1 More on simulating landscapes

The philosophy of rmetasim is to provide flexible and powerful ways to simulate realistic demography underlying population genetics. Usually when a software author uses the words "flexible" and "powerful", it usually means "hard to use". rmetasim has proven to be a bit impenetrable to users starting off so, empirically, this software fits into that category. This vignette is an attempt to explain some of the approaches to simulation that rmetasim can help implement, and lower the activation energy associated with its use.

1.1 Alternatives to landscape.simulate()

The main simulation function, `landscape.simulate()` is the typical approach to simulations in rmetasim. Each simulation step (year) is composed of several substeps:

1. choose populations for extirpation and if any, kill them off
2. reproduce
3. impose survival and growth to new stages
4. reduce populations to the carrying capacity
5. advance the year counter and return to step 1. This is repeated 'numit' times.

These steps are implemented n C++ for speed. It is possible, however, to run each of these steps separately. This can help in debugging a landscape or implementing a simulation where survival precedes reproduction, or changing the time in which extinction occurs or just for fun.

Here is a simulation using landscape.simulate()

```
library(rmetasim)
rland <- landscape.new.example()
rland <- landscape.simulate(rland,10)
landscape.amova(rland)

##        Phi        Phi        Phi
## 0.04082899 0.07007084 0.03248193
```

Here is the same simulation with the individual steps implemented in R functions

```
rland <- landscape.new.example()
for (gen in 1:10)
    {
        rland <- landscape.extinct(rland)
        rland <- landscape.reproduce(rland)
        rland <- landscape.survive(rland)
        rland <- landscape.carry(rland)
        rland <- landscape.advance(rland)
    }
landscape.amova(rland)

##        Phi        Phi        Phi
## 0.05532262 0.04533110 0.03620814
```

```
library(magrittr)
rland <- landscape.new.example()
for (gen in 1:10)
    {
        rland <- rland %>% landscape.extinct() %>%  landscape.reproduce() %>%
            landscape.survive() %>% landscape.carry()%>%landscape.advance()
    }
landscape.amova(rland)

##        Phi        Phi        Phi
## 0.02600957 0.16855691 0.05903673
```

or with `magrittr` These approaches are a little slower because there is conversion between the R version of a landscape (a list) and the internal C++ backend representation more often.

1.2 Examining temporal dynamics

You can see in the previous section how the same landscape can be the input and output of a simulation. You can use this with loops to examine the temporal dynamics of a simulation through time.

The following runs a simulation for 400 years and checks the among-population differentiation every 20 years. Finally it plots the results. This landscape has no migration among the two populations, so the among-pop differentiation should be an increasing function.

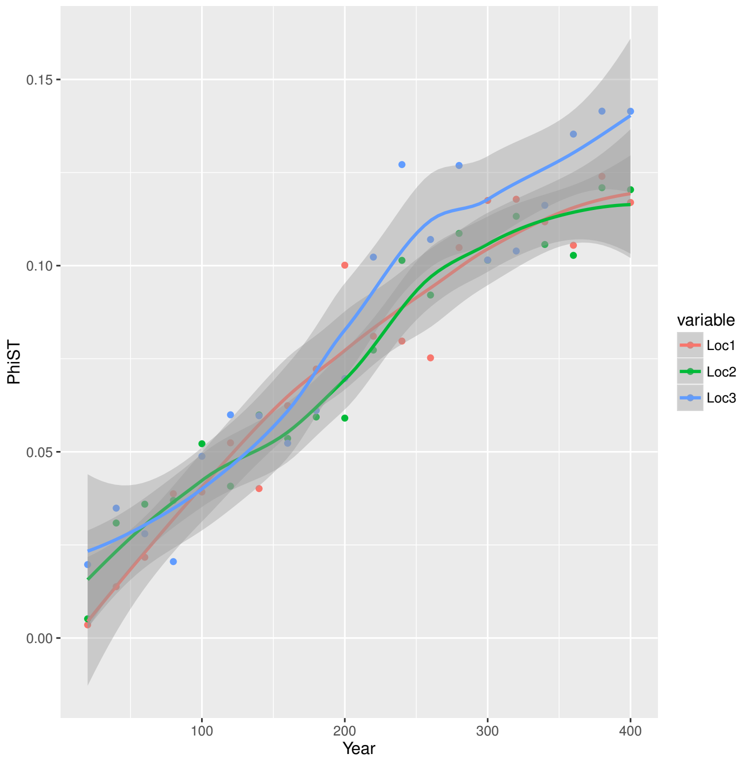
```
### CREATE A LANDSCAPE
###first set up the matrices for local demographies
S <- matrix(c(0, 0, 1, 0), byrow = TRUE, nrow = 2)
R <- matrix(c(0, 1.1, 0, 0), byrow = TRUE, nrow = 2)
M <- matrix(c(0, 0, 0, 1), byrow = TRUE, nrow = 2)
```

```r
#and epochs
S.epoch <- matrix(rep(0, 36), nrow = 6)
R.epoch <- matrix(rep(0, 36), nrow = 6)
M.epoch <- matrix(rep(0, 36), nrow = 6)



##now create the landscape
rland <- landscape.new.empty() %>%
    landscape.new.intparam(h=3,s=2) %>%
    landscape.new.switchparam(mp=0) %>%
    landscape.new.floatparam() %>%
    landscape.new.local.demo( S, R, M) %>%
    landscape.new.epoch(S = S.epoch, R = R.epoch, M = M.epoch,
                        carry = c(1000, 1000, 1000)) %>%
    landscape.new.locus(type = 1, ploidy = 2,
                        mutationrate = 0.001, transmission = 0, numalleles = 5) %>%
    landscape.new.locus(type = 0, ploidy = 1,
                        mutationrate = 0.005, numalleles = 3, frequencies = c(0.2,
                                                                          0.2, 0.6)) %>%
    landscape.new.locus(type = 2, ploidy = 1,
                        mutationrate = 0.007, transmission = 1, numalleles = 3,
                        allelesize = 75) %>%
    landscape.new.individuals(rep(c(500,500),3))


retval <- matrix(0,ncol=4,nrow=20) #store the results col1 = gen, cols2-3 PhiST
retval[1,] <- c(0,landscape.amova(rland)) #before any evolution occurs. Both population
for (i in 1:20)
    {
        rland <- landscape.simulate(rland,20)
        retval[i,] <- c(rland$intparam$currentgen,landscape.amova(rland))
    }
###the rest is just plotting the matrix of PhiSTs
###you can use any kind of graphics, of course.  using ggplot2 here.
colnames(retval) <- c("gen","Loc1","Loc2","Loc3")
library(ggplot2)
library(reshape2)
pl <- ggplot(melt(as.data.frame(retval),measure.vars=c("Loc1","Loc2","Loc3")),
             aes(x=gen,y=value,group=variable,color=variable))
pl <- pl + labs(y="PhiST",x="Year")
pl <- pl + geom_point() + geom_smooth()
pl
```



1.3 Different ways to allow demography to change during the course of the simulation

1.3.1 Random changes in local demographies (playing with local demographies)

1.3.2 Deterministic changes through time (using epochs)

1.3.3 Deterministic changes through time (directly modifying the landscape)