

Week1_lab

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```
library(devtools)
devtools::install_github("BruceKendall/PVA")

## Skipping install of 'PVA' from a github remote, the SHA1 (fa5d2aed) has not changed since last install
## Use `force = TRUE` to force installation

devtools::install_github("BruceKendall/mpmtools")

## Skipping install of 'mpmtools' from a github remote, the SHA1 (ff1984db) has not changed since last install
## Use `force = TRUE` to force installation
```

1. Enter Matrix model

creating matrix

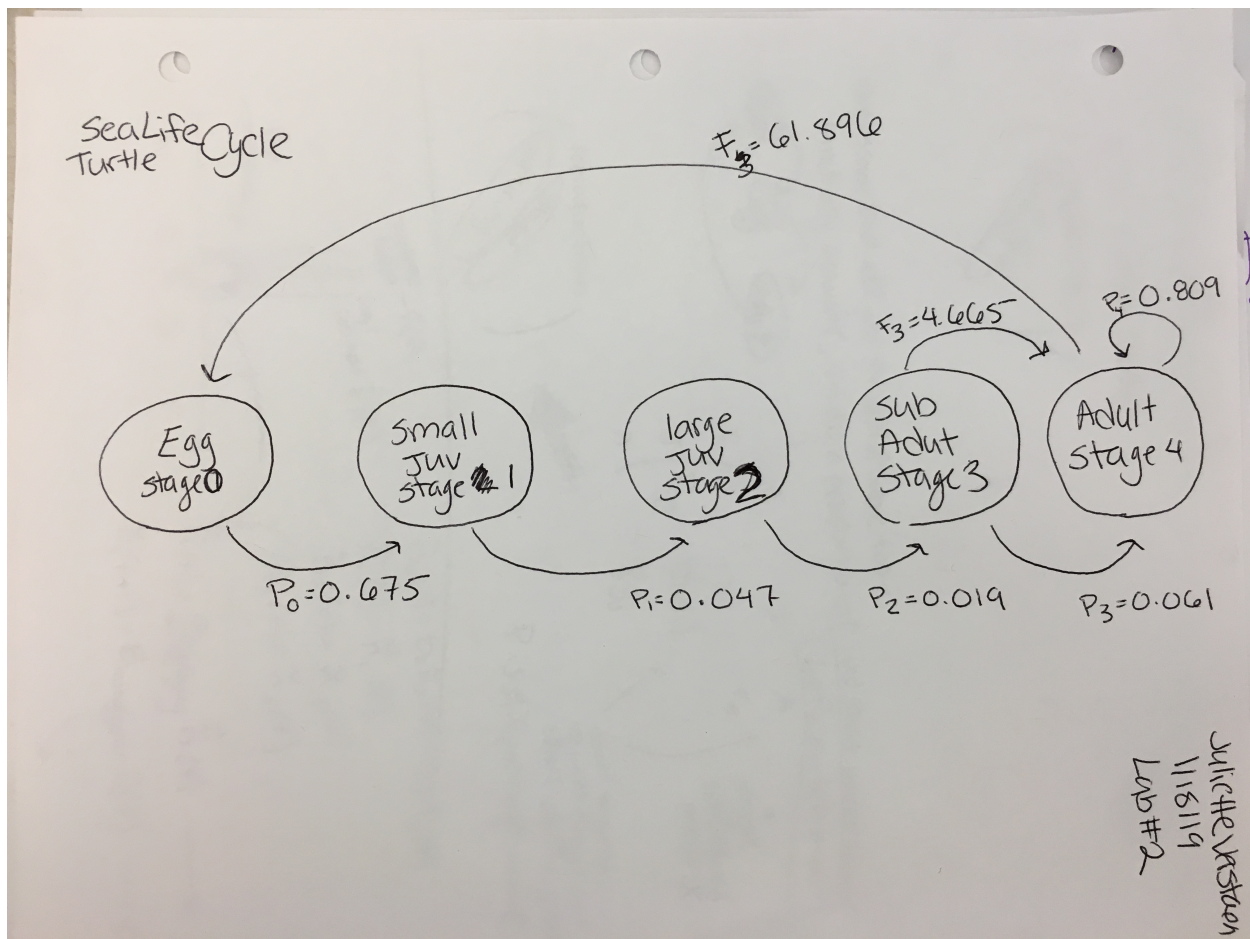
```
A <- matrix(c(0,      0,      0,      4.665, 61.896,
              0.675, 0.703, 0,      0,      0,
              0,      0.047, 0.657, 0,      0,
              0,      0,      0.019, 0.682, 0,
              0,      0,      0,      0.061, 0.809),
            nrow = 5, ncol = 5, byrow = TRUE)
```

giving matrix row and/or column names below is naming by column, if wanted to name by row would have to use byrow=FALSE

```
class_names <- c("Egg", "Sm Juv", "Lg Juv", "Subadult", "Adult")
A <- matrix(c(0,      0,      0,      4.665, 61.896,
              0.675, 0.703, 0,      0,      0,
              0,      0.047, 0.657, 0,      0,
              0,      0,      0.019, 0.682, 0,
              0,      0,      0,      0.061, 0.809),
            nrow = 5, ncol = 5, byrow = TRUE, dimnames = list(class_names, class_names))
```

Life Cycle

```
library(knitr)
include_graphics("life_cycle.png")
```



1.1 Matrix Conventions

- RC Cola: indexed first by *Row* and then by *Column*
- A capital bold letters are matrices and n lower case are vectors
- use brackets to return the elements you want to look at. example = $A[4,3]$ element in 4th row and 3rd column

A

```
##           Egg Sm Juv Lg Juv Subadult  Adult
## Egg      0.000 0.000 0.000      4.665 61.896
## Sm Juv   0.675 0.703 0.000      0.000 0.000
## Lg Juv   0.000 0.047 0.657      0.000 0.000
## Subadult 0.000 0.000 0.019      0.682 0.000
## Adult    0.000 0.000 0.000      0.061 0.809
```

$A[4,3]$

```
## [1] 0.019
```

$A[,3]$

```
##      Egg  Sm Juv  Lg Juv Subadult  Adult
##      0.000  0.000  0.657    0.019  0.000
```

```
A[4,]

##      Egg   Sm Juv   Lg Juv Subadult   Adult
##    0.000   0.000   0.019   0.682   0.000

A[, c(3,5)]

##      Lg Juv   Adult
## Egg      0.000 61.896
## Sm Juv    0.000  0.000
## Lg Juv    0.657  0.000
## Subadult  0.019  0.000
## Adult     0.000  0.809

A[3:4, 3]

##   Lg Juv Subadult
##   0.657    0.019
```

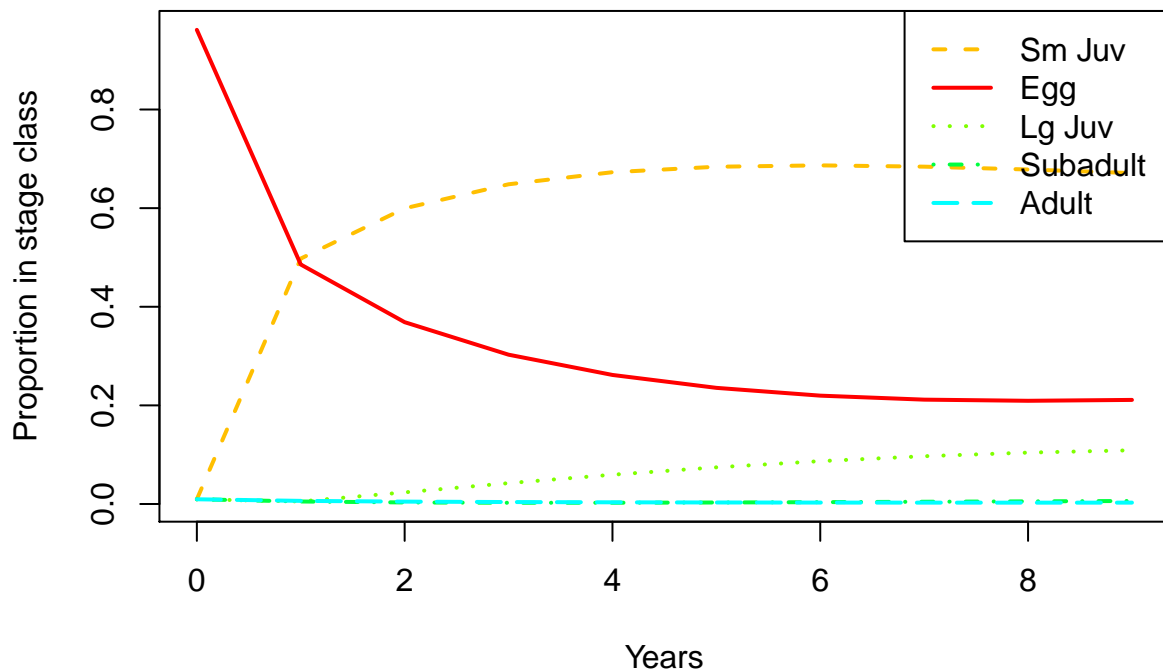
2. Projecting the population matrix

```
library(popbio)

# Initial abundance
n_0 <- c(1000, 10, 10, 10, 10)

# Project the matrix
pop <- pop.projection(A, n_0, iterations = 10)

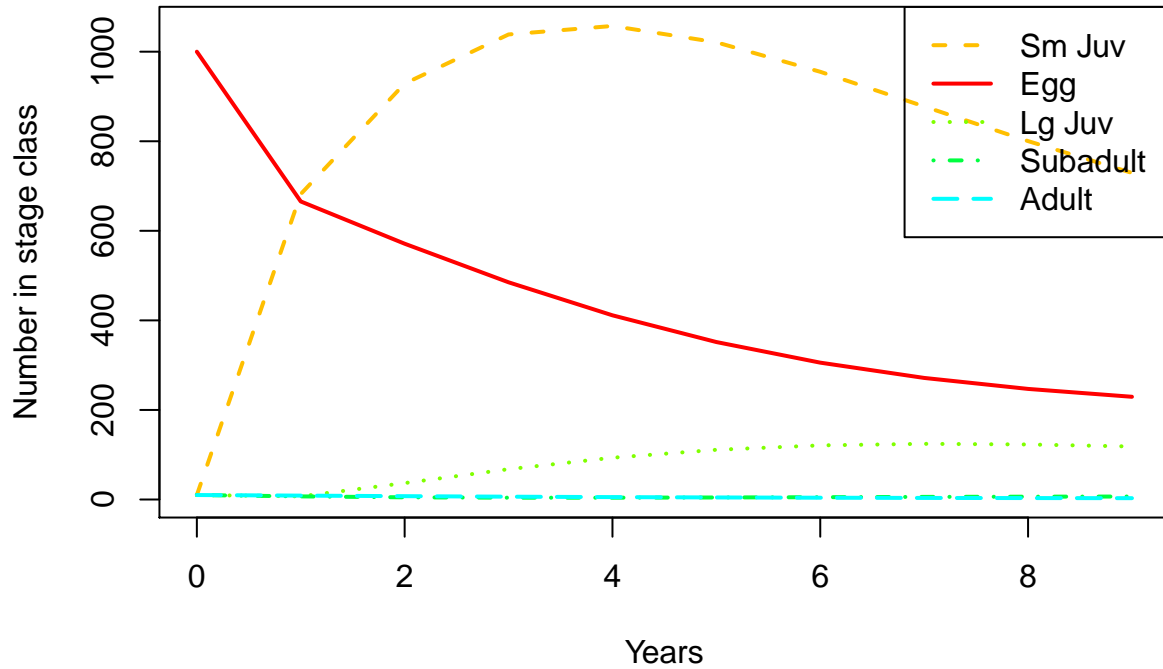
# Plot each stage through time
stage.vector.plot(pop$stage.vector)
```



```
#these are proportions in each stage through time
```

Actual abundances through time

```
stage.vector.plot(pop$stage.vector, proportions = FALSE)
```



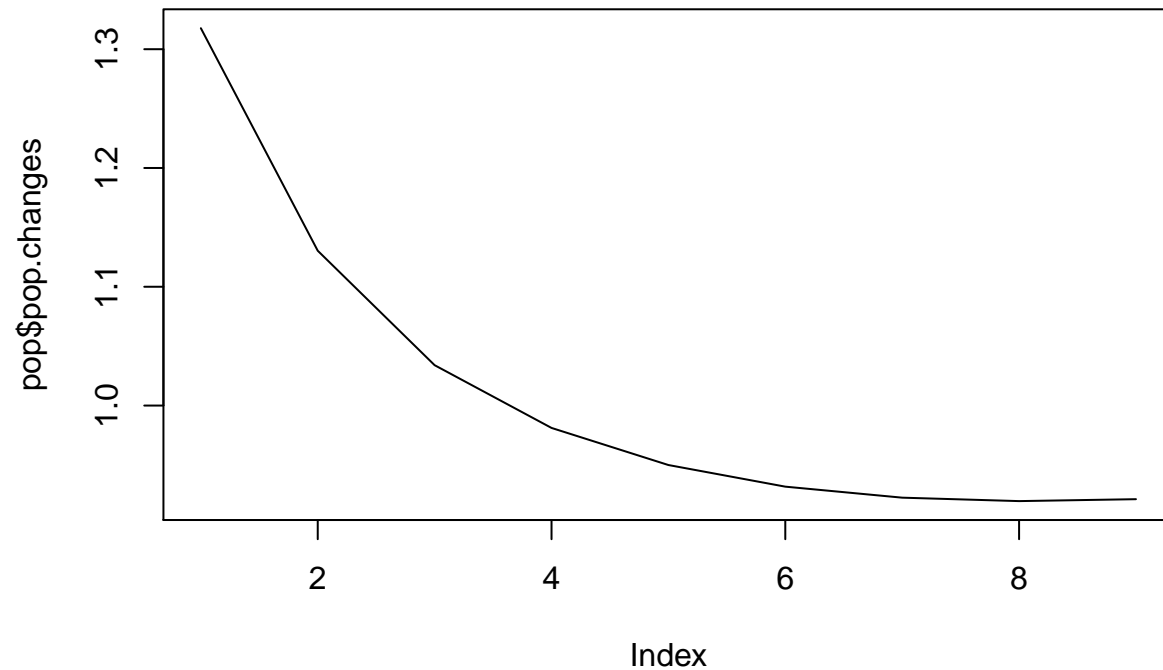
This

graph shows the number of turtles in each stage class over 10 years.

```
plot(pop$pop.sizes, type = "l")
```



```
plot(pop$pop.changes, type = "l")
```

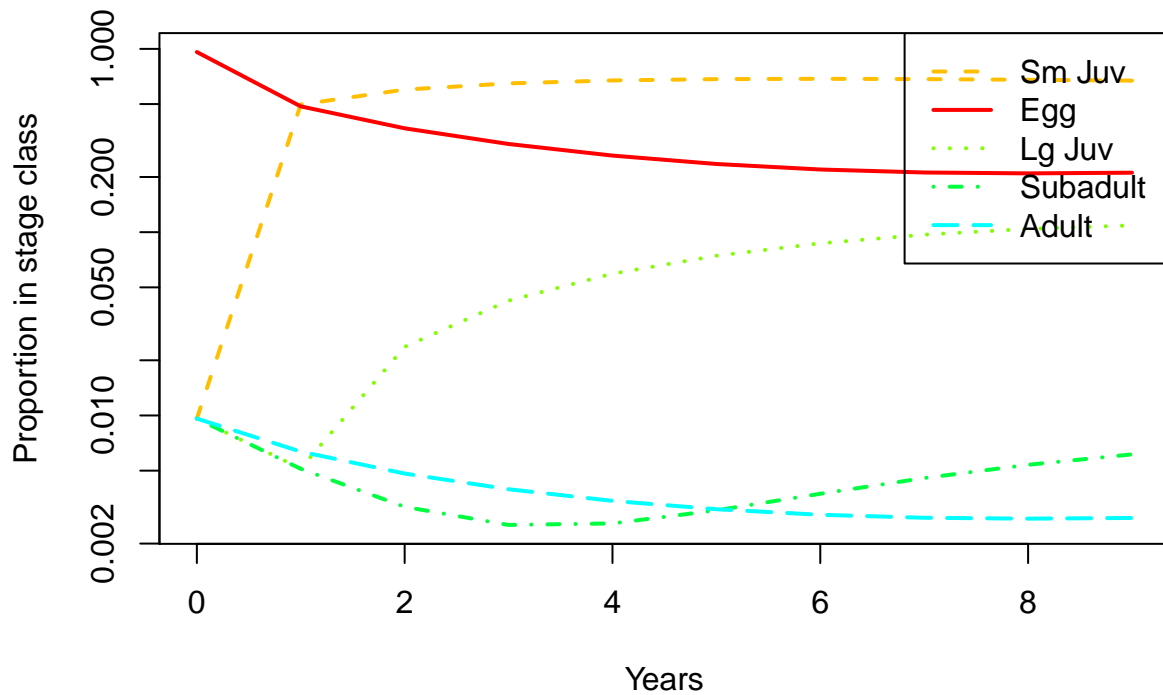


The population size is going down, which we could tell from the previous graphs that are separated out by stage classes. The changes in population is going down also which corresponds to the decrease in population size.

plot proportions in log to see if reaching stable

- they are not fully straight yet at 10 years so not stable
- when project out to 50 years you can tell that year 10 is when they start to be stable

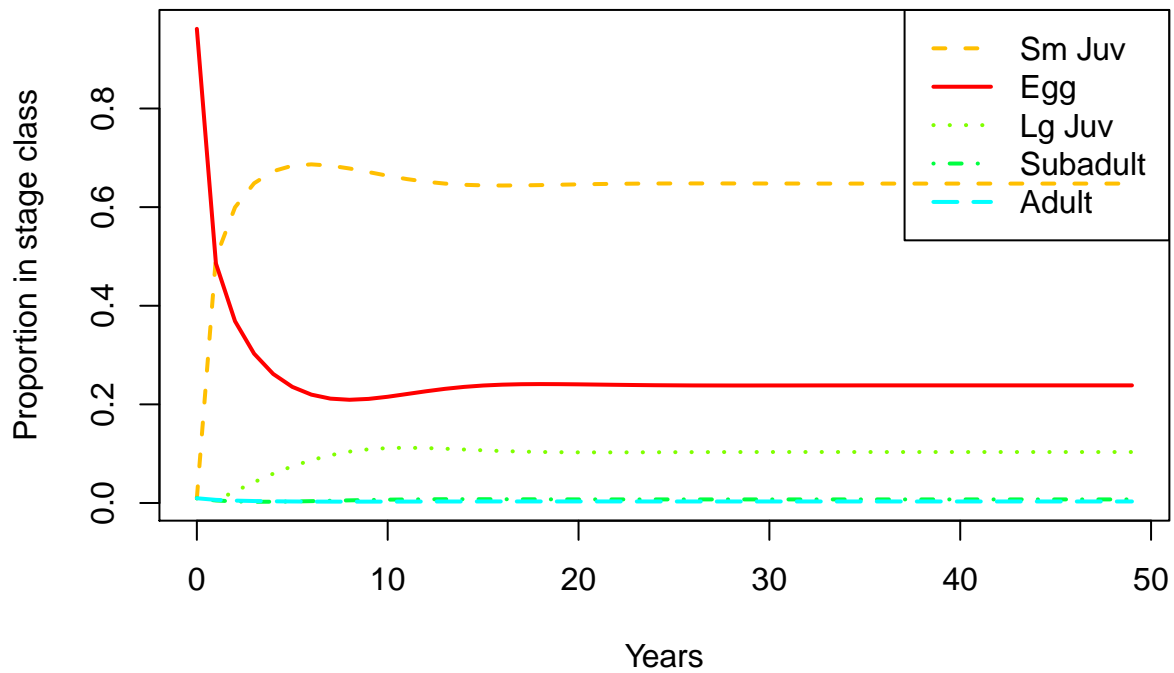
```
stage.vector.plot(pop$stage.vector, log = "y")
```



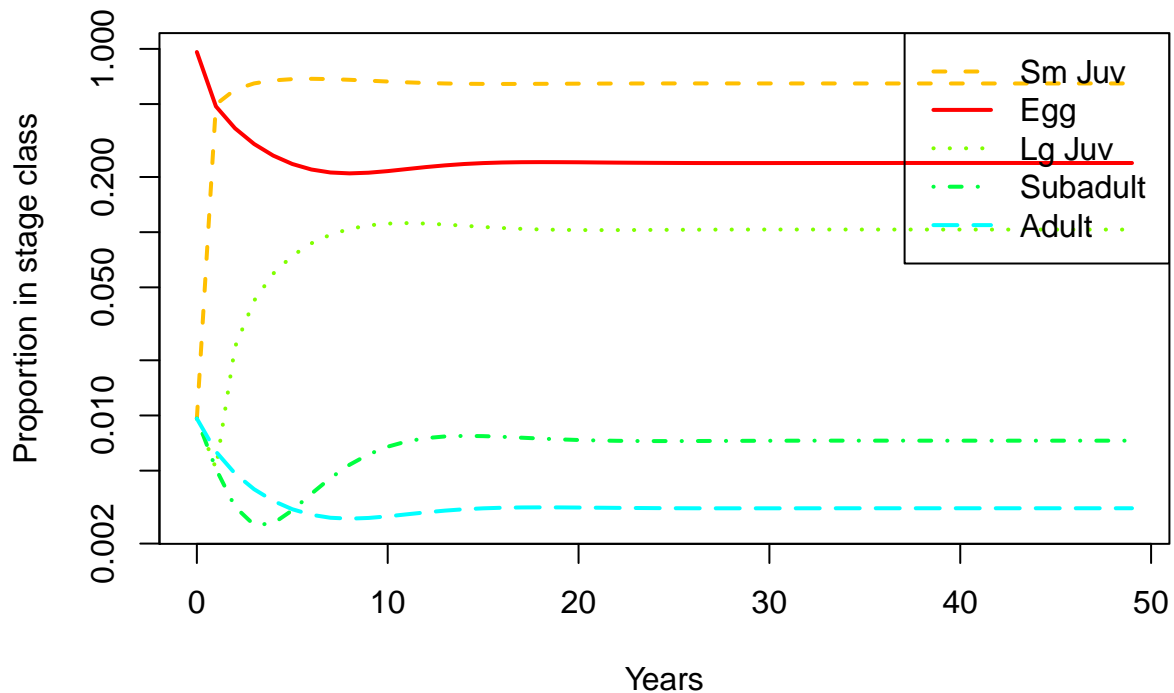
```
pop_50 <- pop.projection(A, n_0, iterations = 50)
```

```
# Plot each stage through time
```

```
stage.vector.plot(pop_50$stage.vector)
```



```
stage.vector.plot(pop_50$stage.vector, log = "y")
```



- Plot-

ting out to 50 years we can see that the populations become more stable at each time stage

-It seems that 10 years out is when the populaiton begins to stable

- The log version of out graph confirms that sometime after 10 years the population is reaching a stable state because they are straight

3. Analyzing the population matrix

SSD (stable stage distribution)

```
lambda(A)
```

```
## [1] 0.9515489
```

```
stable.stage(A)
```

```
##      Egg      Sm Juv      Lg Juv      Subadult      Adult
## 0.238508404 0.647732505 0.103356123 0.007285382 0.003117586
```

```
pop_50
```

```
## $lambda
```

```
## [1] 0.9515473
```

```
##
```

```
## $stable.stage
```

```
##      Egg      Sm Juv      Lg Juv      Subadult      Adult
## 0.238507035 0.647734069 0.103356048 0.007285280 0.003117568
```

```
##
```

```
## $stage.vectors
```

```
##      0      1      2      3      4      5
## Egg    1000 665.61 571.19685 485.036481 411.289802 351.626280
## Sm Juv   10 682.03 928.75384 1038.471823 1057.445316 1021.004674
## Lg Juv   10  7.04 36.68069  67.750644  93.320349 111.011399
```

## Subadult	10	7.01	4.91458	4.048677	4.048460	4.534136
## Adult	10	8.70	7.46591	6.339711	5.375795	4.595974
##	6	7	8	9	10	11
## Egg	305.624171	271.522516	246.937023	229.398165	216.689085	207.013033
## Sm Juv	955.114025	877.741474	800.329955	729.314449	667.551819	615.554061
## Lg Juv	120.921709	124.335922	122.942550	118.388763	112.059197	104.997828
## Subadult	5.201497	5.844934	6.348627	6.665672	6.795375	6.763570
## Adult	3.994726	3.549024	3.227702	2.998477	2.832374	2.705908
##	12	13	14	15	16	17
## Egg	199.036955	191.857183	184.924804	177.957788	170.857081	163.635883
## Sm Juv	572.468302	536.795161	506.870597	481.154272	458.372960	437.564721
## Lg Juv	97.914614	91.235911	85.171366	79.780506	75.030043	70.838267
## Subadult	6.607714	6.366838	6.075666	5.761860	5.445418	5.139346
## Adult	2.601658	2.507812	2.417197	2.326128	2.233311	2.138919
##	18	19	20	21	22	23
## Egg	156.365578	149.138074	142.042252	135.151381	128.518302	122.175557
## Sm Juv	418.062220	399.444506	381.477688	364.057335	347.159488	330.802974
## Lg Juv	67.106284	63.737753	60.649595	57.776235	55.069681	52.497277
## Subadult	4.850961	4.583375	4.336879	4.110094	3.900832	3.706692
## Adult	2.043886	1.949412	1.856660	1.766588	1.679885	1.596978
##	24	25	26	27	28	29
## Egg	116.138261	110.408094	104.977401	99.832788	94.957964	90.335776
## Sm Juv	315.022992	299.854489	285.323169	271.441933	258.210811	245.618826
## Lg Juv	50.038451	47.681343	45.419803	43.251000	41.173678	39.187014
## Subadult	3.525412	3.355062	3.194097	3.041351	2.895970	2.757352
## Adult	1.518063	1.443163	1.372178	1.304932	1.241212	1.180795
##	30	31	32	33	34	
## Egg	85.949527	81.783712	77.824334	74.0589335	70.4764600	
## Sm Juv	233.646683	222.269549	211.459499	201.1874534	191.4245598	
## Lg Juv	37.289953	35.480893	33.757616	32.1173500	30.5569093	
## Subadult	2.625067	2.498805	2.378322	2.2634102	2.1538754	
## Adult	1.123462	1.069009	1.017256	0.9680375	0.9212104	
##	35	36	37	38	39	
## Egg	67.0670671	63.8218873	60.7328261	57.7923908	54.9935583	
## Sm Juv	182.1430760	173.3168527	164.9215214	156.9344872	149.3348083	
## Lg Juv	29.0728437	27.6615829	26.3195520	25.0432572	23.8293409	
## Subadult	2.0495243	1.9501596	1.8555789	1.7655763	1.6799449	
## Adult	0.8766456	0.8342273	0.7938496	0.7554146	0.7188306	
##	40	41	42	43	44	
## Egg	52.3296821	49.7944288	47.3817401	45.0858102	42.9010741	
## Sm Juv	142.1030221	135.2209599	128.6715743	122.4387913	116.5073922	
## Lg Juv	22.6746129	21.5760627	20.5308583	19.5363379	18.5899972	
## Subadult	1.5984799	1.5209810	1.4472542	1.3771137	1.3103819	
## Adult	0.6840106	0.6508718	0.6193352	0.5893247	0.5607676	
##	45	46	47	48	49	
## Egg	40.8222019	38.8440948	36.9618823	35.1709173	33.4667716	
## Sm Juv	110.8629217	105.4916202	100.3803730	95.5166728	90.8885901	
## Lg Juv	17.6894756	16.8325428	16.0170868	15.2411035	14.5026886	
## Subadult	1.2468904	1.1864793	1.1289972	1.0743007	1.0222541	
## Adult	0.5335943	0.5077381	0.4831353	0.4597253	0.4374501	
##						
## \$pop.sizes						
## [1]	1040.0000	1370.3900	1549.0119	1601.6473	1571.4797	1492.7725
## [8]	1282.9939	1179.7859	1086.7655	1005.9278	937.0344	878.6292
						828.7629


```
## [15] 785.4596 746.9806 711.9388 679.3171 648.4289 618.8531 590.3631
## [22] 562.8616 536.3282 510.7795 486.2432 462.7422 440.2866 418.8720
## [29] 398.4796 379.0798 360.6347 343.1020 326.4370 310.5952 295.5330
## [36] 281.2092 267.5847 254.6233 242.2911 230.5565 219.3898 208.7633
## [43] 198.6508 189.0274 179.8696 171.1551 162.8625 154.9715 147.4627
## [50] 140.3178
##
## $pop.changes
## [1] 1.3176827 1.1303438 1.0339800 0.9811646 0.9499152 0.9317268 0.9224490
## [8] 0.9195569 0.9211549 0.9256163 0.9315125 0.9376702 0.9432453 0.9477495
## [15] 0.9510108 0.9530888 0.9541791 0.9545305 0.9543885 0.9539632 0.9534161
## [22] 0.9528597 0.9523637 0.9519630 0.9516682 0.9514730 0.9513620 0.9513160
## [29] 0.9513153 0.9513425 0.9513837 0.9514286 0.9514705 0.9515055 0.9515321
## [36] 0.9515505 0.9515616 0.9515669 0.9515680 0.9515664 0.9515634 0.9515598
## [43] 0.9515563 0.9515532 0.9515509 0.9515492 0.9515481 0.9515475 0.9515473
```

Comparing lambda and the population vector are different because:

1. lambda and stable.stage project out to as far as needed to reach stable asymptotic (goes out as many years as needs to)
2. when we call to pop_ something it is only looking at until the number of iterations/years that we ran it

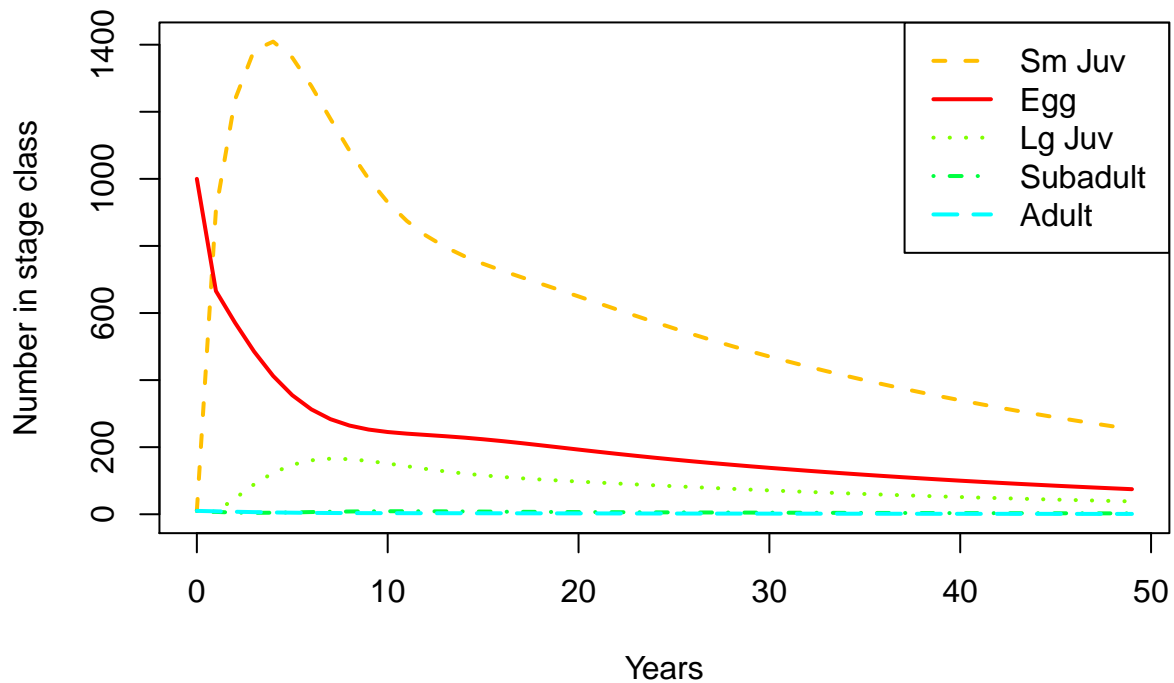
Informating management decisions for turtle conservation

```
#increase egg survival
class_names <- c("Egg", "Sm Juv", "Lg Juv", "Subadult", "Adult")
egg_increase <- matrix(c(0, 0, 0, 4.665, 61.896,
  0.9, 0.703, 0, 0, 0,
  0, 0.047, 0.657, 0, 0,
  0, 0, 0.019, 0.682, 0,
  0, 0, 0, 0.061, 0.809),
  nrow = 5, ncol = 5, byrow = TRUE, dimnames = list(class_names, class_names))

# Initial abundance
n_0_egg <-c(1000, 10, 10, 10, 10)

# Project the matrix
pop_egg <- pop.projection(egg_increase, n_0_egg, iterations = 50)

# Plot each stage through time
stage.vector.plot(pop_egg$stage.vector, proportions = FALSE)
```



```
lambda(egg_increase)
```

```
## [1] 0.9680462
```

```
###increasing egg survival does not seem to matter much
```

```
#increase egg survival
```

```
class_names <- c("Egg", "Sm Juv", "Lg Juv", "Subadult", "Adult")
```

```
adults_increase <- matrix(c(0, 0, 0, 4.665, 61.896,
                             0.675, 0.703, 0, 0, 0,
                             0, 0.047, 0.657, 0, 0,
                             0, 0, 0.019, 0.682, 0,
                             0, 0, 0, 0.061, 0.9),
                           nrow = 5, ncol = 5, byrow = TRUE, dimnames = list(class_names, class_names))
```

```
# Initial abundance
```

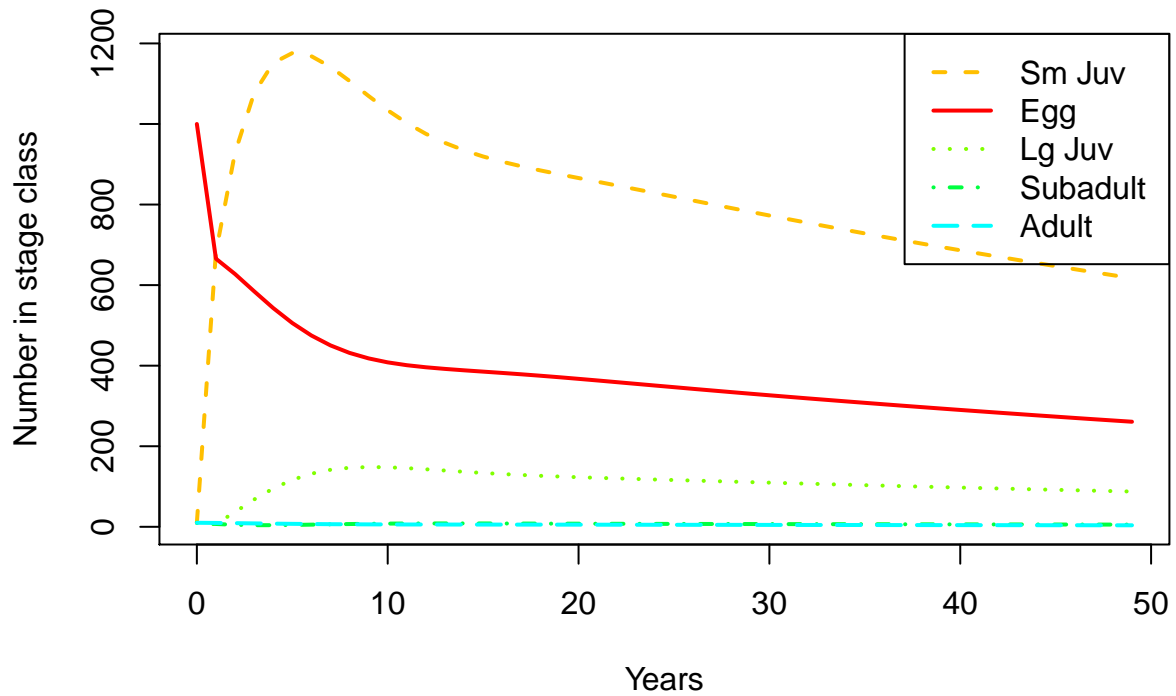
```
n_0_adults <-c(1000, 10, 10, 10, 10)
```

```
# Project the matrix
```

```
pop_adults <- pop.projection(adults_increase, n_0_adults, iterations = 50)
```

```
# Plot each stage through time
```

```
stage.vector.plot(pop_adults$stage.vector, proportions = FALSE)
```



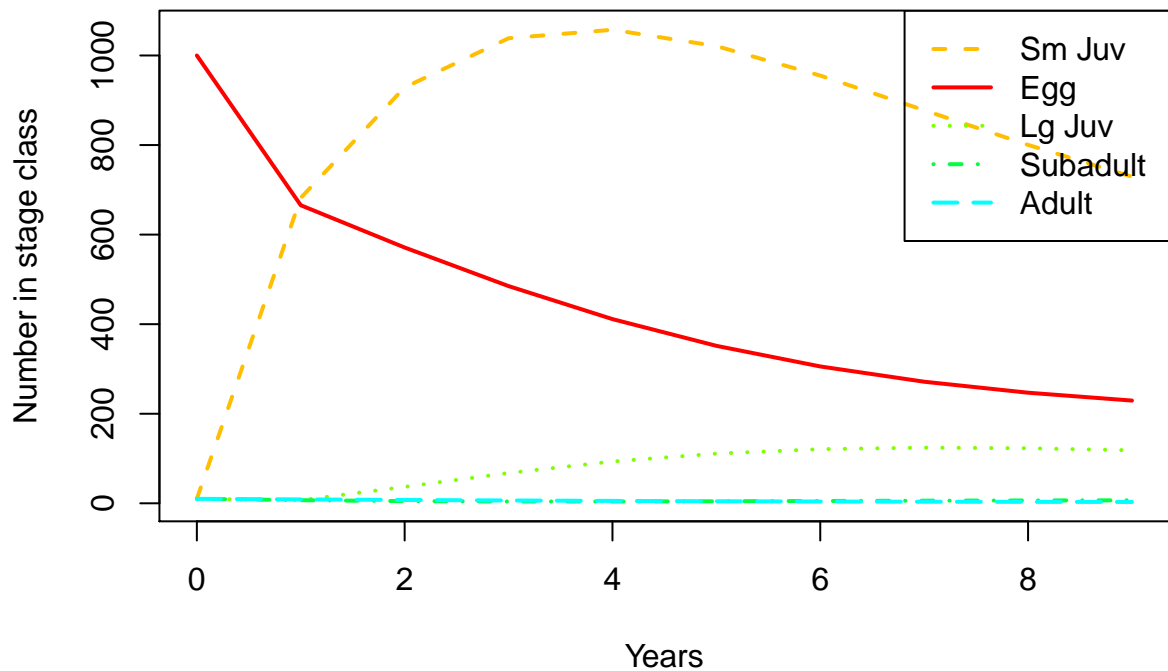
```
lambda(adults_increase)
```

```
## [1] 0.988256
```

Increasing the survival of the eggs does not make a big difference in the numbers of total turtles. However, changing the survival rate of the adult turtles does.

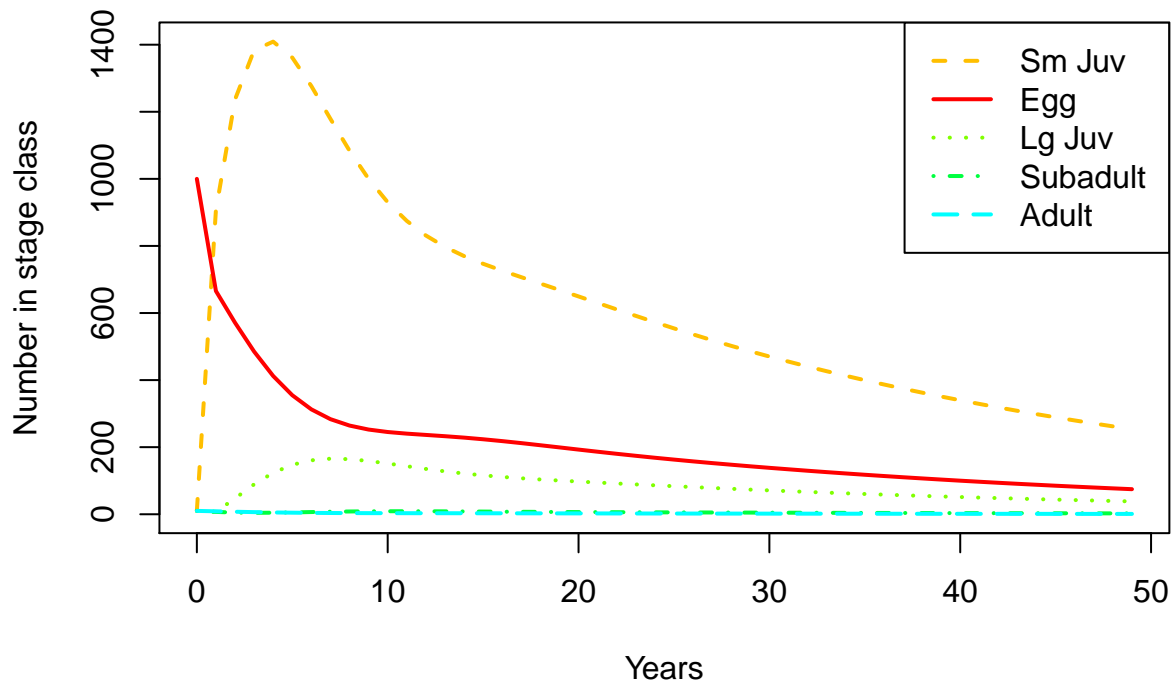
```
#normal
```

```
stage.vector.plot(pop$stage.vector, proportions = FALSE)
```

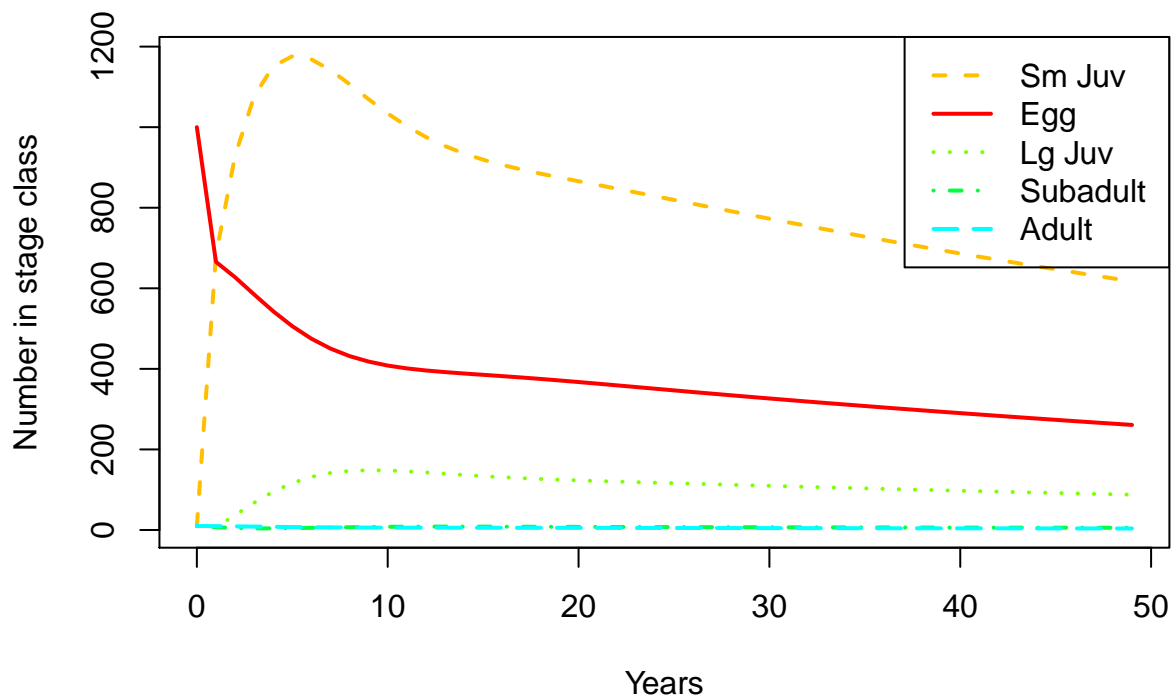


```
#increase egg survival
```

```
stage.vector.plot(pop_egg$stage.vector, proportions = FALSE)
```



```
#increase adult
stage.vector.plot(pop_adults$stage.vector, proportions = FALSE)
```



In order to construct a viable conservation sea turtle plan, we need to increase the survival of the adults. This can be done by decreasing deaths. Many sea turtle deaths are now caused by human activity such as net entanglement, prop strikes, and runoff pollution/algae blooms. In order to properly write a conservation plan, the writer will need to know which area the conservation action will occur and what the main causes of death are.