tree$sampleTimes )
tree$edge.length <- tree$edge.length / 365
bdt <- DatedTree( tree, sampleTimes, tree$sampleStates, tol = Inf)

D <- cophenetic.phylo( bdt )
cat( 'mean genetic divergence if rate = .0015\n' )

mean genetic divergence if rate = .0015

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print( mean(D ) * .0015 )

[1] 0.1489217

n<- bdt$n

treeSampleStates <- tree$sampleStates
cd4s <- setNames( sapply( 1:nrow(treeSampleStates), function(k){
  deme <- DEMES[ which.max(treeSampleStates[k,] ) ]
  stage <- strsplit( deme, '.' , fixed=T)[[1]][1]
  stage <- as.numeric( tail( strsplit(stage, '')[[1]], 1 ) )
  if (stage==1) return(1e3)
  if (stage==2) return(750)
  if (stage==3) return(400)
  if (stage==4) return(300)
  if (stage==5) return(100)
}), tree$tip.label)
ehis <- setNames( sapply( 1:nrow( treeSampleStates), function(k){
  deme <- DEMES[ which.max(treeSampleStates[k,] ) ]
  stage <- strsplit( deme, '.' , fixed=T)[[1]][1]
  stage <- as.numeric( tail( strsplit(stage, '')[[1]], 1 ) )
  ifelse( stage==1, TRUE, FALSE)
}), tree$tip.label)
sampleDemes <- setNames( sapply( 1:n, function(u) DEMES[which.max( treeSampleStates[u,]) ] )

system.time(
  W <- phylo.source.attribution.hiv.msm( bdt
    , bdt$sampleTimes # must use years
    , cd4s = cd4s[bdt$tip.label] # named numeric vector
    , ehi = ehis[bdt$tip.label] # named logical vector
    , numberPeopleLivingWithHIV = plwhiv# scalar
    , numberNewInfectionsPerYear = newinf # scalar
    , maxHeight = MH
    , res = 1e3
    , treeErrorTol = Inf
    , minEdgeLength = 1/52
  )
)

[1] "NOTE : sample times must be in units of years"
[1] "start source attrib"
[1] "Wed Jun 21 18:51:40 2017"

Error in sourceAttribMultiDemeCpp2(heights, Fs[fgyi], Gs[fgyi], Ys[fgyi],
: c++ exception (unknown reason)

Timing stopped at: 19.304 8.026 27.421

```