Kat Leigh pre-class 10/20/21 FSH552

#==Q1

# Find the maximum difference in successive dates

biggest\_gap <- max(difftime(tripData$Date[2:nrow(tripData)], tripData$Date[1:nrow(tripData)-1], units = 'days'))

# Find the row index of this biggest gap

tmp <- difftime(tripData$Date[2:nrow(tripData)], tripData$Date[1:nrow(tripData)-1], units = 'days')

row\_inx\_biggest\_gap <- which(tmp ==biggest\_gap)

check\_gap <- difftime(tripData[row\_inx\_biggest\_gap+1,]$Date, tripData[row\_inx\_biggest\_gap,]$Date)

# Display rows of tripData immediately before (three rows) and after (three rows) the biggest gap

tripData[c(row\_inx\_biggest\_gap -3, row\_inx\_biggest\_gap -2, row\_inx\_biggest\_gap -1, row\_inx\_biggest\_gap +3, row\_inx\_biggest\_gap +2, row\_inx\_biggest\_gap +1),]

#==Q2

# 1. Create a data frame by subsetting speciesData to include all rockfish species (scientific name Sebastes) using speciesCode to find the corresponding codes

**rockFishCode <- speciesCode[grep('Sebastes', speciesCode$Scientific),'SpeciesCode']** # search for matching string 'rockfish' in common column pf speciescode dataframe; return the indices of these matches; return all rows matching these indicies and only the speciescode column.

**rockFish <- speciesData[speciesData$SpeciesCode %in% rockFishCode,]** # subset the speciesdata dataframe to just include the rows where the speciescode matches those corresponding to the codes for 'Sebastes' found in the previous line.

# 2. Provide a table() of the fates of rockfish by species code

**rockFishTable <- table(rockFish$SpeciesCode, as.character(rockFish$Fate))** # get frequency summaries for each value in the fate column for all the rockfish entries. But remove the blank value in the fate column by converting to character.

# 3. Calculate the minimum and maximum length recorded for each rockfish species

**min\_max\_rockFish <- tapply(rockFish$Length, as.factor(rockFish$SpeciesCode), range, na.rm=TRUE)** # apply the range function (calculates the min and max) across all the rockfish data, grouping by species code so that the ranges returned are per species.