Run simulated epidemic history

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

Load packages

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

Source C functions

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

Define 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
	Age progression rate [a]	
α_1	Group 1 [18-27)	$1/9/365\ day^{-1}$
α_2	Group 2 [27-33)	$1/6/365\ day^{-1}$
α_3	Group 3 [33-40)	$1/7/365\ day^{-1}$
α_4	Group 4 [40-80.5)	$1/40.5/365\ day^{-1}$
	Stage progression rate[b]	
γ_1	Stage 1 (early HIV infection)	$1/0.5/365\ day^{-1}$
γ_2	Stage 2 (CD4 $<$ 500 cells/mm3)	$1/3.32/365\ day^{-1}$
γ_3	Stage 3 (350 $<$ CD4 $\leq$ 500 cells/mm3)	$1/2.7/365\ day^{-1}$
γ_4	Stage 4 (200 $<$ CD4 $\leq$ 350 cells/mm3)	$1/5.5/365\ day^{-1}$
γ_5	Stage 5 (CD4 $\leq$ 200 cells/mm3)	$1/5.06/365\ day^{-1}$
	Fraction of individuals transitioning from [b]	
π_1	Stage 1 to stage 2	0.76
π_2	Stage 1 to stage 3	0.19
π_3	Stage 1 to stage 4	0.05
π_4	Stage 1 to stage 5	0
a	Age assortativity factor [c]	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	$1/3/365\ day^{-1}$
s	Initial size of source compartment	1000
i	Incidence scaling factor for London MSM [d]	0.03
	Diagnosis rate	
d_{85}	Fixed rate prior to 1985	$1/10\ year^{-1}$
μ_d	Maximum value of logistic function after 1985 [d]	$1/3\ year^{-1}$
k_d	Steepness of logistic function after 1985 [d]	$1/7\ year^{-1}$
	Treatment rate	
t_{95}	Fixed rate prior to 1995	0
μ_t	Maximum value of logistic function after 1995	1
k_t	Steepness of logistic function after 1995	0.5
e	Treatment effectiveness	0.95
	Transmission weight conferred to individuals in	
w_{s1}	Stage 1	1
w_{s2} to w_{s4}	Stages 2 to 4	0.1
w_{s5}	Stage 5	0.3
w_{a1} to w_{a4}	Age groups 1 to 4	1
w_{c1}	Care status 1 (undiagnosed)	1
w_{c2}	Care status 2 (diagnosed and untreated)	0.5
w_{c3}	Care status 3 (diagnosed and treated)	0.05
w_{r1}	Risk status 1 (low risk)	1
w_{r2}	Risk status 2 (high risk)	10

[a] From quartiles of age of MSM diagnosed in London available in UKDRDB
[b] From Cori et al. AIDS 2015
[c] Arbitrary factor raised to the power of age class difference
[d] Initial value later fitted to retrieve observed number of diagnosed cases ...

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

every individuals start infection at EHI stage

prRecipMat: - prob that recipient get infection, conditionning on - prob of being risk level 1 (80%) vs risk level 2 (20%) - EHI stage (only those recipient get infection) - care status (only undiagnosed get infection) - age assortativity (power of age class difference) - intervenes in F matrix [F(i,j) = incidence * w * prRecipMat(i,j), with w = beta_NH * beta_age * beta_care * beta_risk]

prStageRecipMat: - Prob for EHI recipient to jump to next other CD4 stage