Run simulated epidemic history

Stephane

3/27/2017

Run simulated epidemic history

```
library(knitr)
read_chunk('model0.R')
```

load libraries

```
require(phydynR) # replaces rcolgem
require(deSolve)
require(Rcpp)
```

source C functions

```
sourceCpp( 'model0.cpp' ) # F_matrix and G_matrix fns
```

input parameters

```
##- Age progression
##(by quantiles: 18.0, 27.0, 33.0, 40.0, 80.5)
age_rates <- c(agerate1 = 1/9/365
    , agerate2 = 1/6/365
    , agerate3 = 1/7/365
    , agerate4 = 1/40.5/365
)

##- Natural history (from Cori et al. AIDS 2015)
stage_prog_yrs <- c( .5, 3.32, 2.7, 5.50, 5.06 )
stageprog_rates <- setNames( 1 / (stage_prog_yrs  * 365 )
 , c('gamma1', 'gamma2', 'gamma3', 'gamma4', 'gamma5')  )

pstarts <- c( pstartstage1 = 0 #NA
 , pstartstage2 = 0.76
 , pstartstage3 = 0.19
 , pstartstage4 = 0.05
 , pstartstage5 = 0
)

theta <- c( age_assort_factor = .5 # power of age difference
  , pRiskLevel1 = .8 # proportion in low risk group
  , srcMigrationRate = 1/50/365 # per lineage rate of migration to source
  , srcGrowthRate = 1 / 3 / 365 #
  , src0 = 1e3  # initial source size
  , inc_scale = 0.09401734 # based on docking (see below) # initial = .03
  , max_diag_rate = 0.66227809 # based on docking (see below) # initial = 1/3 (time 2 diag of 3 yrs)
  , diag_rate_85 = 1/10
  , accel_diag_rate = 0.03196171 # based on docking (see below ) # initial = 1/7 # accel of logistic fu
  , treatmentEffectiveness = .95 # slows stage progression
  , pstarts
```

```
    , age_rates
    , stageprog_rates
)

theta_default <- theta
```

Notation	Parameter	Value	Unit
α_1	Age progression rate in age group 1	1/9/365	day^{-1}
α_2	Age progression rate in age group 2	1/6/365	day^{-1}
α_3	Age progression rate in age group 3	1/7/365	day^{-1}
α_4	Age progression rate in age group 4	1/40.5/365	day^{-1}
γ_1	Stage progression rate in stage 1 (early HIV infection)	1/0.5/365	day^{-1}
γ_2	Stage progression rate in stage 2 (CD4 $<$ 500 cells/mm3)	1/3.32/365	day^{-1}
γ_3	Stage progression rate in stage 3 (350 $<$ CD4 $\leq$ 500 cells/mm3)	1/2.7/365	day^{-1}
γ_4	Stage progression rate in stage 4 (200 $<$ CD4 $\leq$ 350 cells/mm3)	1/5.5/365	day^{-1}
γ_5	Stage progression rate in stage 5 (CD4 $\leq$ 200 cells/mm3)	1/5.06/365	day^{-1}
π_1	Fraction of individuals transitioning from stage 1 to stage 2	0.76	
π_2	Fraction of individuals transitioning from stage 1 to stage 3	0.19	
π_3	Fraction of individuals transitioning from stage 1 to stage 4	0.05	
π_4	Fraction of individuals transitioning from stage 1 to stage 5	0	
a	Age assortativity factor	0.5	
p	Proportion of individuals in low-risk group	0.8	
m	Per lineage rate of migration to source compartment	1/50/365	day^{-1}
g	Rate of growth of source compartment	1/3/0365	day^{-1}
s	Initial size of source compartment	1000	
i	Incidence scaling factor for London MSM	0.03	
d	Diagnosis rate prior to 1985	1/10	$year^{-1}$
μ_d	Maximum value of diagnosis rate post 1985 (logistic function)	1/3	$year^{-1}$
k_d	Steepness of diagnosis rate post 1985 (logistic function)	1/7	
μ_t	Maximum value of treatment rate post 1995 (logistic function)	1	$year^{-1}$
k_t	Steepness of treatment rate post 1995 (logistic function)	1/2	
e	Treatment effectiveness	0.95	
w_{s1}	Transmission weight for individuals in stage 1	1	
w_{s2}, w_{s3}, w_{s4}	Transmission weights for individuals in stages 2 to 4	0.1	
w_{s5}	Transmission weight for individuals in stage 5	0.3	
$w_{a1}, w_{a2}, w_{a3}, w_{a4}$	Transmission weights for individuals in age groups 1 to 4	1	
w_{c1}	Transmission weight for individuals undiagnosed	1	
w_{c2}	Transmission weight for individuals diagnosed and untreated	0.5	
w_{c3}	Transmission weight for individuals diagnosed and treated	0.05	
w_{r1}	Transmission weight for individuals in low risk category	1	
w_{r2}	Transmission weight for individuals in high risk category	10	

Note: incidence and diagnosis rate scaling factors are a priori. Now, there are fitted doi:10.1371/journal.pone.0055312.g002 (Fig 2.A)