

Summarizing Age Data

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Preliminaries

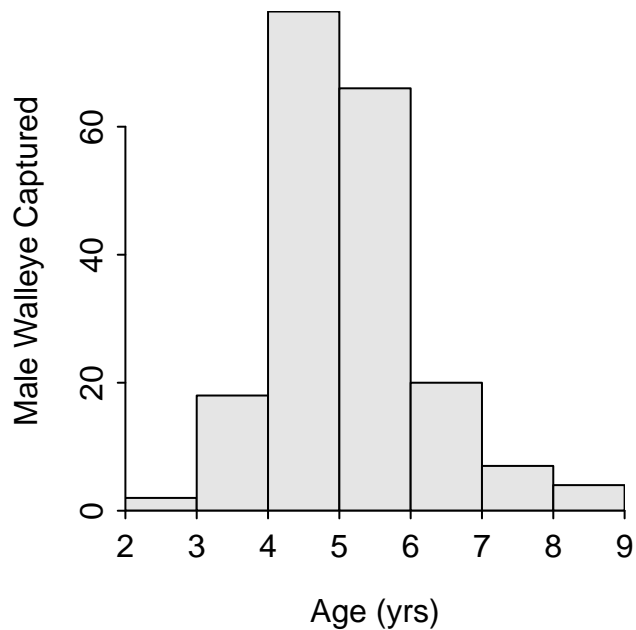
```
> # clears objects in R workspace  
> rm(list = ls())
```

```
> # sourcing the script that constructed and applied the ALK  
> # may need to adjust if you named your script differently  
> source("02_AgeLengthKey.R")
```

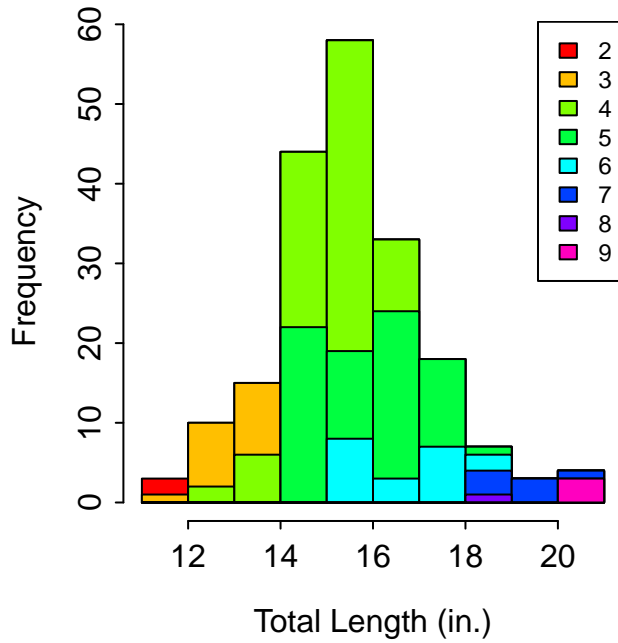
Warning in rm(hook1): object 'hook1' not found

```
> # to demonstrate what is in the workspace after the sourcing  
> ls()  
[1] "waeF.fnl" "waeM.fnl"
```

```
> hist(~Age..observed.annuli.,data=waeM.fnl,xlab="Age (yrs)",ylab="Male Walleye Captured")
```



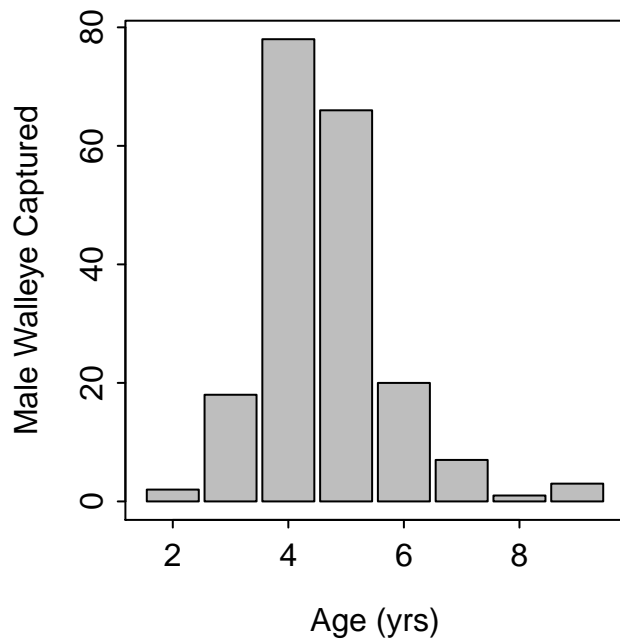
```
> histStack(Length.or.Lower.Length.IN~Age..observed.annuli.,data=waeM.fnl,xlab="Total Length (in.)",
  right=FALSE,legend.pos="topright")
Warning in histStack.default(mf[, 1], mf[, 2], breaks = breaks, col = col, : z was converted to a
factor
```



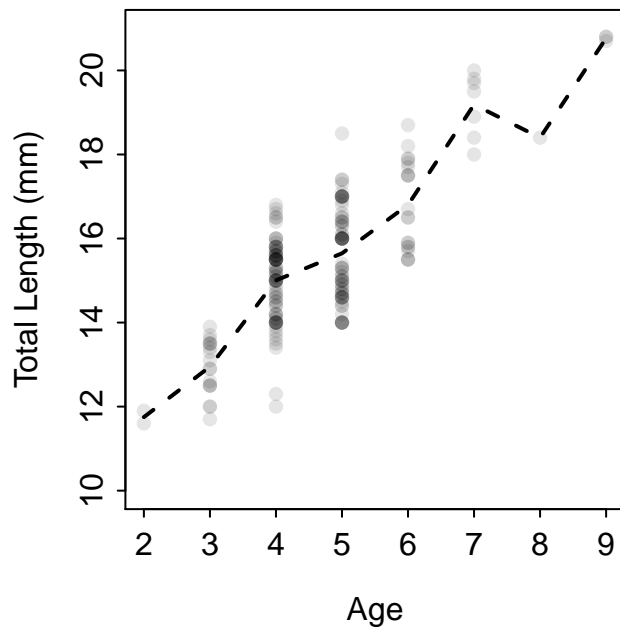
```
> waeM.sumlen <- waeM.fnl %>%
  group_by(Age..observed.annuli.) %>%
  summarize(n=n(),mean=mean(Length.or.Lower.Length.IN),sd=sd(Length.or.Lower.Length.IN),
    min=min(Length.or.Lower.Length.IN),max=max(Length.or.Lower.Length.IN))
> waeM.sumlen
Source: local data frame [8 x 6]
```

	Age..observed.annuli.	n	mean	sd	min	max
1	2	2	11.75000	0.21213203	11.6	11.9
2	3	18	12.95000	0.65282193	11.7	13.9
3	4	78	15.00385	0.94008045	12.0	16.8
4	5	66	15.64697	1.09336737	14.0	18.5
5	6	20	16.80000	1.06028795	15.5	18.7
6	7	7	19.18571	0.76469726	18.0	20.0
7	8	1	18.40000	NaN	18.4	18.4
8	9	3	20.76667	0.05773503	20.7	20.8

```
> plotH(n~Age..observed.annuli.,data=waeM.sumlen,xlab="Age (yrs)",ylab="Male Walleye Captured",
        xlim=c(1.5,9.5),width=0.9)
```



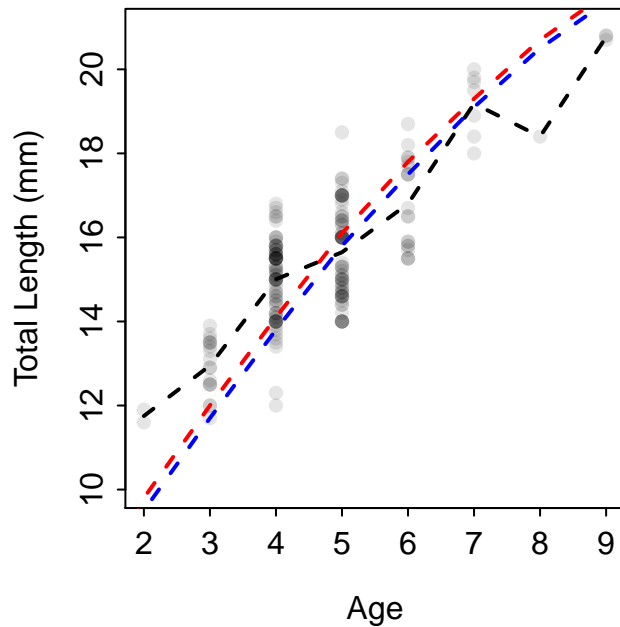
```
> plot(Length.or.Lower.Length.IN~Age..observed.annuli.,data=waeM.fn1,pch=16,col=rgb(0,0,0,1/10),
        xlab="Age",ylab="Total Length (mm)",ylim=c(10,21))
> lines(mean~Age..observed.annuli.,data=waeM.sumlen,lwd=2,lty=2)
```



```

> plot(Length.or.Lower.Length.IN~Age..observed.annuli.,data=waeM.fn1,pch=16,col=rgb(0,0,0,1/10),
      xlab="Age",ylab="Total Length (mm)",ylim=c(10,21))
> lines(mean~Age..observed.annuli.,data=waeM.sumlen,lwd=2,lty=2)
>
> wae.JM <- data.frame(age=1:17,
                      state=c(6.5,9.8,12.0,14.1,16.1,17.8,19.3,20.7,21.8,
                              22.9,23.8,24.5,25.1,25.9,25.5,25.8,25.2),
                      NOR=c(6.4,9.5,11.7,13.8,15.8,17.5,19.1,20.5,21.6,
                             22.7,23.7,24.4,25.2,25.8,25.6,25.6,NA))
> lines(state~age,data=wae.JM,lwd=2,lty=2,col="red")
> lines(NOR~age,data=wae.JM,lwd=2,lty=2,col="blue")

```



Construct and Apply an Age-Length Key – Females

Copy the code from above and convert the 'M's to 'F's

Application Assignment

Create a script that performs the following tasks:

1. Continue or `source()` your script from the previous handout.
2. Summarize the age distribution from all of the fish in your sample.
3. Show the mean length-at-age for all fish in your sample in both tabular and graphical forms.
4. (*Time Permitting*) Show the length frequency for all fish in your sample.
5. (*Time Permitting*) Repeat the above for your second sex or species.

Save your script!