Programing fundamentals

- * A program is a set of instructions for a computer to follow
- Programs are often used to manipulate data (in all type and formats you discussed last week)
- Simple to complex
 - the scripts you wrote last week (simple)
 - instructions to analyze relationships in census data and visualize them
 - a model of global climate

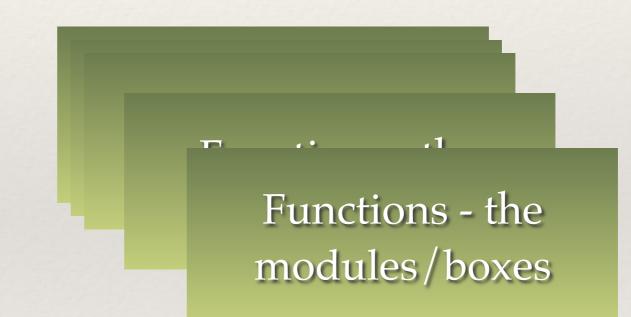
Programing fundamentals

- Operations (=,+,-,...concatenate, copy)
- Data structures (simple variables, arrays, lists...)
- Control structures (if then, loops)
- * Modules...

Concepts common to all languages through the syntax may be different

Modularity

Main controls the overall flow of program- calls to the functions/ modules/building blocks



- * A program is often multiple pieces put together
- * These pieces or modules can be used multiple times

Programing fundamentals

Box 1. Summary of Best Practices

- 1. Write programs for people, not computers.
- (a) A program should not require its readers to hold more than a handful of facts in memory at once.
- (b) Make names consistent, distinctive, and meaningful.
- (c) Make code style and formatting consistent.
- 2. Let the computer do the work.
- (a) Make the computer repeat tasks.
- (b) Save recent commands in a file for re-use.
- (c) Use a build tool to automate workflows.
- 3. Make incremental changes.
- (a) Work in small steps with frequent feedback and course correction.
- (b) Use a version control system.
- (c) Put everything that has been created manually in version control.
- 4. Don't repeat yourself (or others).
- (a) Every piece of data must have a single authoritative representation in the system.
- (b) Modularize code rather than copying and pasting.
- (c) Re-use code instead of rewriting it.

- 5. Plan for mistakes.
- (a) Add assertions to programs to check their operation
- (b) Use an off-the-shelf unit testing library.
- (c) Turn bugs into test cases.
- (d) Use a symbolic debugger.
- 6. Optimize software only after it works correctly.
- (a) Use a profiler to identify bottlenecks.
- (b) Write code in the highest-level language possible.
- 7. Document design and purpose, not mechanics.
- (a) Document interfaces and reasons, not implementation
- (b) Refactor code in preference to explaining how it we
- (c) Embed the documentation for a piece of software in software.
- 8. Collaborate.
- (a) Use pre-merge code reviews.
- (b) Use pair programming when bringing someone new speed and when tackling particularly tricky problem
- (c) Use an issue tracking tool.

Best practices for software development

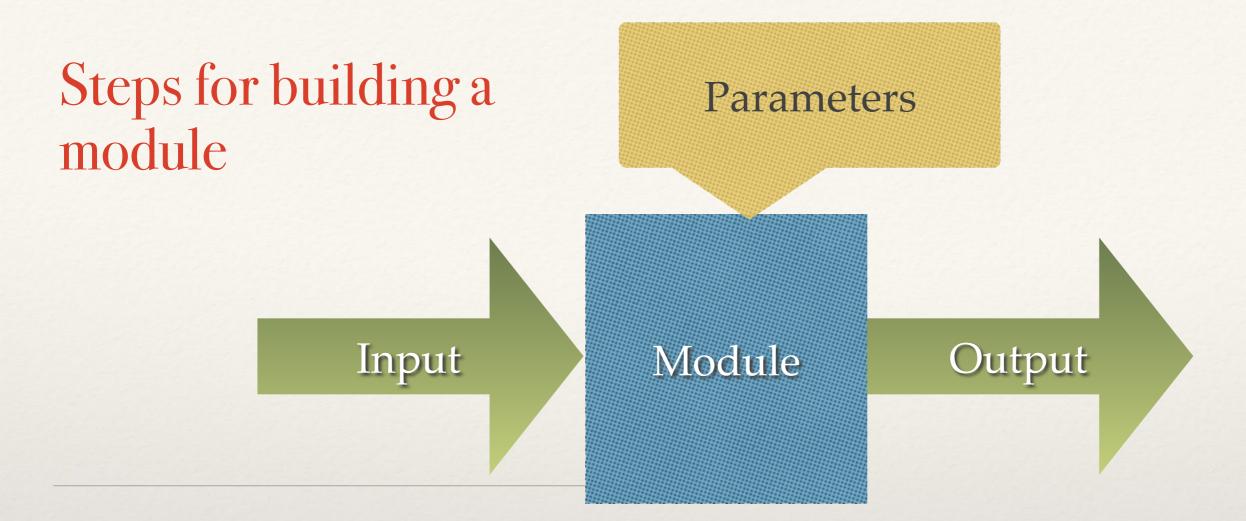
- Read: Wilson G, Aruliah DA, Brown CT, Chue Hong NP, Davis M, et al. (2014) Best Practices for Scientific Computing. PLoS Biol 12(1): e1001745. doi:10.1371/journal.pbio.1001745
- Blanton, B and Lenhardt, C 2014. A Scientist's Perspective on Sustainable Scientific Software. Journal of Open Research Software 2(1):e17, DOI: http://dx.doi.org/10.5334/jors.ba
- but also
- * <u>http://simpleprogrammer.com/2013/02/17/principles-are-</u> <u>timeless-best-practices-are-fads/</u>

Best practices for model (software) development

- Common problems
 - Unreadable code (hard to understand, easy to forget how it works, hard to find errors, hard to expand)
 - Overly complex, disorganized code (hard to find errors; hard to modify-expand)
 - Insufficient testing (both during development and after)
 - Not tracking code changes (multiple versions, which is correct?)

STEPS: Program Design

- 1. Clearly define your goal as precisely as possible, what do you want your program to do
 - 1. inputs/parameters
 - 2. outputs
- 2. Implement and document
- 3. Test
- 4. Refine



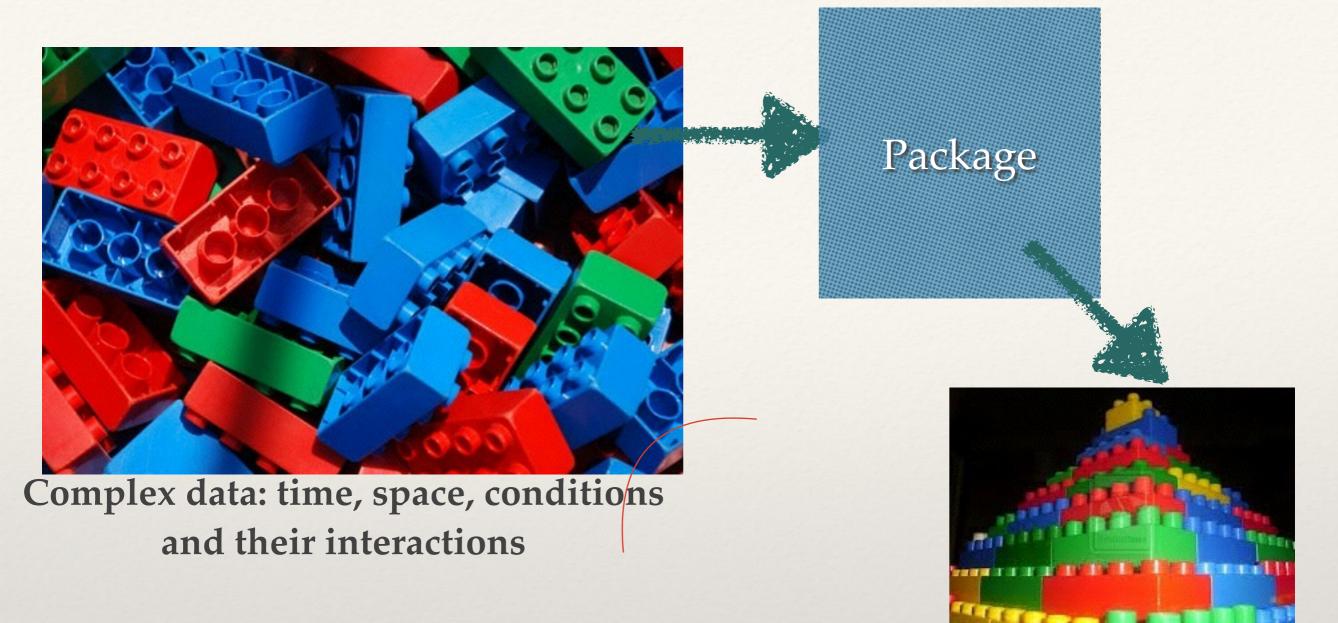
- 1. Design the program "conceptually" "on paper" in words or figures
- 2. Translate into a step by step representation
- 3. Choose programming language
- 4. Define inputs (data type, units)
- 5. Define output (data type, units)
- 6. Define structure
- 7. Write program
- 8. Document the program
- 9. Test the program
- 10. Refine...

Best practices for software development

- * Automated tools (useful for more complex code development
- * (note that GP's often create programs > 100 lines of code)
- Automated documentation
 - http://www.stack.nl/~dimitri/doxygen/
 - http://roxygen.org/roxygen2-manual.pdf
- Automated test case development
 - http://r-pkgs.had.co.nz/tests.html
- * Automated code evolution tracking (Version Control)
 - https://github.com/

Designing Programs

- What's in the box (the program itself) that gives you a relationship between outputs and inputs
 - * the link between inputs and output
 - breaks this down into bite-sized steps or calls to other boxes)
 - think of programs as made up building blocks
 - * the design of this set of sets should be easy to follow



Building Packages

We often have a project that has a set of different functions and data sets - we can combine these together as a package

Functions in R

* Format for a basic function in R

#' documentation that describes inputs, outputs and what the function does
FUNCTION NAME = function(inputs, parameters) {
 body of the function (manipulation of inputs)
 return(values to return)

In R, inputs and parameters are treated the same; but it is useful to think about them separately in designing the model - collectively they are sometimes referred to as arguments

ALWAYS USE Meaningful names for your function, its parameters and variables calculated within the function

Use Lists to return more complex info

```
#' Summary information about spring climate
#'
#' computes summary information about spring temperature and precipitation
#' @param clim.data data frame with columns tmax, tmin (C)
#' rain (precip in mm), year, month (integer), day
#' @param months (as integer) to include in spring; default 4,5,6
#' @return returns a list containing, mean spring temperature (mean.springT, (C))
#' year with lowest spring temperature (coldest.spring (year))
#' mean spring precipitation (mean.springP (mm))
#' spring (as year) with highest precip (wettest.spring (year))
spring.summary = function(clim.data, spring.months = c(4:6)) {
 spring = subset(clim.data, clim.data$month %in% spring.months)
 springT = (spring$tmax+spring$tmin)/2.0
 all.springT = aggregate(springT, by =list(spring$year), mean)
 mean.springT = mean(c(spring$tmax, spring$tmin))
 lowyear = spring$year[which.min(spring$tmin)]
 spring.precip = as.data.frame(matrix(nrow=unique(spring$year), ncol=2))
 colnames(spring.precip)=c("precip","year")
 spring.precip = aggregate(spring$rain, by=list(spring$year), sum)
 colnames(spring.precip) = c("year", "precip")
 mean.spring.precip = mean(spring.precip$precip)
 wettest.spring = spring.precip$year[which.max(spring.precip$precip)]
 return(list(mean.springT = mean.springT, coldest.spring=lowyear,
              mean.springP=mean.spring.precip,wettest.spring=wettest.spring,
      all.springP = spring.precip, all.springT = all.springT ))
}
```

- * Packages in R are ways to organize code/data
- We've used many packages (e.g dplyr) that contain different functions (e.g manipulate())
- You can create your own package to organize code that you might use for a particular project
 - sharing
 - standardization

- * Packages have a precise directory structure to store your code, data, documentation and tests that is easy for R to read
- * A file named DESCRIPTION with descriptions of the package, author, and license conditions meta data
- * in a structured text format that is readable by computers and by people.
- A man / subdirectory of documentation files.
- • An R/ subdirectory of R code.
- A data / subdirectory of datasets.
- * There can be other components but this is a start

- * This package ("classexamples") is now a directory structure to store your code, data, documentation and tests that is easy for R to read
- * A file named DESCRIPTION with descriptions of the package, author, and license conditions
- * in a structured text format that is readable by computers and by people.
- A man/ subdirectory of documentation files.
- • An R/ subdirectory of R code.
- A data / subdirectory of datasets.
- * There can be other components but this is a start

- * To create a package in R studio
 - start a new project
 - create R package
 - * at creation you can add things (.R code, .RData data)
 - notice how it creates a project, and subdirectories any .R files you created will go in R directory

- use load_all() to load everything in your package into your current workspace
- * DESCRIPTION
 - * edit this file to describe your function



* Data

- to add data to your package; store as an .RData file in the Data subdirectory
 - * use save(name, file="data/name.RData")
 - * you may have to create data

* R

- to add code to your package; store as a .R file in the R subdirectory
- * See example in esm237examples

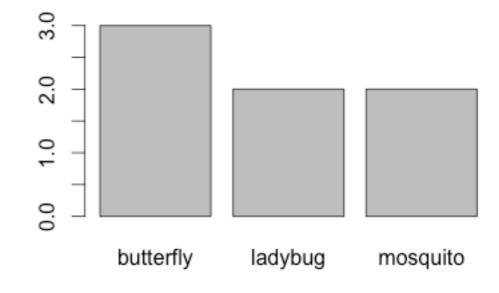
- * vectors (c)
- * matrices, arrays
- * data frames
- * lists
- * factors

- * Factors (a bit tricky, basically a vector of "things" that has different levels (classes); not really numeric - so you can't average them!)
- * But can be useful for doing "calculations" with categories

```
>
> a = c(1,5,2.5,9,5,2.5)
> a
[1] 1.0 5.0 2.5 9.0 5.0 2.5
> mean(a)
[1] 4.166667
> a = as.factor(c(1,5,2.5,9,5,2.5))
> mean(a)
[1] NA
Warning message:
In mean.default(a) : argument is not numeric or logical: returning NA
> a
[1] 1 5 2.5 9 5 2.5
Levels: 1 2.5 5 9
> summary(a)
  12.5 5
             9
   2
         2
             1
  1
```

summary can be used with factors to get frequencies in each category (or "level")

```
>
>
> species.recorded = c("butterfly","butterfly","mosquito","butterfly","
ladybug", "ladybug", "mosquito")
> species.recorded = as.factor(species.recorded)
> species.recorded
[1] butterfly butterfly mosquito butterfly ladybug ladybug
                                                                mosquit
0
Levels: butterfly ladybug mosquito
> summary(species.recorded)
butterfly ladybug mosquito
        3
                  2
                            2
> plot(species.recorded)
>
```



```
>
                                              > species.recorded = c("butterfly","butterfly","mosquito","butterfly","
                                              ladybug", "ladybug", "mosquito")
                                              > species.recorded = as.factor(species.recorded)
                                              > species.recorded
                                              [1] butterfly butterfly mosquito butterfly ladybug
                                                                                               ladybug
                                                                                                        mosquit
                                              Levels: butterfly ladybug mosquito
                                              > summary(species.recorded)
> mean(summary(species.recorded))
                                              butterfly ladybug mosquito
                                                      3
                                                               2
                                                                        2
[1] 2.333333
                                              > plot(species.recorded)
> max(summary(species.recorded))
                                              >
[1] 3
> sum(summary(species.recorded))
[1] 7
                                                                            You can "do things" (apply
> sum(species.recorded)
Error in Summary.factor(c(1L, 1L, 3L, 1L, 2L, 2L, 3L), na.rm = FALSE) :
                                                                             functions) to the summary
  sum not meaningful for factors
                                                                             (frequency of each "factor"
> species.recorded
[1] butterfly butterfly mosquito butterfly ladybug
                                                                                          level
                                                        ladybug
[7] mosquito
Levels: butterfly ladybug mosquito
> summary(species.recorded)[1]
butterfly
> summary(species.recorded)[2]
ladybug
      2
> summary(species.recorded)[3]
mosquito
       2
>
```

- * A simple model that takes advantage of factors
- A model to compute an index of species diversity from a list of recorded species

$$D = \Sigma (n / N)^2$$

where n is the number of individuals in each species, and N is total number

```
# '
   Simpson's Species Diversity Index
# '
# '
   Compute a species diversity index
# '
   @param species list of species (names, or code)
# '
   @return value of Species Diversity Index
# '
   @examples
   compute simpson index(c("butterfly","butterfly","mosquito","butterfly",
#' "ladybug", "ladybug")))
#' @references
  http://www.tiem.utk.edu/~gross/bioed/bealsmodules/simpsonDI.html
# '
```

compute_simpson_index = function(species) {

```
species = as.factor(species)
tmp = (summary(species)/sum(summary(species))) ** 2
diversity = sum(tmp)
return(diversity)
}
```

lm is an
 example of a function that
 returns a list >> res = lm(obs\$prices~obs\$forestC) > names(res) [1] "coefficients" "residuals" "effects" [4] "rank" "fitted.values" "assign" [7] "qr" "df.residual" "xlevels" [10] "call" "terms" "model" > res\$coefficients (Intercept) obs\$forestC 14.9789368 0.1865644 > res\$model obs\$prices obs\$forestC 23 59 1 2 44 88 3 60 100 4 10 4 5 2 8 33 79 6 7 59 300

>

- a bit more on factors; a list of numbers can also be a factor but then they are not treated as actual numbers you could think of them as "codes" or addresses or..
- use *as.numeric* or *as.character* to go back to a regular
 vector from a factor

```
> items = c(1,5,1,5,6,3)
> mean(items)
[1] 3.5
> items = as.factor(c(1,5,1,5,6,3))
> mean(items)
[1] NA
Warning message:
In mean.default(items) : argument is not numeric or logical: returning
NA
> summary(items)
1356
2121
> tmp = as.numeric(items)
> tmp
[1] 1 3 1 3 4 2
> mean(tmp)
[1] 2.333333
>
```

Generating "fake" or example data - sample

tmp = c("ponderosa","jack","white","lodgepole","douglasfir","oak")
obs.trees= list(species=sample(tmp, replace=T, size=100))

```
obs.trees$carbon = runif(min=5, max=20, n=100)
```

```
# run our functions
compute_simpson_index(obs.trees$species)
```

```
# save data for use in your R package
save(obs.trees, file="data/obstrees.RData")
```

- * vector, (c)
- * matrices, arrays
- * data frames
- * lists
- * factors

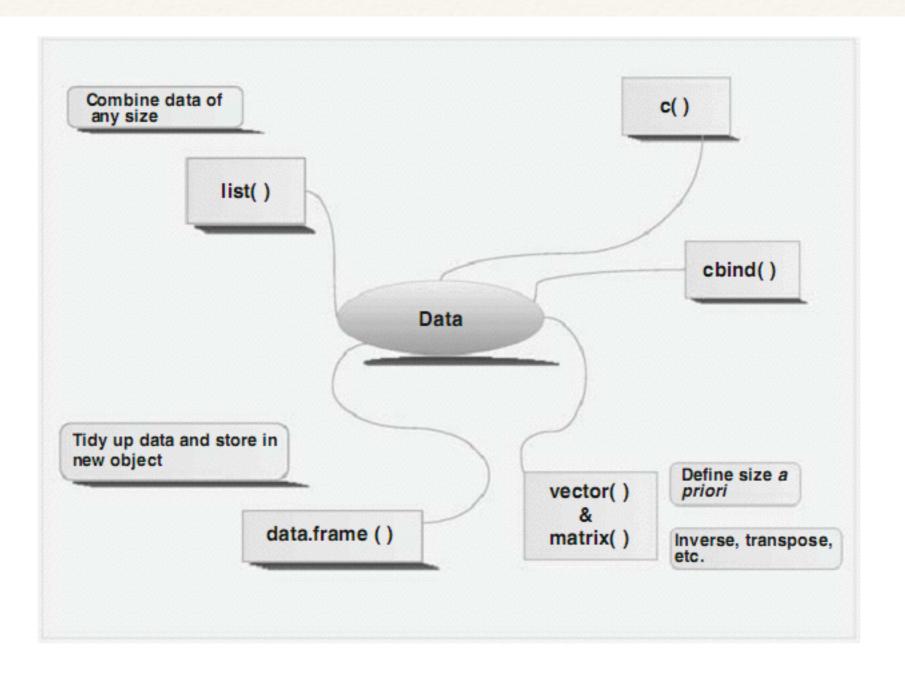
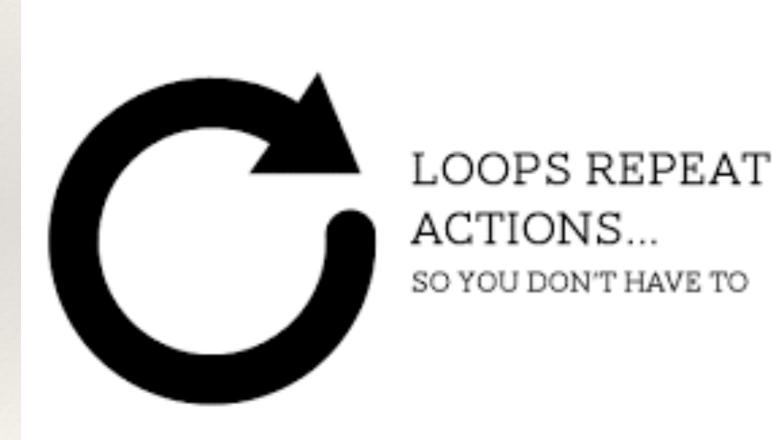
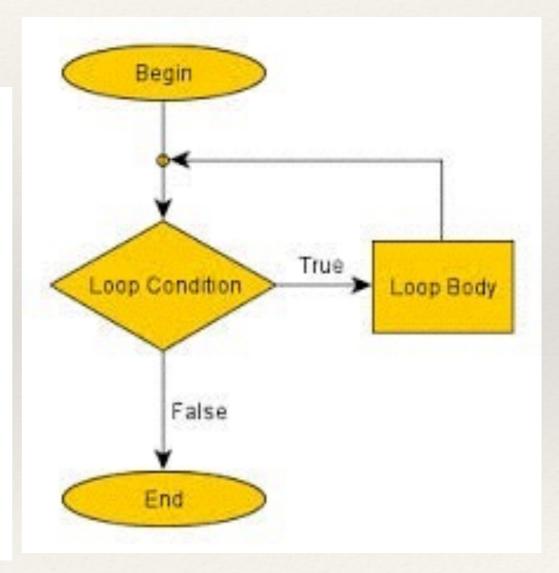


Fig. 2.1 Overview of various methods of storing data. The data stored by cbind, matrix, or data.frame assume that data in each row correspond to the same observation (sample, case)

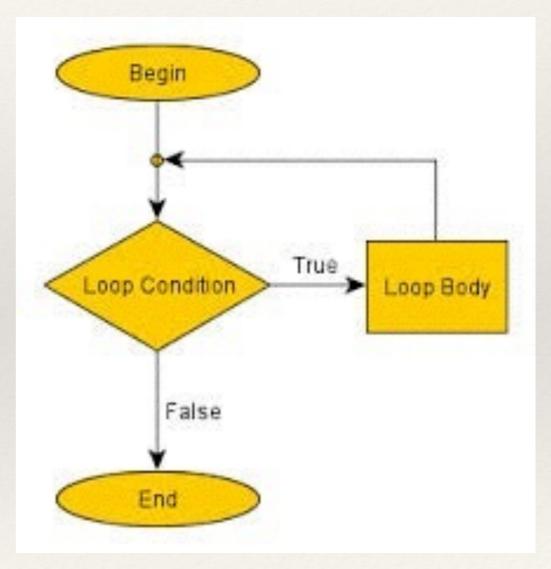
http://www.simonqueenborough.com/R/basic/figure/data-types.png

 Loops are fundamental in all programming languages: and are frequently used in models

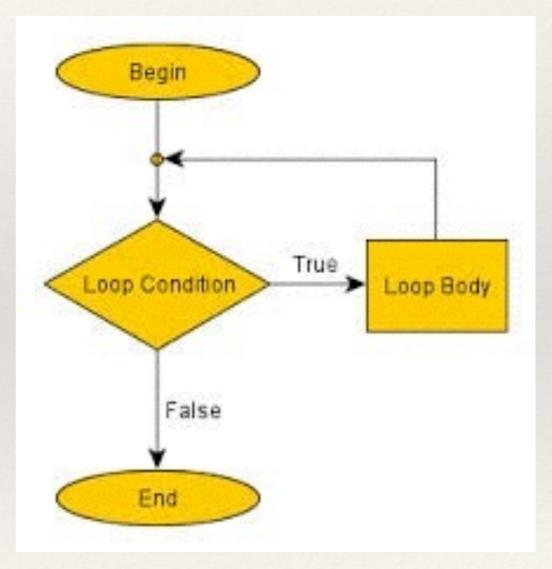




- * Two distinctive reasons for looping
- Apply the same equations (e.g for power generation) over a range of parameter values
- Evolve a variable through time (or space), when the variable's value at the next time step depends on the previous one (e.g growing a population)



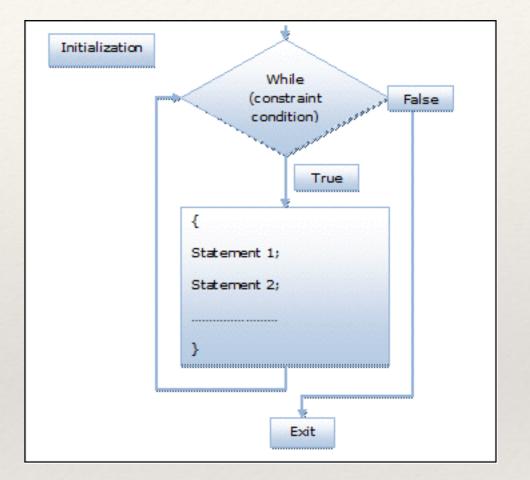
 All loops have this basic structure - repeat statements (loop body) until a condition is true



- * In R, the most commonly used loop is the *For* loop
- * for (i in 1:n) { statements }
- * In "for" loops the i (or whatever variable you want to use as the counter, is automatically incremented each time the loop is gone through; and the looping ends when i (the counter) reaches n
- * What is x? alpha? after this loop is run

>x=0> for (alpha in 1:4) { x = x+alpha} >
>
>
x=0
> for (alpha in 1:4) { x = x+alpha}
>
>
> alpha
[1] 4
> x
[1] 10

- Another useful looping construct is the While loop
- keep looping until a condition is met
- Useful when you don't know what "n" in the for 1 in to "n" is
- often used in models where you are evolving
 - accumulate something until a threshold is reached (population, energy, biomass?



* A simple *while* loop example

>
>
> alpha = 0
> x = 0
> while (alpha < 100) { alpha = alpha + x; x = x+1}
> x
[1] 15
> alpha
[1] 105
>

* alpha = (1+2+3+4+5+6+7+8+9+10+11+12+13+14) = 105

- * A more useful *while* loop example
- A question: if a metal toxin in a lake increases by 1% per year, how many years will it take for the metal level to be greater than 30 units, if toxin is current at 5 units
- there are other ways to do this, but a while loop would do it

why won't this work?

> pollutant.level = 5
> while (pollutant.level < 30) {
+ pollutant.level = pollutant.level + 0.01* pollutant.level
+ yr = yr + 1
+ }
>

```
> yr=1
> pollutant.level = 5
> while (pollutant.level < 30 ) {
+ pollutant.level = pollutant.level + 0.01* pollutant.level
+ yr = yr + 1
+ }
> > yr
[1] 182
> pollutant.level
[1] 30.2788
```

* Most programming languages have For and while loops

File Loops

```
# average5.py
# Computes the average of numbers listed in a file.
def main():
    fileName = raw_input("What file are the numbers in? ")
    infile = open(fileName,'r')
    sum = 0.0
    count = 0
    for line in infile.readlines():
        sum = sum + eval(line)
        count = count + 1
    print "\nThe average of the numbers is", sum / count
```

mcsp.wartburg.edu/zelle/python/ppics1/.../Chapter08.p

Python Programming, 1/e

36

Key Programming concepts: Control Structures

* if(cond) expression

> > a=4 > b=10 > if(a > b) win = "a" > if(b > a) win = "b" > win [1] "b"

>

* ifelse(cond, true, false)
>
> win = ifelse(a > b, "a", "b")
> win
[1] "b"
>

Conditions: == equal > greater than >= greater than or equal to < less than <= less than or equal to %in% is in a list of something

&& AND || OR is.null()

Key Programming concepts: Control Structures

If can also be used to choose what you return from a function

```
compute_seasonal_flow = function(str,kind) {
  str$season = ifelse( str$month %in% c(1,2,3,10,11,12),"winter","summer")
  tmp = subset(str, str$season=="winter")
  if(kind=="mean") winter= mean(tmp$mm)
  if(kind=="min") winter=min(tmp$mm)
  tmp = subset(str, str$season=="summer")
  if(kind=="mean") summer= mean(tmp$mm)
  if(kind=="mean") summer= max(tmp$mm)
  if(kind=="min") summer=max(tmp$mm)
  if(kind=="min") summer=min(tmp$mm)
  if(kind=="min") summer=min(tmp$min")
  if(kind=="mi
```

Key Programming concepts: Control Structures

If can also be used to choose what you return from a function

> compute_seasonal_flow(streamflow,"mean") \$summer [1] 1.538304 \$winter [1] 0.6200728 > compute_seasonal_flow(streamflow,"max") \$summer [1] 23.66069 \$winter [1] 71.97168

Key Programming concepts: Review of data types

```
#' compute_NPV
#'
#' compute net present value
#' @param value/cost ($)
#' @param time in the future that cost/value occurs (years)
#' @param discount rate, default 0.01
#' @return value in $
```

compute_NPV = function(value, time, discount=0.01) {

```
result=0.0
if (length(value) < length(time) )
  value = rep(value, times=length(time))
for (i in 1:length(time) ) {
  result = result + value[i] / (1 + discount)**time[i]
}</pre>
```

return(result)

}

Key Programming concepts: Review of data types

```
compute carbon
# '
   computes growth given species, and spring temperature and precipitation
   @param currentbiomass (mgC)
  @param species (name of species)
  @param species.parm (data frame with species, maxrate (%C/yr), topt (C), pmax
(mm), pmin(mm)
  @param springt (C) springtime temperature
#'
#' @param springp (mm) springtime rainfall
#' @return growth (mgC/year)
compute carbon = function(currentbiomass, species, species.parm, springt, springp)
  idx = match(obs.trees$species, coeff.species.growth$species)
  growth.rate = species.parm$maxrate[idx]
  growth.rate = growth.rate - abs(springt-species.parm$topt[idx])/20
 peffect = (springp -species.parm$pmin[idx])/
      (species.parm$pmin[idx]-species.parm$pmax[idx])*species.parm$maxrate[idx]
  growth.rate = ifelse(springp < species.parm$pmin[idx], 0,</pre>
```

ifelse(springp > species.parm\$pmax[idx], growth.rate,

```
growth.rate-peffect) )
```

```
new.carbon = currentbiomass*growth.rate
return(new.carbon)
```

load "stuff" in your package including R
load_all()
result = spring.summary(clim)
View(result)

save data for use in your R package save(clim, file="data/clim.RData")

generate data
tmp = c("ponderosa","jack","white","lodgepole","douglasfir","oak")
obs.trees= list(species=sample(tmp, replace=T, size=100))

```
obs.trees$carbon = runif(min=5, max=20, n=100)
```

coeff.species.growth = data.frame(species=c("ponderosa","jack","white","lodgepole","douglasfir","oak"), maxrate=c(1.2,1.1,1.3,1.6,1.9,1.2), topt = c(9,7,6,5,7,12), pmax = c(300,300,300,400,600,400), pmin = c(100,200,200,250,250,100))

run our functions
compute_simpson_index(obs.trees\$species)
compute_NPV(value=100, time=20, discount=0.01)
compute_carbon(obs.trees\$carbon, obs.trees\$species, coeff.species.growth, 9, 200)

save data for use in your R package save(obs.trees, file="data/obstrees.RData") save(coeff.species.growth, file="data/coeff.species.growth.RData")

- * Loops can be "nested" one loop inside the other
- * For example, if we want to calculate NPV for a range of different interest rates and a range of damages that may be incurred 10 years in the future
 - * using a function called compute_npv
- * Steps
 - define inputs (interest rates, damages)
 - define a data structure to store results
 - define function/model (already available)
 - * use looping to run model for all inputs and store in data structure

- * Now we can start to build a more complex program
- Lets say we want to figure out the benefits of a forest, that include both carbon storage and biodiversity
- Conceptual model
- Implementation using our building blocks

```
#' Forest Ecosystem Benefit Computer
```

```
#'
```

```
#' compute_ecobenefit()
```

```
#'
```

* Computes an estimate of forest ecosystem benefits that include both biodiversity and carbon

- #' @param tree dataframe with species and current biomass
- #' @param carbonprice (\$) price paid for carbon
- #' @param biodiversityprice (\$) price paid for biodiversity in a given year
- #' @param paramters for growth model
- #' @param clim dataframe with tmax, tmin and precip for each day
- #' @param discount discount rates
- #' @return annual.benefit and NPV of all benefits over all years

#'@examples

compute_ecobenefit = function(tree, carbonprice, biodiversityprice, coeff.species.growth, clim, discount) {

```
spring = spring.summary(clim)
benefit = matrix(nrow=nrow(spring$all.springT), ncol=length(tree$species))
for (i in 1:nrow(spring$all.springT)) {
    benefit[i,]=compute_carbon(tree$carbon,trees$species, coeff.species.growth,
    spring$all.springT$x[i], spring$all.springP$precip[i])
```

```
benefit = as.data.frame(benefit)*carbonprice
```

benefit\$biodiversity = compute_simpson_index(tree\$species)*biodiversityprice

```
annual.benefit = apply(benefit,1,sum)
```

present.benefit = compute_NPV(value=annual.benefit, time=seq(from=1,to=length(annual.benefit)),
discount)

return(list(annual.benefit=annual.benefit, NPV=present.benefit))

Run our more complex function - different discount rates

compute_ecobenefit(obs.trees, 20, 10, coeff.species.growth, clim, 0.01) compute_ecobenefit(obs.trees, 20, 10, coeff.species.growth, clim, 0.05)