

rtsetse example1 savannah grass boundary

Andy South

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This document shows results of a [rtsetse](#) simulation on a simple 50 x 50 grid, half savannah and half grassland with parameters set for *G. morsitans*. This was set up to compare results with an equivalent run in Hat-trick done by Steve.

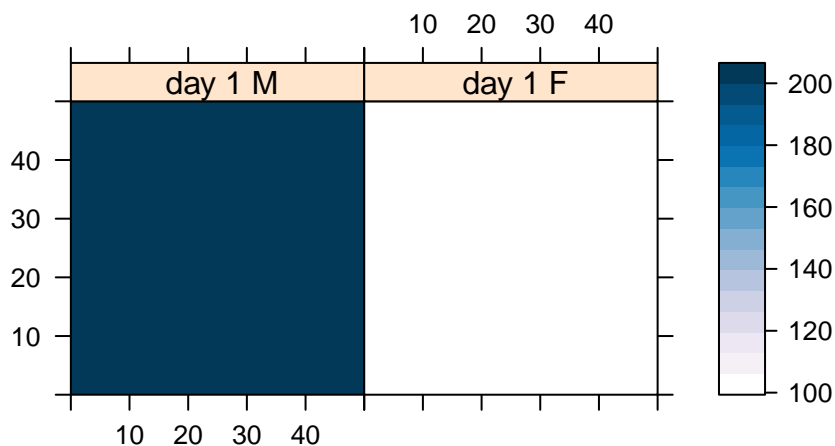


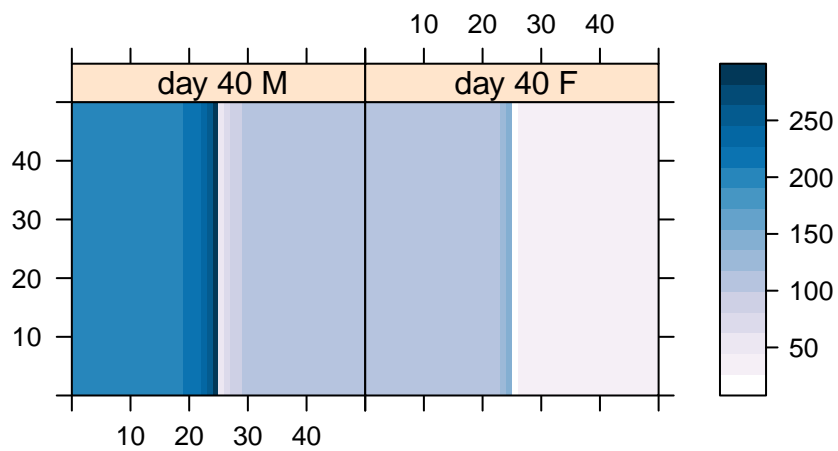
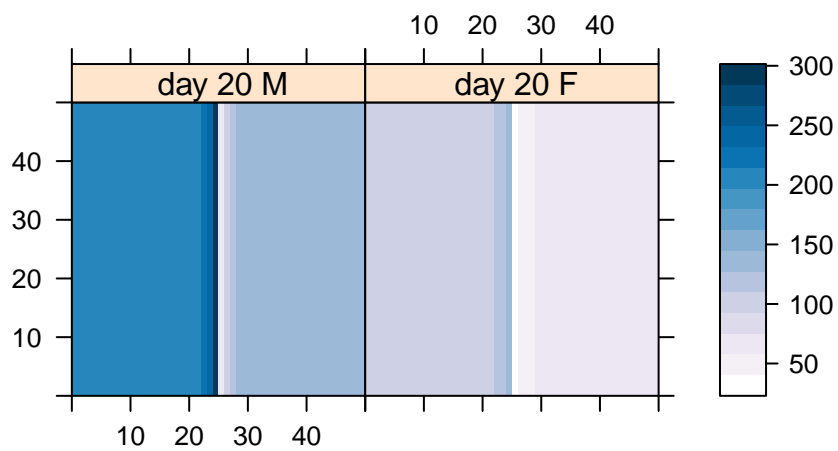
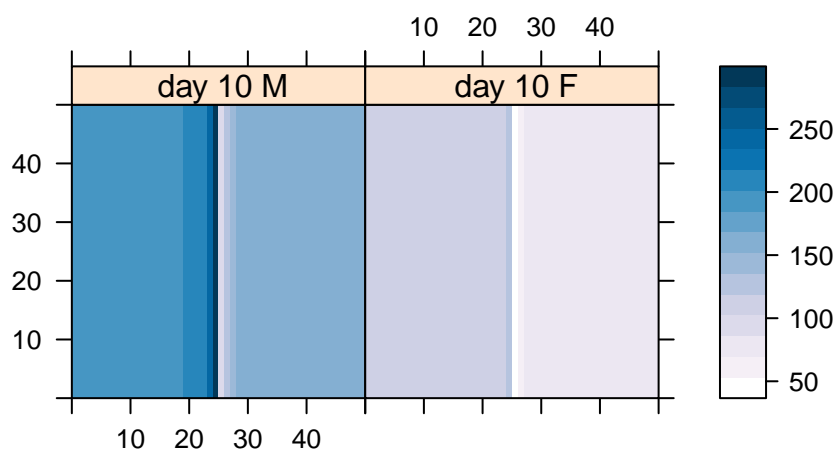
The following maps show the distribution of males and females over the progress of the simulation as it approaches equilibrium. Later ones show the same for flies older than 20.

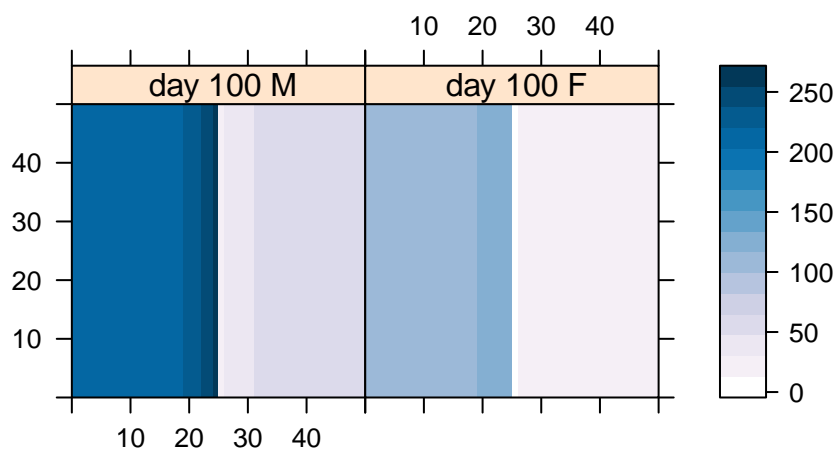
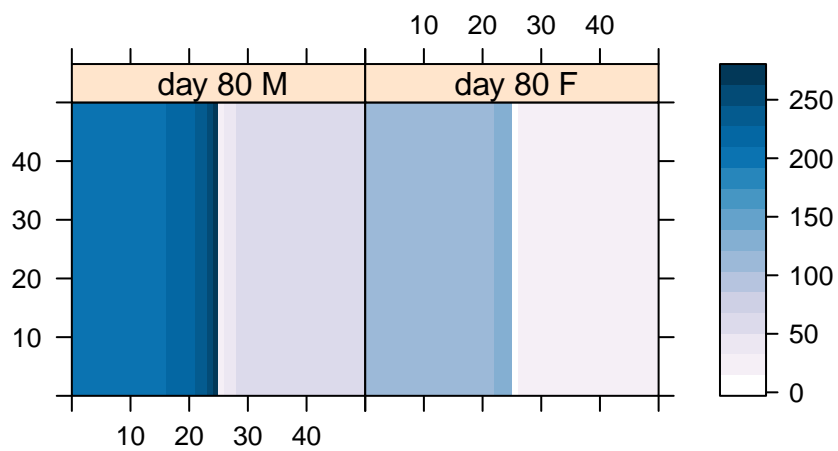
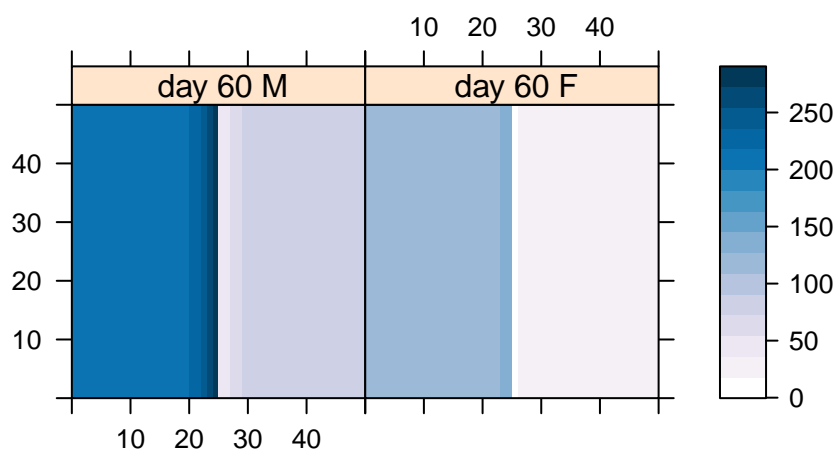
Over time differential mortality causes the densities to decline in the poorer habitat on the east half. Densities change in the boundary between the two habitats due to the interaction between mortalities and dispersal.

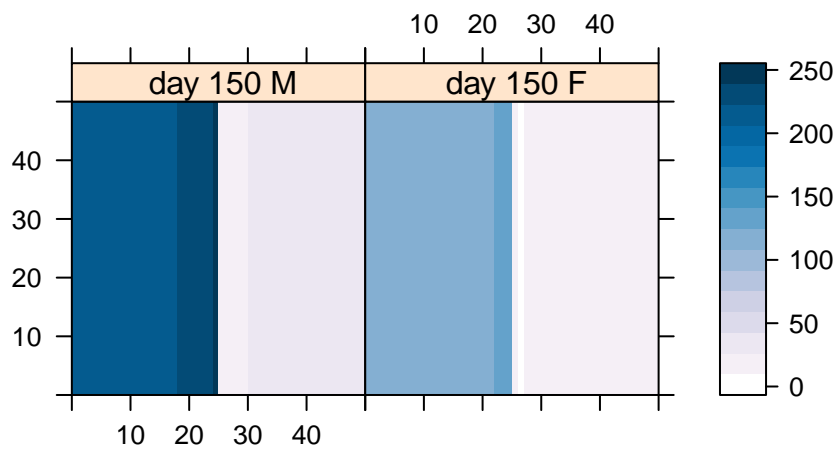
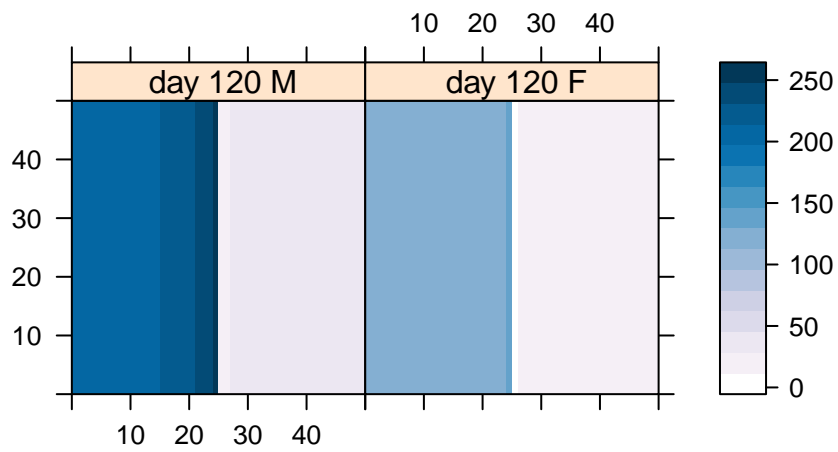
By the 150 days shown here the population hasn't quite reached equilibrium but the pattern changes little after this.

Is this pattern sufficiently similar to what happens in Hat-trick ?

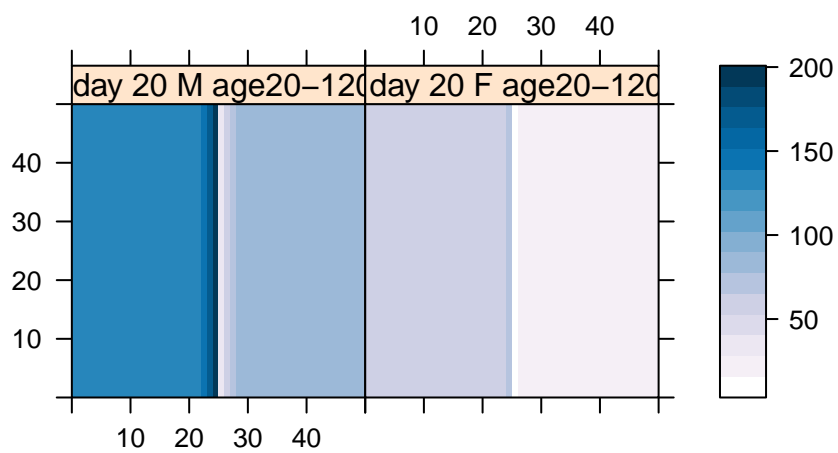
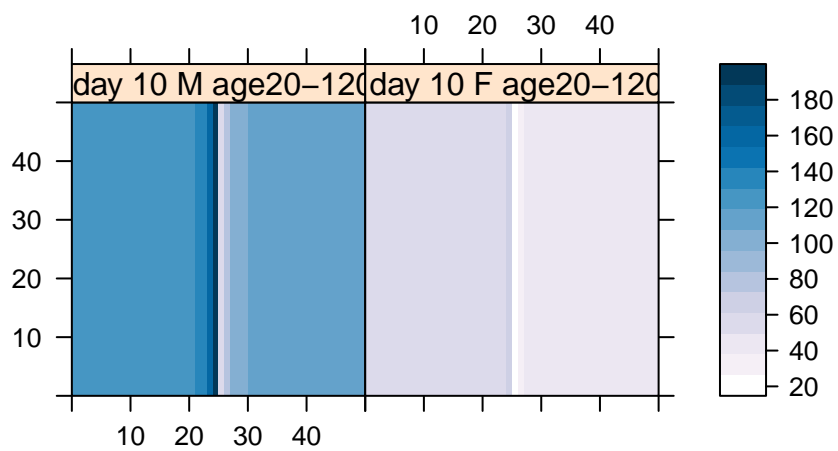
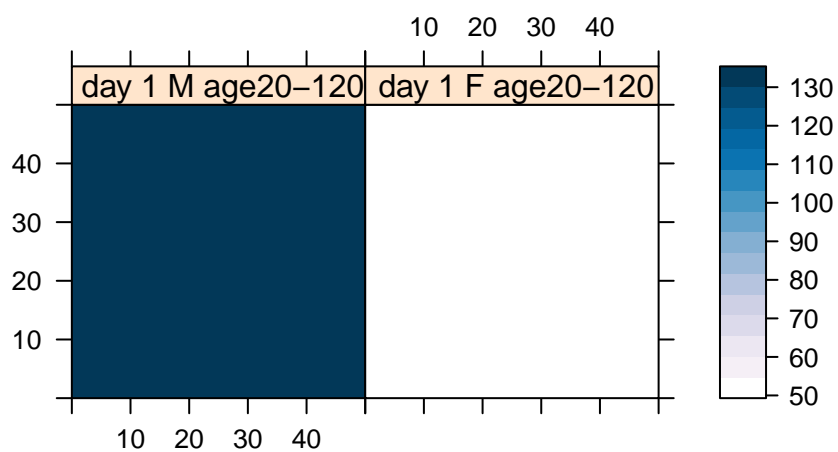


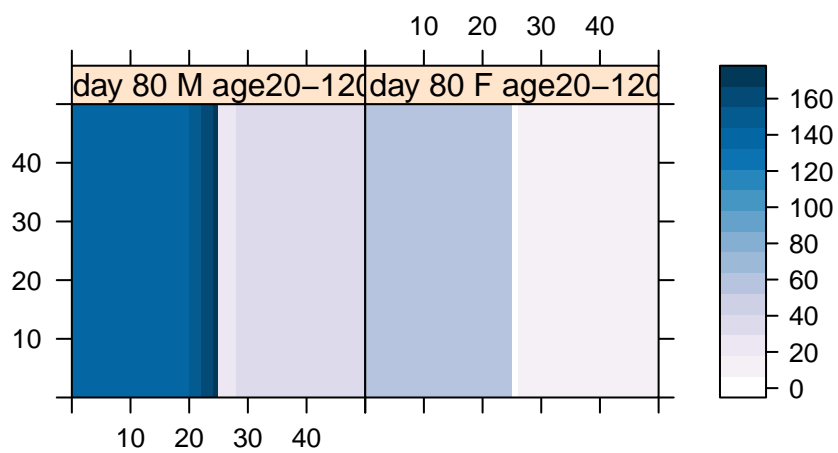
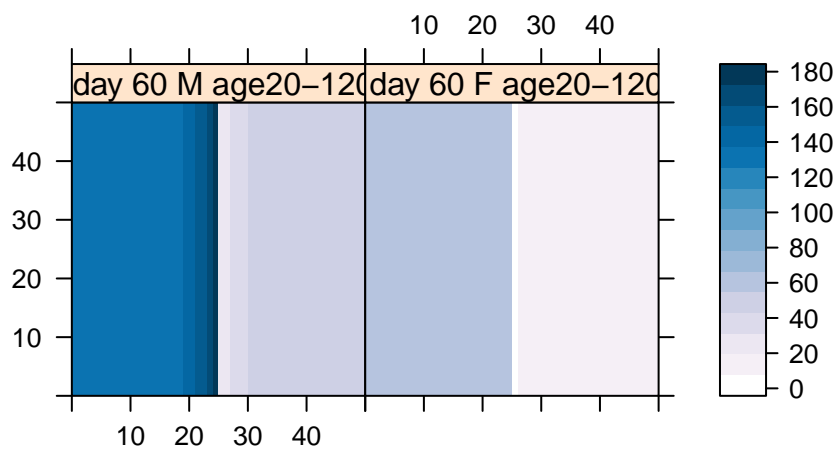
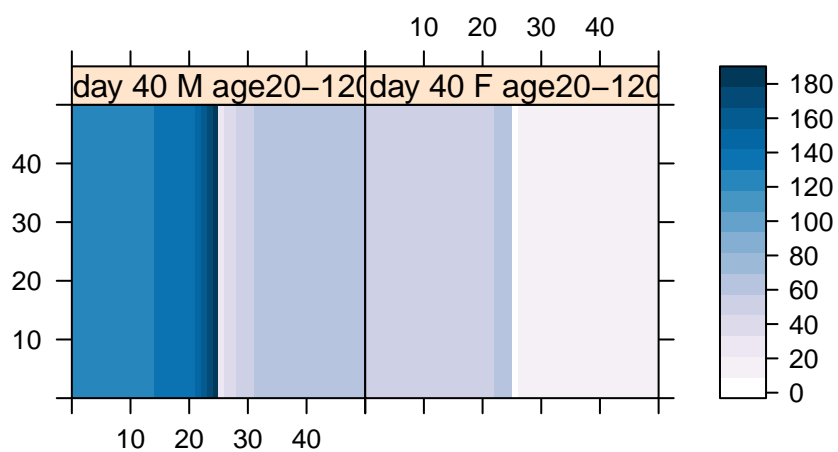


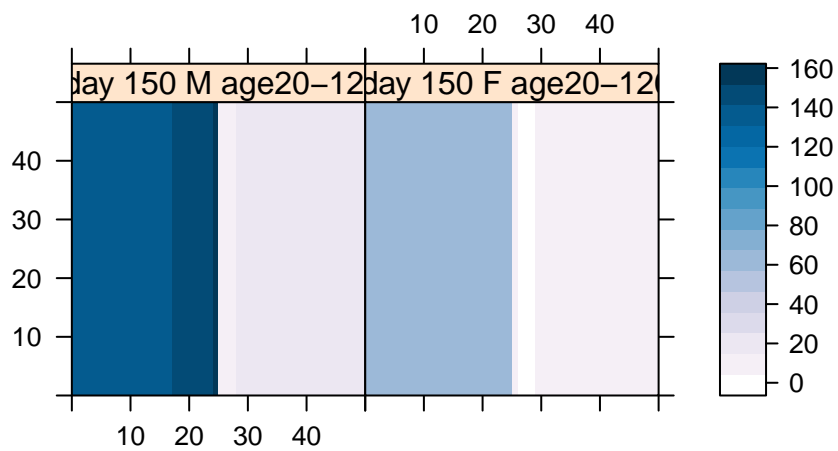
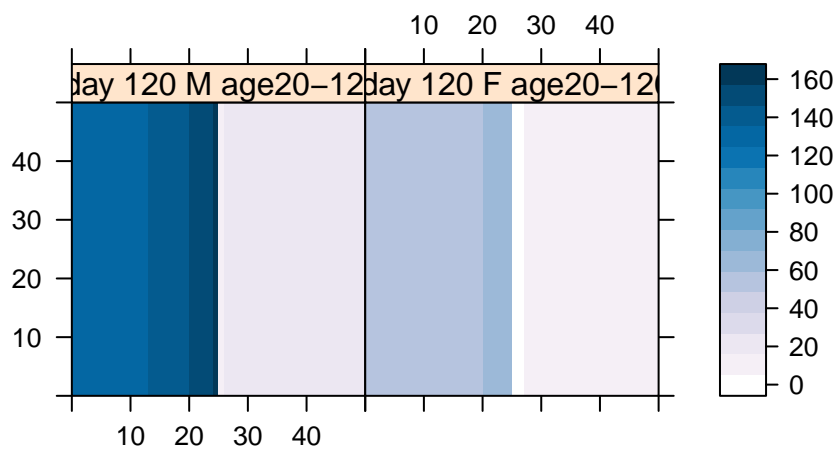
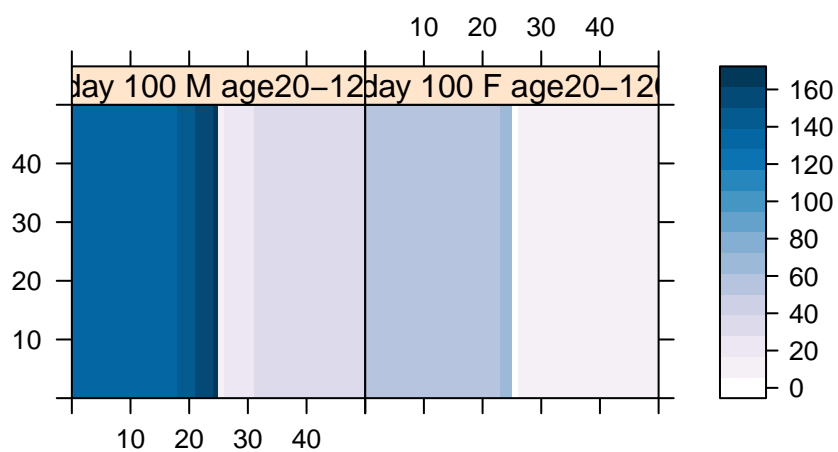




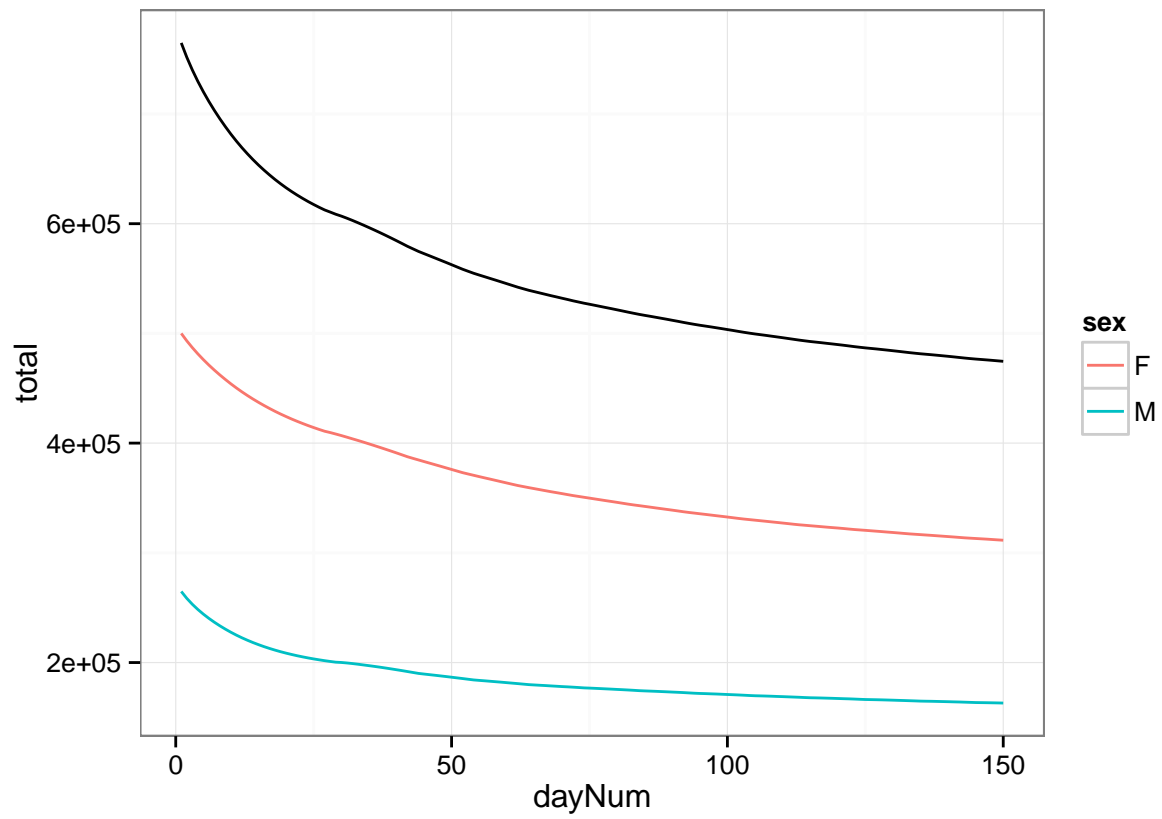
The plots below are for the same time periods as above, but just show the older flies.



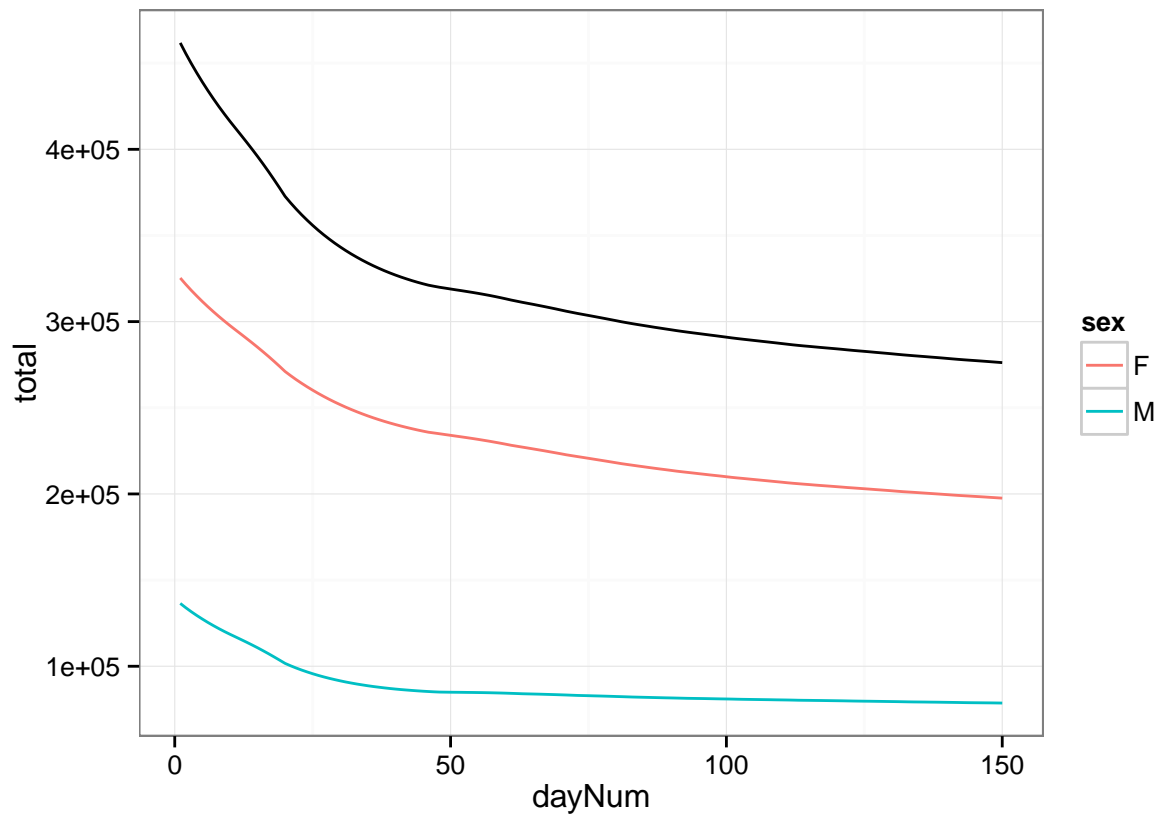




Adult population over time summed for the whole grid.



Adults over 20 days summed for the whole grid.



appendix : code used to run this simulation, showing param values used.

```
iDays <- 150
aRecord <- rt_runGrid ( pMoveF=0.6, pMoveM=0.3, iDays=iDays, pMortF=0.082, pMortM=0.139,
pMortPupa=0.2, fStartPopPropCC=1, iCarryCapF=200, propMortAdultDD=0.25, iFirstLarva=16,
iInterLarva=10, pMortLarva=0.05, propMortLarvaDD=0.25, propMortPupaDD=0.25, mVegCats =sys-
tem.file("extdata","vegHalfSavannahHalfGrass50x50.txt", package="rtsetse"), dfMortByVeg=list(code =
c("D", "T", "O", "S", "B", "G", "N"), name = c("Dense Forest", "Thicket", "Open Forest", "Savannah",
"Bush", "Grass", "No-go area"), mortality = c(200, 150, 110, 100, 110, 210, 999), pupmortality = c(120, 110,
105, 100, 120, 170, 999)) )
```