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```
title: "Final Project; Categorical Data Analysis"
author: "Abby Smith, Miruna Baronschi, Martha Eichlersmith"
date: "2019-12-05"
output:
 pdf_document:
    fig_caption: yes
    number_sections: yes
header-includes:
  \usepackage{color}
  \usepackage{mathtools}
  \usepackage{bbm} #for mathbb for numbers
  \usepackage{amsbsy}
 \usepackage{caption}
  \usepackage{booktabs}
  \usepackage{geometry}
\usepackage{float} #to hold things in place
  \usepackage{lastpage}
  \usepackage{fancyhdr}
  \usepackage{graphicx}
  \pagestyle{fancy}
  \floatplacement{figure}{H}
  \fancyhf{}
- \fancyhead[L]{STAT 455 Fall 2019 \\ Final Project}
- \[R]{Abby, Miruna, Martha \ \ Page \ \ pageref*{LastPage}}\]
- \setlength{\headheight}{22.5pt} #to remove \fancyhead error for head height
geometry: left=0.75in,right=0.75in,top=1.1in,bottom=1in
```{r setup, include=F}
knitr::opts_chunk$set(message=F, warning=F)
require(tidyverse)
require(janitor)
require(rgdal)
require(sp)
require(sf)
require(raster)
require(Rcapture)
require(dga)
require(rgeos)
require(MASS)
library(bookdown) #for fig captions
library(kableExtra)
knitr::opts_chunk$set(fig.width = 10, fig.height = 4)
knitr::onts chunk$set(echo=FALSE)
knitr::opts_chunk$set(fig.pos='H')
Estimates of Killing in Casanare
Casanare is a large, rural state in Colombia that includes 19 municipalities and a population of almost 300,000 inhabitants. Located in the foothills of
So how many people have been killed or disappeared? We review the Human Rights Data Analysis Group (HRDAG)'s reporting on this issue of population estim
The datasets come from state agencies - including government, security, forensic and judicial bodies - and from civil society organizations. Across thes
Multiple Systems Estimation (MSE), Capture Re-Capture
The goal is to estimate the overall population of victims by first estimating the victims who are not captured by any of the datasets. MSE estimates th
```{r img.MSE, fig.height=3, fig.cap="Multiple System Estimation^[Green, Amelia Hoover (2013) Multiple Systems Estimation: Stratification and Estimation
library(png)
library(grid)
img <- readPNG("mse_review.png")</pre>
 grid.raster(img)
#![](mse_review.png) need to cite this
## MSE Assumptions
There are several MSE assumptions that are need for when there are two "systems" (lists), but not more than that. The assumptions are:
1. *Closed system*: The population of interest does not change during the measurement period. This means that the object of measurement, whether that i
2. *Perfect matching (record linkage!)*: The overlap between systems (i.e., the group of cases recorded in more than one list) is perfectly identified.
3. *Equal probability of capture*: For every data system, each individual has an equal probability of being captured. For example, every death has proba
4. *Independence of lists*: Capture in one list does not affect probability of capture in another list. For example, being reported to one NGO does not
Like differences in capture probability, dependencies between systems are impossible to account for in the two-system setting. A common example here
# Overview of Data
```

```
```{r data-sources}
casanare<- read_delim('summary-table.csv', delim= "|")</pre>
casanare_capture_recapture <- casanare %>%
 dplyr::select(-c(vln, muni, year)) #just want a matrix of 0s and 1s
cols_lists <- casanare_capture_recapture %>% dplyr::select(starts_with("d_"))
#this function returns any instance of a "capture" for each org
return_1 <-function(x) {
 casanare_capture_recapture %>%
 filter(x ==1) %>%
 summarize(n=sum(Freq)) %>% dplyr::select(n)
}
#unlist(map(cols_lists, return_1))
unique_records<- casanare_capture_recapture %>%
 mutate(sum_cols = reduce(dplyr::select(., starts_with("d_")), `+`)) %>%
 filter(sum_cols == 1)
unique_records<-unique_records %>%
 group_by(d_CCJ, d_EQU, d_FON, d_IMLD ,d_PN0 ,d_CIN, d_FAM ,
 d_FSR, d_IMLM,
 d_VP, d_CCE, d_CTI, d_FDC, d_GAU , d_PL) %>%
 summarise(n = sum(Freq))
print table with each data source and total records "captured"
org_names <- c("Colombian Commission of Jurists", "Equitas", "Fondelibertad", "National Institute of Forensic Medicine Disappearances", "Policía Naciona
colnames(contigency_table) <- c("Organization", "Total Captures", "Unique", "Type")</pre>
knitr::kable(contigency_table, format="latex", booktabs=T, caption="Contingency Table") %>%
 kableExtra::kable_styling(latex_options="scale_down") %>%
 kableExtra::kable_styling(latex_options = "HOLD_position")
Overall Trends
The following graph shows that violence has been concentrated in Yopal. We can see that the *reported* violence (i.e. the counts in the 15 datasets) ap
```{r mapping-whole-country}
#group deaths by municipality
muni <- casanare %>% mutate(name_2= str_to_title(muni)) %>%group_by(name_2) %>% summarise(count = sum(Freq))
colombia_dat <- getData('GADM', country='COL', level = 2) %>%
  st_as_sf() %>%
  clean names()
casanare_dat <- colombia_dat %>%
  filter(name_1 == "Casanare") %>%
  mutate(name_2 = stringi::stri_trans_general(name_2, "Latin-ASCII"))%> #removes accents for joining purposes
  mutate(name_2 = str_to_title(name_2)) %>%
  left_join( muni, by =c('name_2'))
casanare_overall_plot <- ggplot(casanare_dat, aes(fill = count)) +scale_fill_gradient(low='white', high= 'red')+</pre>
  geom_sf() +
  theme_void() +
  ggtitle('Total Counts in 15 Datasets by Municipality 1998-2007')
```{r mapping-by-muni}
#partition by years
#group deaths by municipality
muni_by_year<- (casanare %%% mutate(name_2 = str_to_title(muni)) %%
group_by(name_2, year) %%
summarise(count = sum(Freq))</pre>
casanare_dat_with_years <- colombia_dat %>%
 filter(name_1 == "Casanare") %>%
mutate(name_2 = stringi::stri_trans_general(name_2, "Latin-ASCII"))%>%
 mutate(name_2 = strIngl..strI_trans_gener
mutate(name_2 = str_to_title(name_2)) %>%
left_join(muni_by_year, by =c('name_2'))
casanare_by_years <- ggplot(casanare_dat_with_years, aes(fill = count)) +scale_fill_gradient(low='white', high= 'red')+</pre>
 geom_sf() +
 theme_void() + facet_wrap(~ year)+
 ggtitle('Yearly Counts in 15 Datasets by Municipality 1998-2007')
```{r gisplots, fig.cap="Overall Trends in 15 Datasets by Municipality"}
gridExtra::grid.arrange(casanare_overall_plot, casanare_by_years, nrow=1)
```

```
Looking just at the totals of the 15 datasets, that data suggest the violence peaked in 2003-2004 and the total number of victims is 3501. However, jus
## Heterogeneity Issues
One of the requirements for MSE is for each individual has equal probability of capture for a given list. However, we can see from the figure below thi
```{r threeorg2004, fig.height=2.5, fig.cap="Counts from Three Different Datasets in 2004"}
gather_cols <-colnames(casanare %>% dplyr::select(starts_with("d_")))
for_2004<- pivot_longer(casanare, cols= gather_cols, names_to='data_lists', values_to='indicator') %>% filter(indicator == 1) %>%
filter(data_lists == "d_PN0" | data_lists == "d_IMLM" | data_lists == "d_CIN") %>% filter(year == 2004) %>%
 mutate(name_2 = str_to_title(muni))
test_this <- colombia_dat %>% filter(name_1 == "Casanare") %>%
 mutate(name_2 = stringi::stri_trans_general(name_2, "Latin-ASCII"))%>%
mutate(name_2 = str_to_title(name_2)) %>%
 full_join(for_2004, by =c('name_2'))
hetromap <- ggplot(test_this, aes(fill= Freq)) + scale_fill_gradient(low='white', high= 'red')+
 geom sf() -
 theme_void() + facet_wrap(~ data_lists)+ ggtitle('Disappearances/Kidnappings Across Municipalities by Different Organizations, in 2004')
hetromap
Different Datasets - Different Stories
We motivate our need for a more sophisticated analysis by showing the reporting patterns of 3 different organizations across 1998-2007. If we relied on
```{r motivation-plot}
#list by year
casanare_long <- gather(casanare, key = "data_lists", value= 'Freq', gather_cols) %>%
filter(data_lists == "d_GAU" | data_lists == "d_IMLM" | data_lists == "d_FAM") %>%
    group_by(data_lists,year) %>% summarise(n = sum(Freq))
motivation.plot <- ggplot(casanare_long, aes(x= factor(year), y= as.integer(n), fill = as.factor(data_lists)))+
    geom_bar(stat='identity', position='dodge') + xlab("Year") + ylab("Reported Disappearances/Deaths") +
    ggtitle('Reported Disappearances/Deaths in Casanare') +</pre>
    guides(fill = guide_legend(title='Lists')) +
theme_bw()
```{r, fig.cap= 'Count Trends for Three Organizations'}
motivation.plot
\newpage
Loglinear Modelling
In order to do our estimation, we will use loglinear modeling. We will describe the model as if we had two datasets (for simplicity). We know the vict
 `{r img.example, fig.height=3,echo=FALSE}
library(png)
library(grid)
#img <- readPNG("2datasetexample.png")</pre>
 #grid.raster(img)
The count of victims captured into a dataset or combination of datasets is n_{11}, n_{10}, n_{01}, and n_{00}. Each of these cells is a count of vi
Our estimates are primarily based on Poisson regression.
Estimating the Total Count of Victims
We are interested in estimating n_{0}, which also allows us to estimate the total number of victims.
The (log of the) expected cell count n_{00} is a function of the other observed cell counts, as shown in the equation below.
\log(n_{00}) = \alpha
+ \beta_1 \cdot (x \in \mathbb{1}(x \in \mathbb{1}(x
+ \beta_2 \cdot m_{1}(x \in n_{01})
This is the saturated form of the log-linear models introduced in Bishop, Fienberg and Holland (1975). To quote from Agresti, "the saturated GLM has a s
When estimation of the total "population" of missing people in Casanare is the goal (as it typically is with multiple-systems estimation), the key value
\begin{aligned}
\log(n_{00}) &= \alpha
\underbrace{
+ \beta_1 \cdot \mathbbm{1}(x\in n_{10})
+ \beta_2 \cdot mathbbm{1}(x in n_{01})
}_{\text{each }=0}
\\[.5ex]
\log(n_{00}) & = \alpha
\\[.5ex]
\bar{n}_{00} & = \exp \left\{ \hat{\alpha} \right\}
\\[3ex]
hat{N} &= n_{11} + n_{10} + n_{01} + hat{n}_{00}
\end{aligned}
As with any regression and data mining model, we want to avoid over-fitting. There is a trade off we need to balance between "goodness of fit", and simp
```

```
We need to find the best model in order to get an accurate estimate of α. Thus, we should determine whether the full (saturated) model above, whi
\log(n_{00}) = \alpha
 \beta_1 \cdot \beta_1
+ \beta_2 \cdot \mathbbm{1}(x\in n_{01})
+ \beta_{12} \cdot m_{1}(x \in n_{11})
In this case, we can clearly write out the possible model. During model selection, we estimate these models and choose the model that minimizes the Bay
Challenges with Loglinear models
 Interpretation: The inclusion of so many variables in loglinear models often makes interpretation very difficult.
 Independence Assumption: The frequency in each cell is independent of frequencies in all other cells, which is not necessarily the case here. We
3. **Sample Size Requirement:** With loglinear models, you need to have at least 5 times the number of cases as cells in your data. If you do not have
Choosing our "Systems"
Our dataset encompasses 15 datasets, far too many to model with a loglinear model. We collapse these 15 datasets into 4 systems (i.e. groups) based on t
```{r adding-systems}
#want to count how many records are in just one of these (or both) of these lists vs. these + another system
cap_indicators<- casanare_capture_recapture %>% #could have used fct_collapse() here
    mutate(security_ind = case_when((d_GAU == 1 | d_FON == 1 | d_PN0==1) ~ 1,
                                                                       TRUE ~ 0),
                   forensic_ind = case\_when((d\_IMLM == 1 | d\_IMLD == 1) \sim 1,
                                                                           TRUE \sim 0)
                 TRUE ~ 0),
                 civil_ind = case_when( (d_EQU=1 \mid d_FAM=1 \mid d_PL == 1 \mid d_CCE==1 \mid d_CIN == 1) \sim 1,
                                                                           TRUE ~ 0)
                   ) %>%
    dplyr::select(-Freq, Freq) # move Freq to last column for closedp() function
table.system <- head(cap indicators %>% dplyr::select(security ind, forensic ind, judicial ind, civil ind, Freq))
knitr::kable(table.system, format="latex", booktabs=T
                                              , caption="Example of Information from Systems"
,linesep=""
                                               ) %>%
    #kableExtra::kable styling(latex options="scale down") %>% for if the table is too large
    kableExtra::kable_styling(latex_options = "HOLD_position")
```{r systems.venndiagram, fig.height=5, fig.wdith=6, fig.cap="Estimated Venn Diagram of Systems"}
for_venn <- cap_indicators[,c(16:20)] %>%
 group_by(security_ind, forensic_ind, judicial_ind, civil_ind) %>%
summarise(new_Freq = sum(Freq))
par(mar=c(.1,1,2,1)) #make margins smaller
dga::venn4(c(2000,for_venn$new_Freq),num.test.points = 100000, main='Overlap of Security, Forensic, Judicial and Civil lists') #rough diagram of overlap
In the above Venn Diagram, the colored dots represent a specific victim. We are trying to estimate the victims that are not captured in one of the list
Model Definitions
Types of Models
Models will be denoted by M, and the subscripts will denote the type of model.
* M_0: The M_0 model is the simplest possible multiple source capture recapture model. It assumes that there is no heterogeneity and that all lists
* M_t: This model relaxes the M_0 model to allow for lists to have different capture rates. M_0: This model relaxes the M_0 model to allow for individual capture heterogeneity.
* $M {th}$: This model allows for both list heterogeneity and capture events having different rates.
Types of Heterogeneity
When heterogeneity in capture probability is present (i.e. the probability of a list capturing a victims differs), there are different forms that this h
 Normal: The log odds of capture follows a Normal distribution.
 Darroch: The log odds of capture among those who were not captured follows a Normal distribution.
* Poisson: The log odds of capture among those who were not captured follows a Poisson distribution.
* Gamma: The log odds of capture among those who were not captured follows a Gamma distribution.
Non-Hierarchical Models
After collapsing the 15 lists into four systems, we fit several loglinear models. We see that the best fits clearly take into account both system and in
We will need the hierarchical structure to perform model selection. It's important to note that a model is not chosen if it bears no resemblance to the
The "number of captured units" is the number of observed elements, in this example, the number of people documented as missing/killed, we usually call t
```{r NOT-HIERCH-models}
test <- cap_indicators[,c(16:20)] %>%
    group_by(security_ind, forensic_ind, judicial_ind, civil_ind) %>%
    summarise(new_Freq = sum(Freq))
loglinear_models <- closedp.t(test, dfreq=T)</pre>
```

```
NonHierchModels <- loglinear_models$results
#table.logmodels <- as.data.frame(loglinear_models)</pre>
 knitr::kable(round(NonHierchModels[,1:6], 3)
                                                                          , format="latex"
                                                                             , booktabs=T
                                                                          , caption="Summary of Models (Non-hierarchical models)"
                                                                                     linesep="") %>%
            #kableExtra::kable_styling(latex_options="scale_down") %>%
            kableExtra::kable_styling(latex_options = "HOLD_position")
Each model controls for a subset of all the possible interactions among the models. In the context of MSE, the two- and three-way interactions estimate
 ```{r NOT-HIERCH-models-boxplot, fig.cap="Boxplot of Residuals for Models"}
par(mar=c(2,1,2,1)) #make margins smaller
boxplot(loglinear_models) #residuals for heterogen.
 These boxplots of residuals offer a general assessment of model fit. These boxplots of residuals offer a general assessment of model fit.
Since the individual cell counts:
n_i \simeq Pois(m_i)
\$E[n i] = Var(n i) = m i \$\$
it follows that the Pearson residuals:
\rianlge frac{n_i - \hat{m_i}}{\langle m_i \rangle}
are approximately mean 0, variance 1. This is why they are sensible residuals to use.
The light dotted line represents zero, and ideally you want the residuals centered around zero. We see that there is significantly less variation in th
Specific Model Results
```{r modelProfileLike, fig.cap='Profile Likelihood of Specific Model'}
par(mar=c(4,4,2,1)) #make margins smaller
profilelike <- profileCI(test,dfreq=T, m = "Mth", h = "Darroch", a=2) #profile likelihood CI
 ```{r modelProfileLikeCI}
knitr::kable(round(profilelike$results, 2), format="latex", booktabs=T, caption="Confidence Interval of Specific Model") %>%
kableExtra::kable_styling(latex_options = "HOLD_position")
 \newpage
Capture Recapture
We display some basic capture-recapture frequency statistics to explore capture patterns. It displays, for $i= 1,...t$, the number of people captured $i
If the n_i statistics vary among capture occasions, there is a temporal effect-- which we clearly see here. We would expect the top panel of the plot
```{r descriptive-stats}
desc<- descriptive(test, dfreq = T)</pre>
descstat <- t(desc$base.freq)</pre>
rownames(descstat) <- c(</pre>
                    "fi: number of units captured i times"
            ,"ui: number of units captured {f for} the first time on occasion i"
                    "vi: number of units captured for the last time on occasion i"
            ,"ni: number of units captured on occasion i" % \left( 1\right) =\left( 1\right) \left( 1\right) 
knitr::kable(descstat, format="latex", booktabs=T, caption="Capture Recapture Statistics") %>%
kableExtra::kable_styling(latex_options = "HOLD_position")
\ \\lambda \\lambda \\lambda \\right) = \\log \\left(\frac{N \times P(i \text{ captures})}{{t \choose i}}\right) = \\log(N(1-p)^{t-i} p^i = \) \]
 ```{r descriptive-plot, fig.height=6, fig.cap="Capture-Recapture Frequency Statistics"}
plot(desc)
 \newpage
Hierarchical Models
 ### More Interactions: Better Fit
We start by fitting three simple models. The first, and simplest, is the model that assumes independence between the four systems. The second model lo
 \begin{aligned}
 \text{text}(Model 1:) \quad \log(\hat{N}) = \alpha + \
 \label{log(hat{N}) &= \alpha_1 + \lambda_2 + \lambda_2 + \lambda_3 + \lambda_4 + \lambda_2 + \lambda_3 + \lambda_4 + \lambda_4 + \lambda_2 + \lambda_3 + \lambda_4 +
 \label{eq:lambda} \ + \lambda_{24} + \lambda_{34}
 \label{log(hat{N}) &= \alpha_1 + \beta_2 + \beta_3 + \beta_4 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \beta_4 + \beta_2 + \beta_3 + \beta_4 +
 \label{eq:lambda_23} $$ \lambda_{23} + \lambda_{24} + \lambda_{34} + \lambda_{123} + \lambda_{234} + \lambda_{
\end{aligned}
```

We perform log-likelihood ratio test and see that the higher the order of the interaction, the better the fit (with saturated model signifying a perfec file:///C:/Users/MarEichler17/Documents/MYE-Documents/SCHOOL/Northwestern/Courses/STAT455/STAT455-Fall2019/Project/Categorical-FinalProj... 5/7

```
\$G^{2}=2 \sum_{i} n_{i} \log \left(n_{i} / \hat{m}_{i}\right)=\sum_{i} d_{i}
We perform log-likelihood ratio test and see that the higher the order of the interaction, the greater the deviance explained. Each LRT for the nested m
 {r hierch_models1}
independence_model <- loglm(new_Freq ~ security_ind + forensic_ind + judicial_ind + civil_ind, data=test)</pre>
no_three <- loglm(new_Freq ~ security_ind*forensic_ind + security_ind*judicial_ind + security_ind*civil_ind + forensic_ind*judicial_ind + forensic_ind*c
no_four_way <- loglm(new_Freq ~ security_ind*forensic_ind*judicial_ind*civil_ind - security_ind:forensic_ind:judicial_ind:civil_ind, data=test)
anovafit <- anova(independence_model, no_three, no_four_way, test="LR") #LRT</pre>
anova.table <- anovafit[1:4,]</pre>
knitr::kable(anova.table, format="latex", booktabs=T, caption="ANOVA for 3 standard models") %>%
kableExtra::kable_styling(latex_options = "HOLD_position")
Iterative Proportional Fitting
We will use iterative proportional fitting to estimate N. The iterative proportional fitting process generates maximum likelihood estimates of the ex
Here the marginal subtables would be:
1. Security by Judicial by Forensic systems
2. Security by Forensic by Civil systems
3. Judicial by Forensic by Civil systems
4. Judicial by Civil by by Security systems
To do this four-dimensional IPF:
1. Proportionally adjust each (three-dimensional) row of cells to equal the pre-determined totals of Marginal 1.
2. Proportionally adjust each column of cells to equal the pre-determined totals of Marginal 2.
3. Proportionally adjust each slice of cells to equal the pre-determined totals of Marginal 3.
4. Proportionally adjust each stack of cells to equal the pre-determined totals of Marginal 4. This is the end of the first 'Iteration'.
5. Repeat the above steps until the desired level of convergence is reached.
Under mild restrictions, we know that the cell-values at the end of this process that satisfy the fitted marginal totals are the MLEs.
Results
Using iterative proportional fitting, we fit all possible second-order interaction models (we restrict to second-order to aid interpretation). These wil
We choose he best model according to the BIC criteria, is below: estimates a total for missing/disappeared people as 8817, which is similar to the $8
```{r hierch-models2}
hierch_models <- closedpMS.t(test, dfreq=T ,h='Poisson', maxorder = 2) #restrict to second order interactions
Top <- hierch_models$results[1:5,]</pre>
Middle <- hierch models$results[30:34,]
Bottom <- hierch_models$results[60:64,]</pre>
HierchModels <- rbind(Top, Middle, Bottom)</pre>
rnames <- rownames(HierchModels)</pre>
rownames(HierchModels)<- gsub("\\[|\\]", "", rnames)</pre>
#get rid fo brackets otherwise booktabs goes all wonky
knitr::kable(HierchModels[,1:6], format="latex"
                        , booktabs=T
                         , caption="`Top' Five, `Middle' Five, and `Bottom' Five Models (Hierarchical models)") %>%
   #kableExtra::kable_styling(latex_options="scale_down") %>%
kableExtra::kable_styling(latex_options = "HOLD_position")
     {r estimaterange}
MAX.EST <- max(hierch_models$results[,1])
MIN.EST <- min(hierch_models$results[,1])
results <- as.data.frame(cbind("abundance"=hierch_models$results[,1], "BIC"=hierch_models$results[,6] ))
BIC.results <- results[results$BIC < 300,]
MAX.goodBIC.EST <- max(BIC.results[,1])
MIN.goodBIC.EST <- min(BIC.results[,1])</pre>
We can see that the independence model listed as "1,2,3,4" has the worst fit -- this is to be expected, as we have demonstrated in previous sections the
The shorthand "14,2,3" means that lists 1 and 4 are independent of 2, and also independent of list 3, i.e. $(1,4) \indep 2$ and $(1,4) \indep 3$. It is
\sl(N) = \alpha_1 + \lambda_1 + \lambda_2 + \lambda_3 + \lambda_4 + \lambda
The shorthand identifies both the model and the margins that must be fitted to obtain MLEs using IPF. Not all shorthands have a conditional independence
These the hierarchical models have different estimates, ranging from 5053 to 9268.
We also plot the BIC values for different models and their accompanying estimates of $\hat{N}$. When we only look at estimates with a corresponding BIC
```{r hierch-modelsBIC, fig.cap="Hiercharical Models BIC Plot"}
plot(hierch_models) #BIC for a bunch of different models
This is the fundamental problem of the frequentist approach. We could just pick the "best" model, i.e., the one with the lowest BIC (note the y-axis is
Unfortunately, just picking one model ignores the error that we introduce by the selection itself. It also forces us to decide which dependencies among
Conclusions
Our findings show that the total number of deaths and disappearances in Casanare is far greater than previously assessed. The initial analysis made by G
```

```
Importantly, given estimation techniques used in our analysis, there is strong evidence that the true total of victims is actually much higher than 3,50
As can be seen, there is a lot of uncertainty about the true total of deaths and disappearances. Nevertheless, the number of deaths and disappearances w
References
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```{r printcode}
#PRINTING THE CODE
#knitr::stitch("HW06.Rmd") to go to latex
                 script="Categorical-FinalProject.Rmd" , system.file("misc", "knitr-template.Rhtml", package="knitr")) #code to HTML
#knitr::stitch(
## Error: <text>:10:3: unexpected input
## 9: header-includes:
## 10: - \
```

The R session information (including the OS info, R version and all packages used):

```
sessionInfo()
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 17763)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252 LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252 LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] grid
                stats
                          graphics grDevices utils
                                                        datasets methods base
##
## other attached packages:
##
   [1] png_0.1-7
                         kableExtra_1.1.0 bookdown_0.12
                                                          MASS 7.3-51.4
                                                                          rgeos_0.5-2
                        Rcapture_1.4-2 raster_3.0-7 janitor 1.2.0 forcats 0.4.6
##
   [6] dga 1.2
                                                          sf 0.8-0
                                                                           rgdal 1.4-8
                                                          stringr_1.4.0
                                         forcats 0.4.0
## [11] sp 1.3-1
                                                                          dplvr 0.8.3
                                                          tibble_2.1.3
##
  [16] purrr_0.3.2
                        readr_1.3.1
                                         tidyr_1.0.0
                                                                           ggplot2_3.2.1
## [21] tidyverse_1.2.1
##
## loaded via a namespace (and not attached):
##
   [1] Rcpp_1.0.2
                          lubridate 1.7.4
                                             lattice 0.20-38
                                                                class 7.3-15
##
   [5] assertthat 0.2.1
                          zeallot 0.1.0
                                             digest 0.6.20
                                                                R6 2.4.0
##
   [9] cellranger_1.1.0
                          chron_2.3-54
                                             backports 1.1.4
                                                                evaluate_0.14
## [13] e1071_1.7-2
                          highr_0.8
                                             httr_1.4.1
                                                                pillar_1.4.2
                          lazyeval_0.2.2
## [17] rlang_0.4.0
                                             readxl_1.3.1
                                                                rstudioapi_0.10
## [21] rmarkdown_1.14
                          labeling_0.3
                                             webshot 0.5.1
                                                                munsell 0.5.0
## [25] broom 0.5.2
                          compiler_3.6.1
                                             modelr 0.1.5
                                                                xfun 0.8
## [29] pkgconfig_2.0.2
                          htmltools 0.3.6
                                             tidyselect_0.2.5
                                                                gridExtra_2.3
## [33] codetools 0.2-16 viridisLite 0.3.0 crayon 1.3.4
                                                                withr 2.1.2
  [37] nlme_3.1-140
                          jsonlite_1.6
                                             gtable_0.3.0
                                                                lifecycle_0.1.0
##
  [41] DBI_1.0.0
                          magrittr_1.5
                                              units 0.6-5
                                                                scales 1.0.0
## [45] KernSmooth_2.23-15 cli_1.1.0
                                             stringi_1.4.3
                                                                snakecase_0.11.0
## [49] xml2 1.2.2
                      ellipsis_0.2.0.1
                                             generics_0.0.2
                                                                vctrs_0.2.0
## [53] tools 3.6.1
                          glue 1.3.1
                                             hms 0.5.0
                                                                vaml 2.2.0
## [57] colorspace 1.4-1 classInt 0.4-2
                                             rvest_0.3.4
                                                                knitr 1.24
## [61] haven_2.1.1
   Sys.time()
## [1] "2019-12-05 09:59:46 CST"
```