

Latest_Analysis

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Initial Set up

Load packages and set the seed for reproducibility

```
#Downloaded packages
library(phyloseq)
library(dada2)
library(ggplot2)
library(biom)
library(devtools)
library(knitr)
library(mixOmics)
library(tidyverse)
library(vegan)
library(mixOmics)
library(readxl)
library(tableone)
library(ReporteRs)
library(magrittr)
library(plyr)
library(RColorBrewer)
library(DESeq2)
library(edgeR)
library(dplyr); packageVersion("dplyr")

## [1] '0.5.0'

#If error in phyloseq load visit this page <https://joey711.github.io/phyloseq/install.html>

set.seed(08152017)
```

Import Meta Data

Import Meta Data as DataFrame

Inorder to input using this code, ensure the file path matches the path to the file on your computer. The file listed is found in the “Latest” folder of the AG data within the sub-folder containing the meta data. Download it to your computer and rewrite the code.

```
library(readr)
Meta <- read_delim("~/Desktop/ag-cleaned.txt", #file path name
  "\t", escape_double = FALSE, col_types = cols(AGE_YEARS = col_number(),
    BMI = col_number(), BMI_CORRECTED = col_number(), "#SampleID" = col_character(), `ENA-BASE-COUNT` =col_number(),HEIGHT_CM = col_number(), VIOSCREEN_FIBER = col_number(),
    VIOSCREEN_LOW_FAT_DAIRY_SERVING = col_number(),
    VIOSCREEN_LYSINE = col_number(),
    VIOSCREEN_MANNITOL = col_number(),
    VIOSCREEN_SFA100 = col_double(), #capric acid
    VIOSCREEN_SFA40 = col_double(),#SFA4:0 Butyric Acid
    VIOSCREEN_SFA170 = col_double(), #margaric acid
    VIOSCREEN_VEG5_DAY = col_number(),
    VIOSCREEN_VEGETABLE_SERVINGS = col_number(),
    chaol_1k = col_double()), trim_ws = TRUE)
```

Data Exploration for demographic information

Here I have summarized only a few of the variables in the dataset. In order to find summaries of other variables replace the variable name in the code.

Univariate Exploration

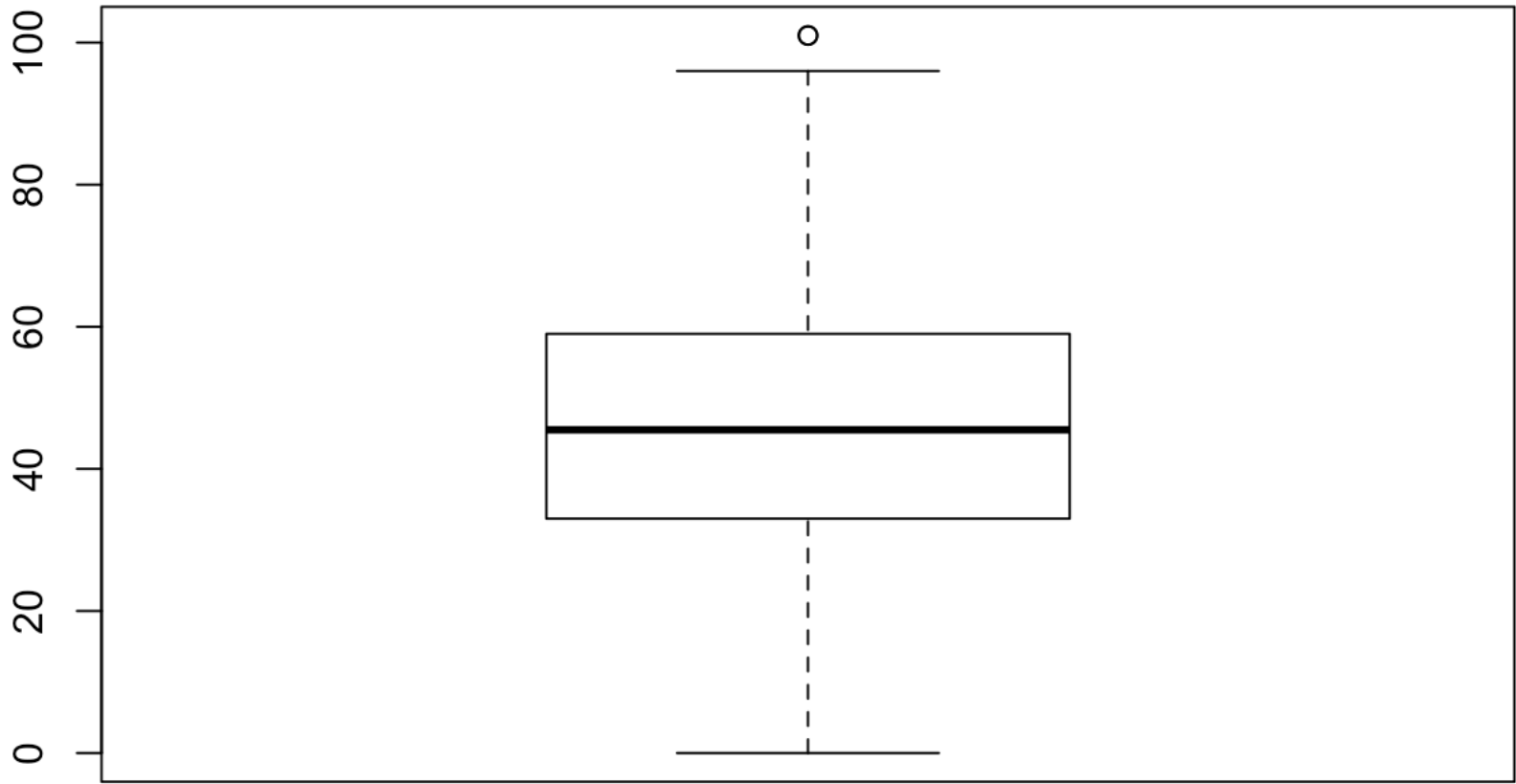
```
#Summary Statistics for continuous variables.
summary(Meta$AGE_YEARS)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      0.00   33.00   45.50   44.75   59.00  101.00   580
```

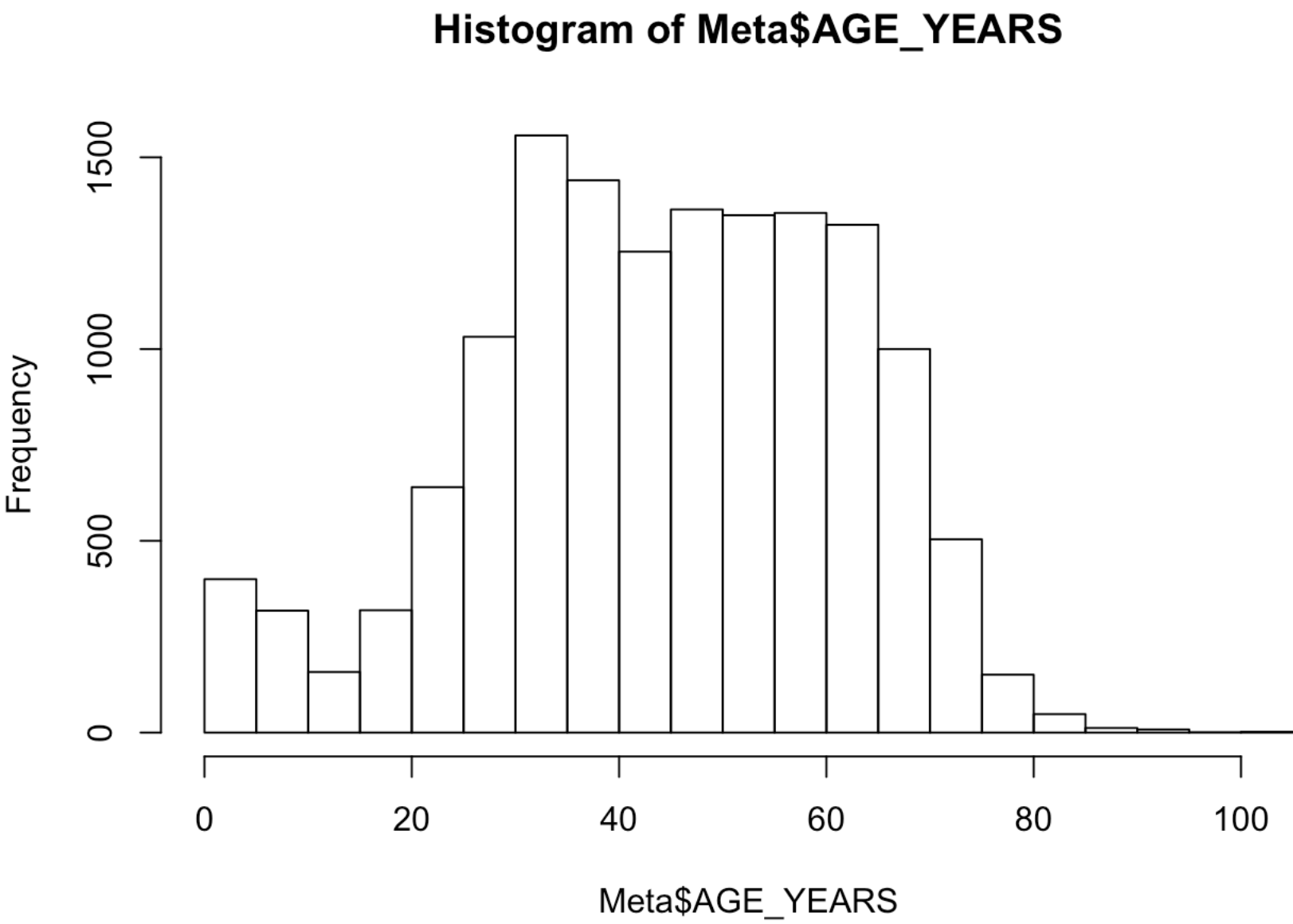
```
summary(Meta$BMI_CORRECTED) #BMI as listed in variable "BMI" listed has implausible values the corrected version has 8213 missing values and a max BMI of 76.89
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
##	9.63	20.81	23.24	23.90	26.32	76.89	8213

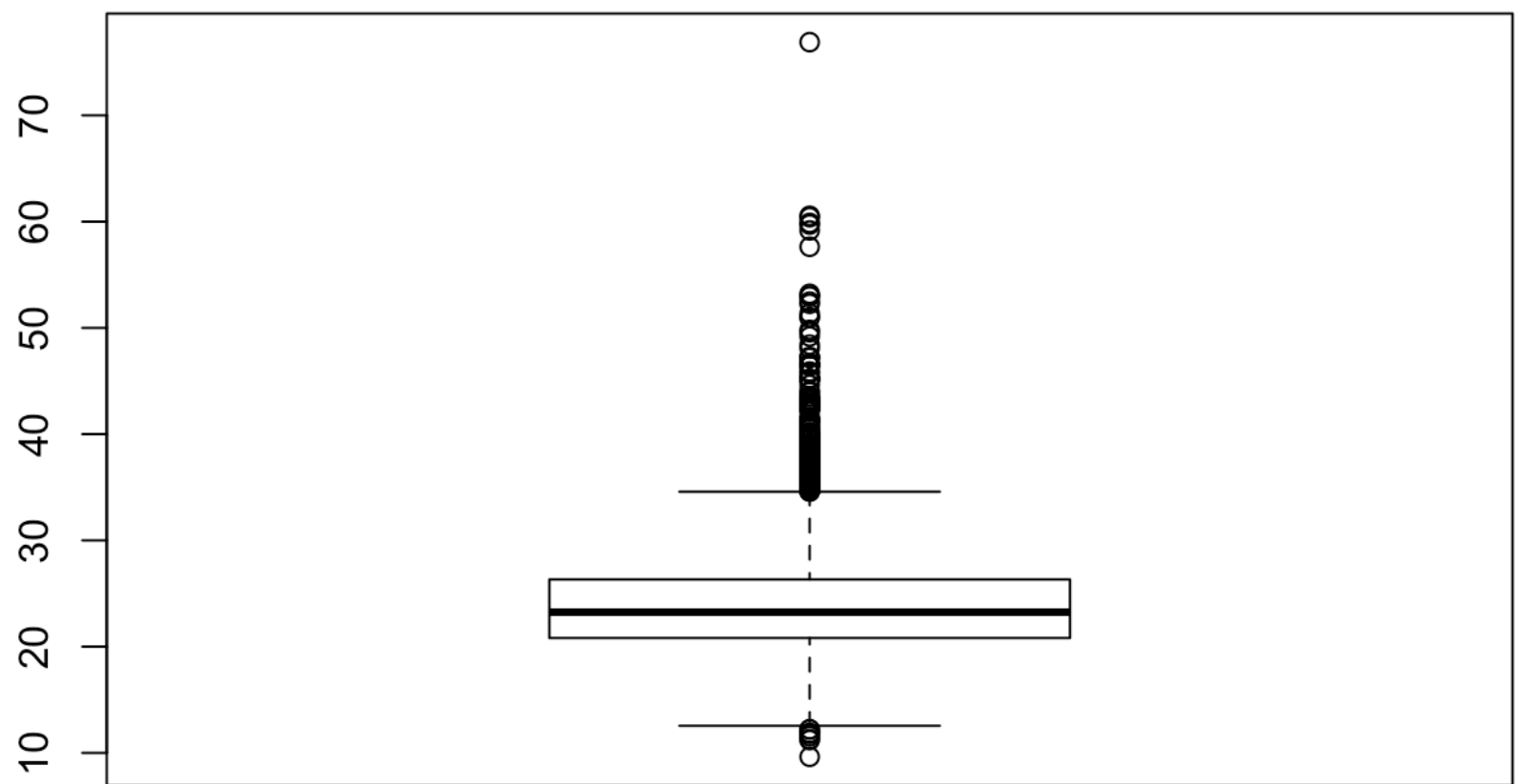
```
#Data Visualization
boxplot(Meta$AGE_YEARS)
```



```
hist(Meta$AGE_YEARS)
```

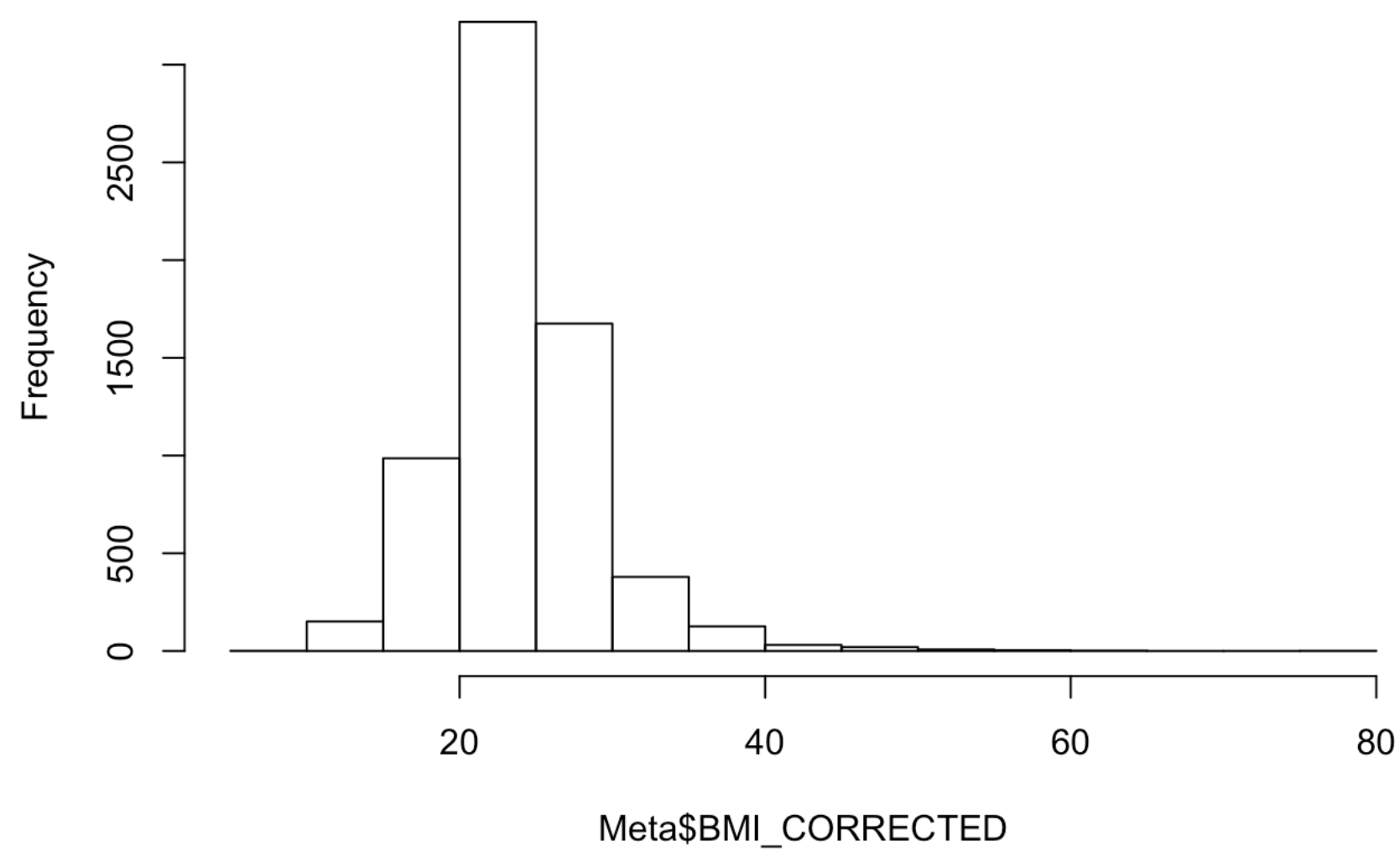


```
boxplot(Meta$BMI_CORRECTED)
```

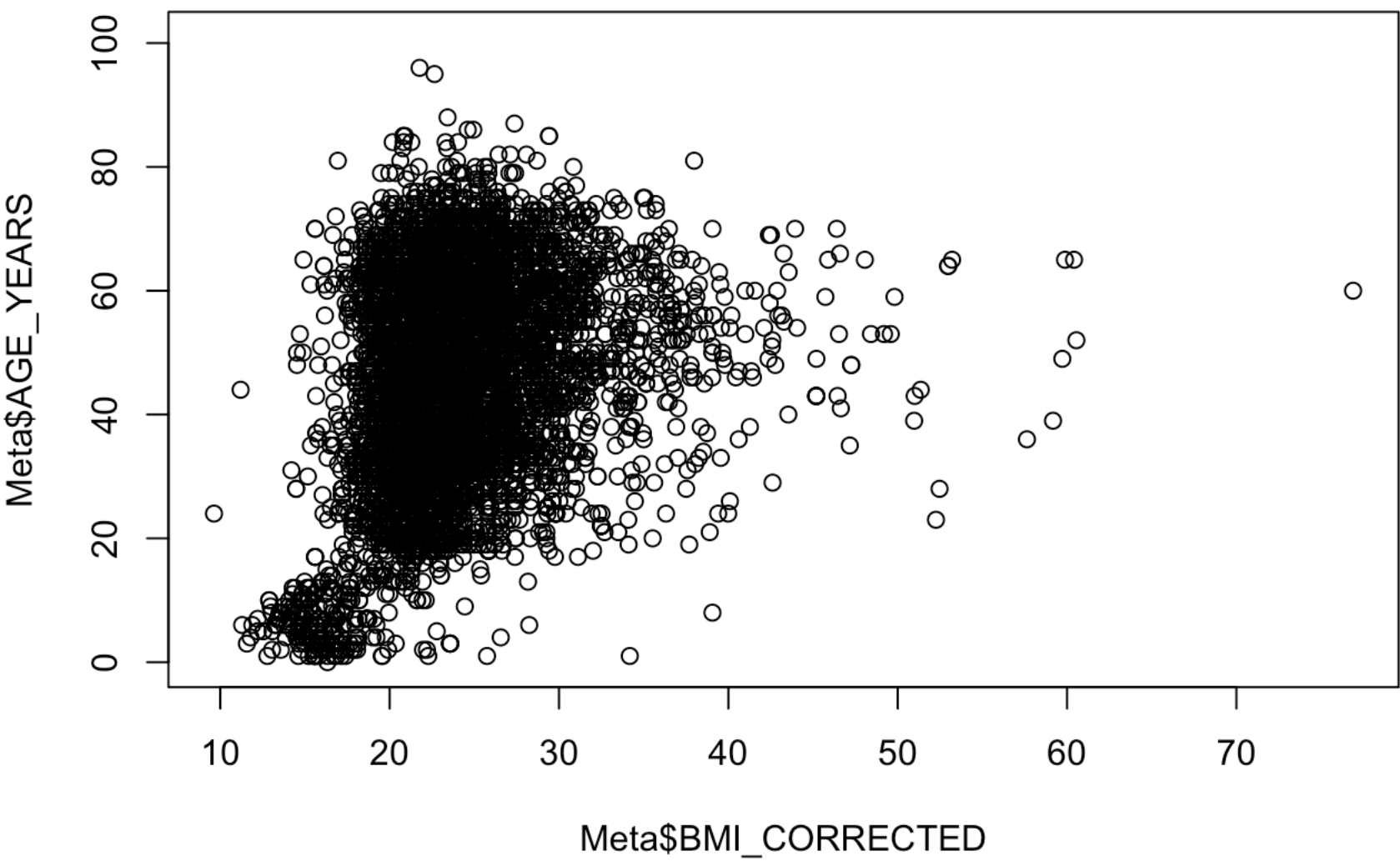


```
hist(Meta$BMI_CORRECTED)
```

Histogram of Meta\$BMI_CORRECTED



```
#Scatterplot BMI*AGE to observe for any trends  
plot(Meta$BMI_CORRECTED, Meta$AGE_YEARS)
```



```
#Summary Of Categorical Variables

Categ_BodySite<- summary(as.factor(Meta$BODY_SITE))
Categ_BodySite
```

##	UBERON:feces	UBERON:nostril	UBERON:skin of hand
##	12811	192	454
##	UBERON:skin of head	UBERON:tongue	
##	323	1036	

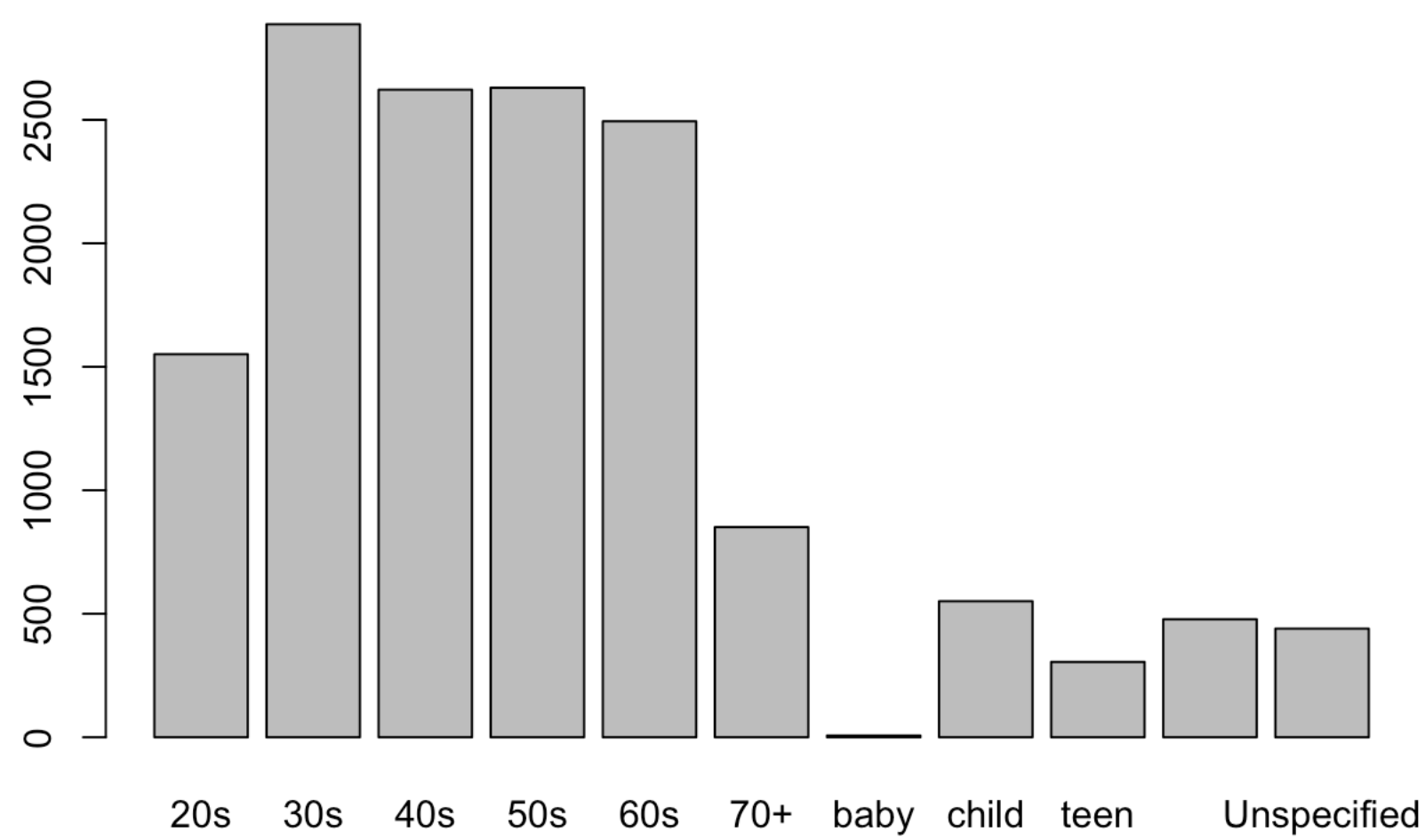
```
barplot(Categ_BodySite)
```



```
Categ_Age<- summary(as.factor(Meta$AGE_CAT))
Categ_Age
```

##	20s	30s	40s	50s	60s	70+
##	1551	2887	2622	2630	2494	851
##	baby	child	teen	Unknown	Unspecified	
##	7	551	305	478	440	

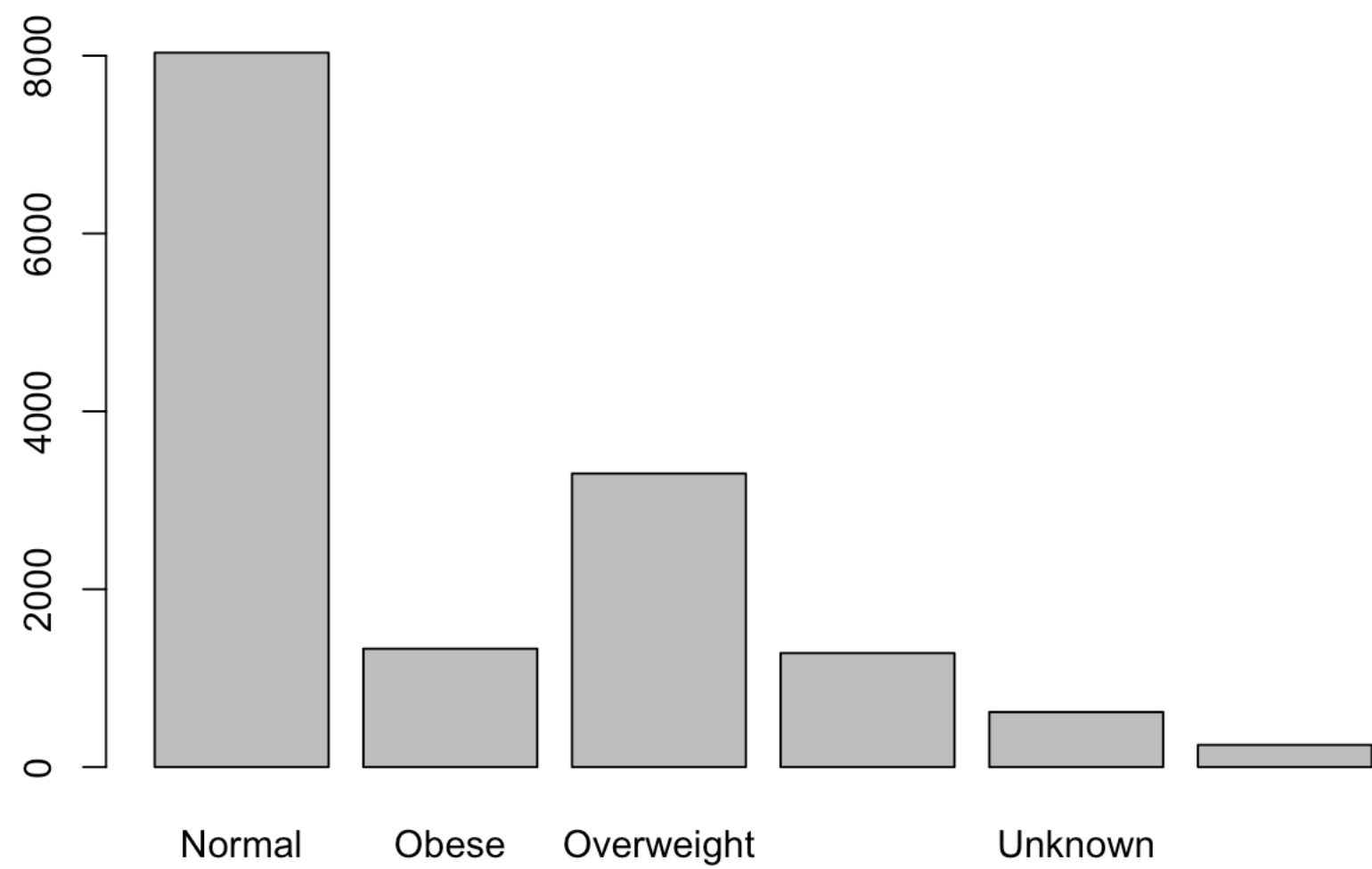
```
barplot(Categ_Age)
```



```
Categ_BMI<- summary(as.factor(Meta$BMI_CAT))
Categ_BMI
```

##	Normal	Obese	Overweight	Underweight	Unknown	Unspecified
##	8034	1331	3301	1282	619	249

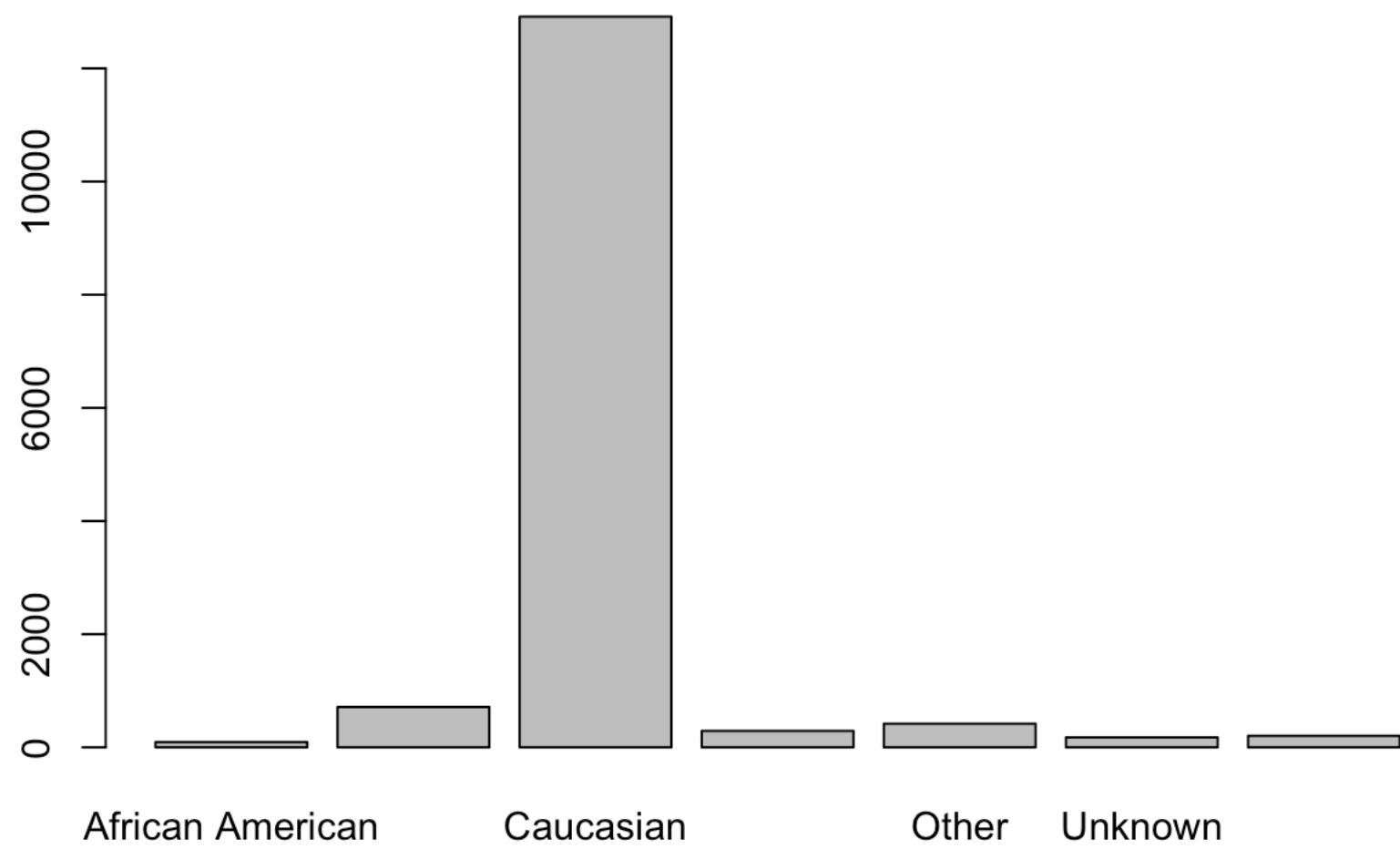
```
barplot(Categ_BMI)
```



```
Categ_Race<- summary(as.factor(Meta$RACE))
Categ_Race
```

##	African American	Asian or Pacific Islander
##	94	714
##	Caucasian	Hispanic
##	12916	292
##	Other	Unknown
##	419	177
##	Unspecified	
##	204	

```
barplot(Categ_Race)
```



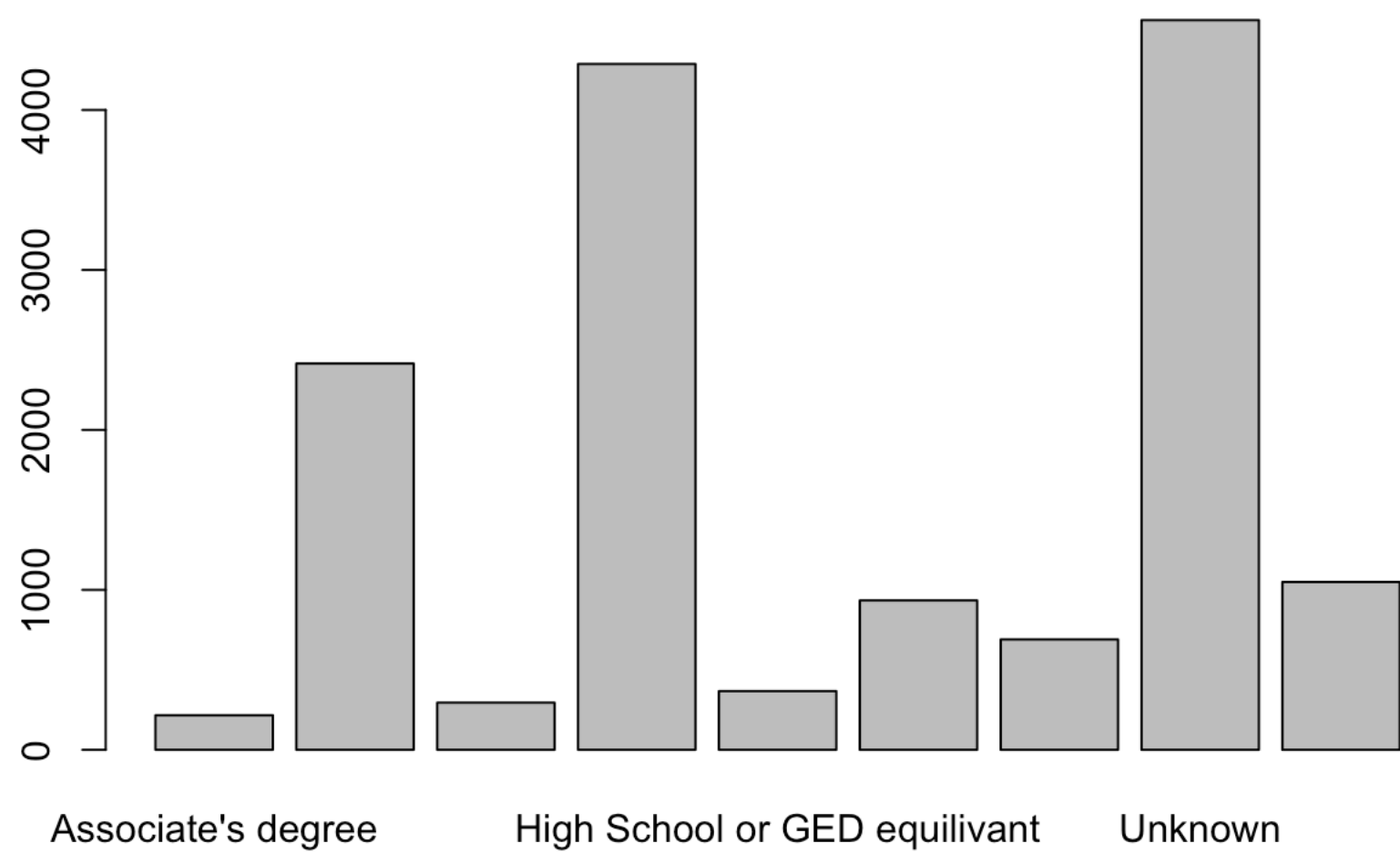
```
Categ_Sex<- summary(as.factor(Meta$SEX))  
Categ_Sex
```

##	female	male	other	Unknown	unspecified
##	7423	6639	14	517	223

```
Categ_Education<- summary(as.factor(Meta$LEVEL_OF_EDUCATION))  
Categ_Education
```

##	Associate's degree	Bachelor's degree
##	216	2415
##	Did not complete high school	Graduate or Professional degree
##	295	4288
##	High School or GED equivlivan	Some college or technical school
##	367	934
##	Some graduate school or professional	Unknown
##	690	4562
##	Unspecified	
##	1049	

```
barplot(Categ_Education)
```



```
Categ_Region<- summary(as.factor(Meta$COUNTRY_RESIDENCE))
Categ_Region
```

##	Australia	Austria
##	94	9
##	Belgium	Belize
##	15	1
##	Brazil	Canada
##	2	61
##	China	Croatia
##	2	2
##	Czech Republic	Denmark
##	4	5
##	Finland	France
##	3	28
##	Georgia	Germany
##	1	38
##	Greece	Hong Kong
##	2	7
##	Iceland	India
##	1	24
##	Ireland	Isle of Man
##	52	4
##	Israel	Italy
##	2	17
##	Japan	Jersey
##	5	2
##	Malta	Mexico
##	1	2
##	Morocco	Netherlands
##	35	15
##	New Zealand	no_data
##	5	7262
##	Norway	Portugal
##	9	4
##	Puerto Rico	Romania
##	1	1
##	Saudi Arabia	Serbia
##	1	5
##	Singapore	Slovakia
##	3	3
##	Spain	Sweden
##	6	30
##	Switzerland	Tanzania, United Republic of
##	61	2
##	Thailand	United Arab Emirates
##	2	4
##	United Kingdom	United States
##	1712	2982
##	Unknown	Unspecified
##	1073	1216

```
Categ_Birth_Country<- summary(as.factor(Meta$COUNTRY_OF_BIRTH))
Categ_Birth_Country
```

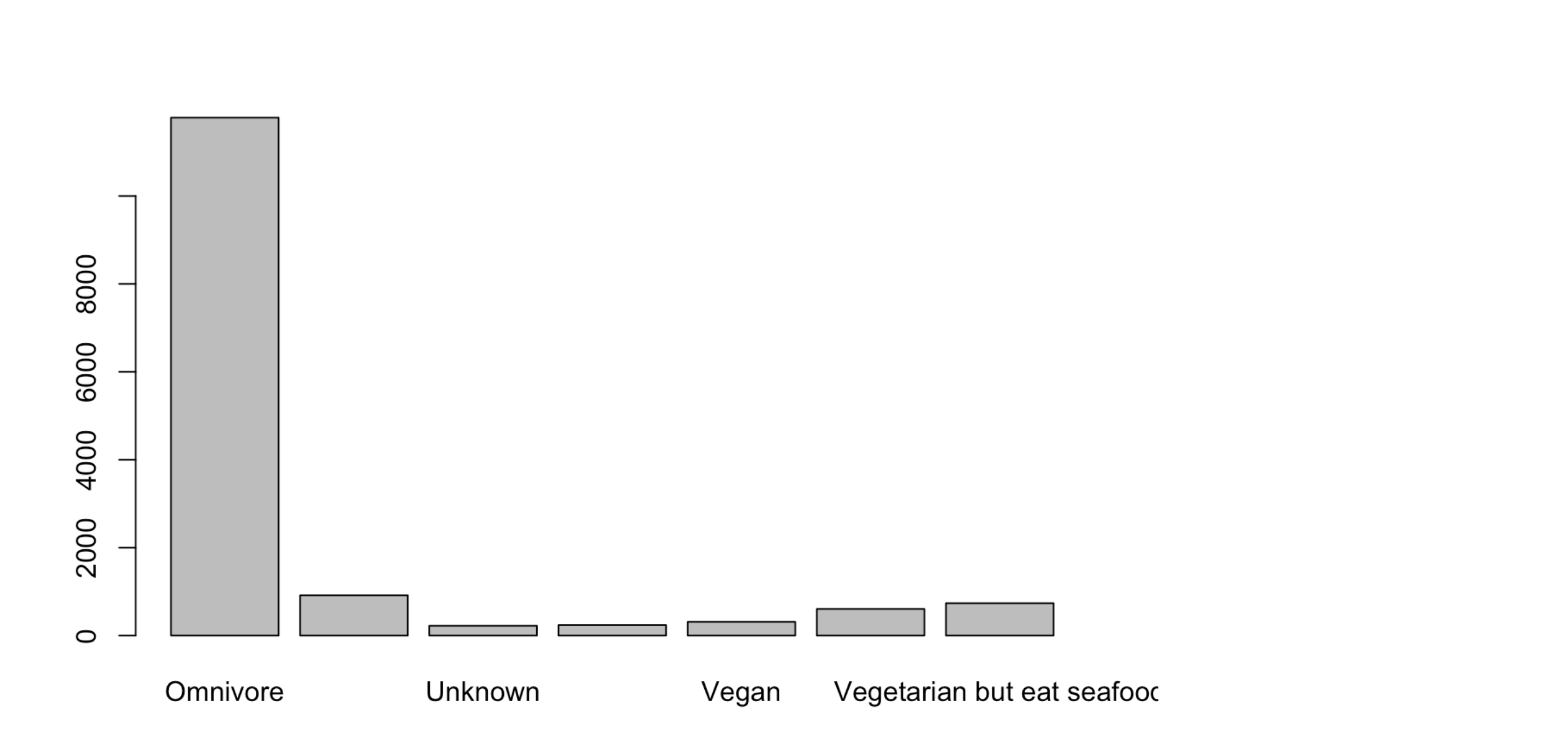
##	United States	United Kingdom
##	9312	2566
##	Australia	Canada
##	341	323
##	Germany	Unspecified
##	185	171
##	India	Unknown
##	150	138
##	Belgium	France
##	114	100
##	Ireland	Poland
##	98	57
##	Italy	Switzerland
##	56	54
##	South Africa	Sweden
##	52	51
##	Iran, Islamic Republic of	New Zealand
##	49	47
##	China	Brazil
##	46	45
##	Netherlands	Spain
##	44	44
##	Hong Kong	Russian Federation

##	39	38
##	Japan	Mexico
##	32	31
##	Afghanistan	Korea, Republic of
##	26	26
##	Denmark	Hungary
##	22	22
##	Norway	Austria
##	22	21
##	Philippines	Israel
##	21	20
##	Czech Republic	Bulgaria
##	19	18
##	Taiwan, Province of China	Malaysia
##	17	16
##	Greece	Puerto Rico
##	15	15
##	Romania	Thailand
##	14	14
##	Finland	Portugal
##	12	12
##	Morocco	Pakistan
##	11	11
##	Singapore	Ukraine
##	11	11
##	Croatia	Indonesia
##	10	10
##	Colombia	Cyprus
##	9	9
##	Zimbabwe	Serbia
##	9	8
##	Sri Lanka	Viet Nam
##	8	8
##	Argentina	Lebanon
##	7	7
##	Tanzania, United Republic of	Turkey
##	7	7
##	Zambia	Belarus
##	7	6
##	Cuba	Nigeria
##	6	6
##	Slovakia	Jamaica
##	6	5
##	Lithuania	Peru
##	5	5
##	Venezuela	Bangladesh
##	5	4
##	Chile	Dominican Republic
##	4	4
##	Egypt	El Salvador
##	4	4
##	Ethiopia	Kuwait
##	4	4
##	Latvia	Malta
##	4	4
##	Saudi Arabia	United States Minor Outlying Islands
##	4	4
##	Bosnia and Herzegovina	Guatemala
##	3	3
##	Iceland	Kenya
##	3	3
##	Paraguay	Uganda
##	3	3
##	United Arab Emirates	Albania
##	3	2
##	Algeria	Azerbaijan
##	2	2
##	Bermuda	Costa Rica
##	2	2
##	Ecuador	Libyan Arab Jamahiriya
##	2	2
##	Luxembourg	Malawi
##	2	2
##	Mauritius	Panama
##	2	2
##	Syrian Arab Republic	(Other)
##	2	18

```
Categ_Diet<- summary(as.factor(Meta$DIET_TYPE))
Categ_Diet
```


##	Omnivore	Omnivore but do not eat red meat
##	11783	917
##	Unknown	Unspecified
##	224	238
##	Vegan	Vegetarian
##	312	605
##	Vegetarian but eat seafood	
##	737	

```
barplot(Categ_Diet)
```



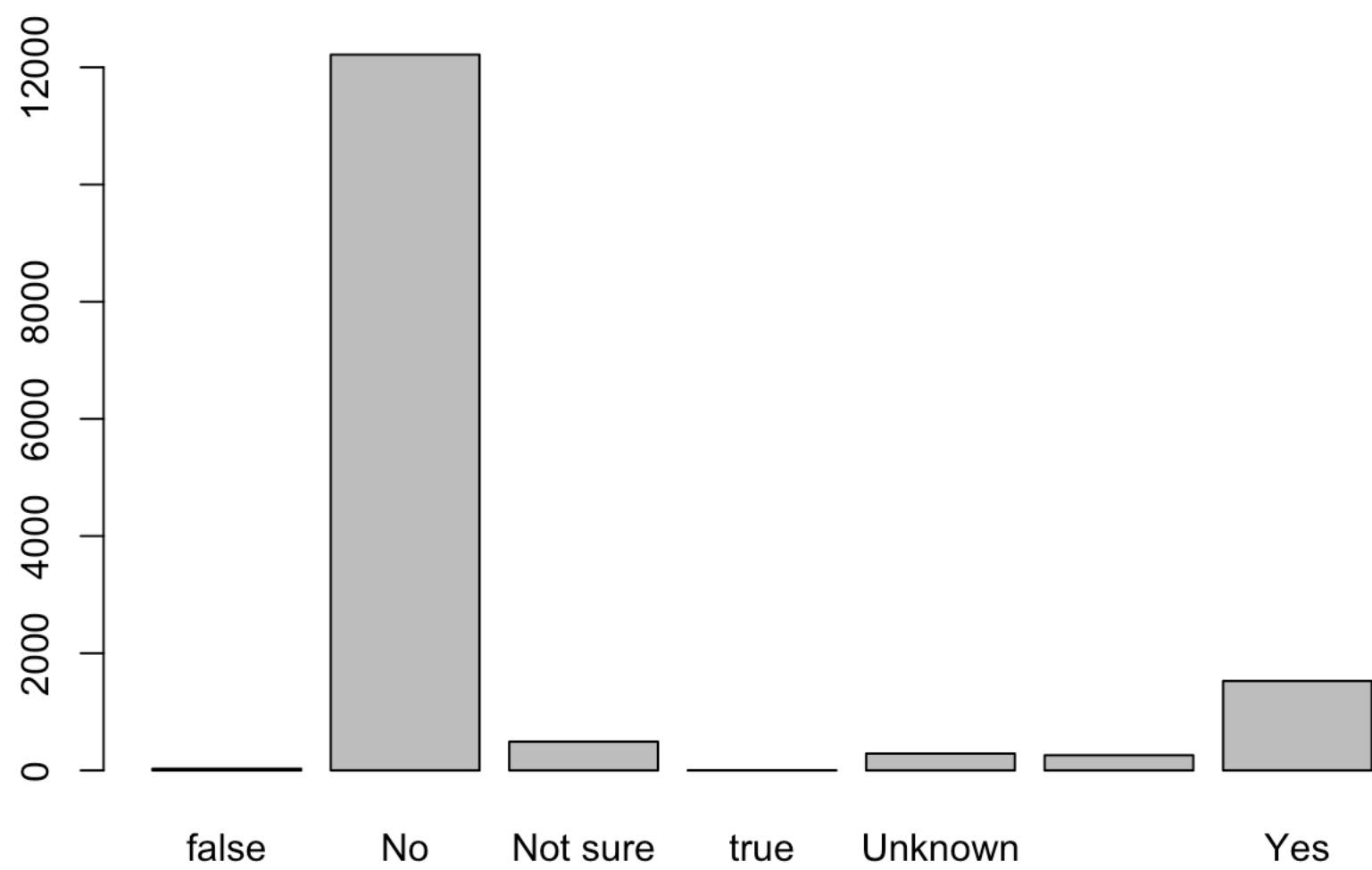
```
Categ_Pregnant<- summary(as.factor(Meta$PREGNANT))
Categ_Pregnant
```

##	false	No	Not sure	true	Unknown	Unspecified
##	600	10066	41	1	3367	672
##	Yes					
##	69					

```
Categ_Delivery<- summary(as.factor(Meta$CSECTION))
Categ_Delivery
```

##	false	No	Not sure	true	Unknown	Unspecified
##	30	12217	491	2	289	260
##	Yes					
##	1527					

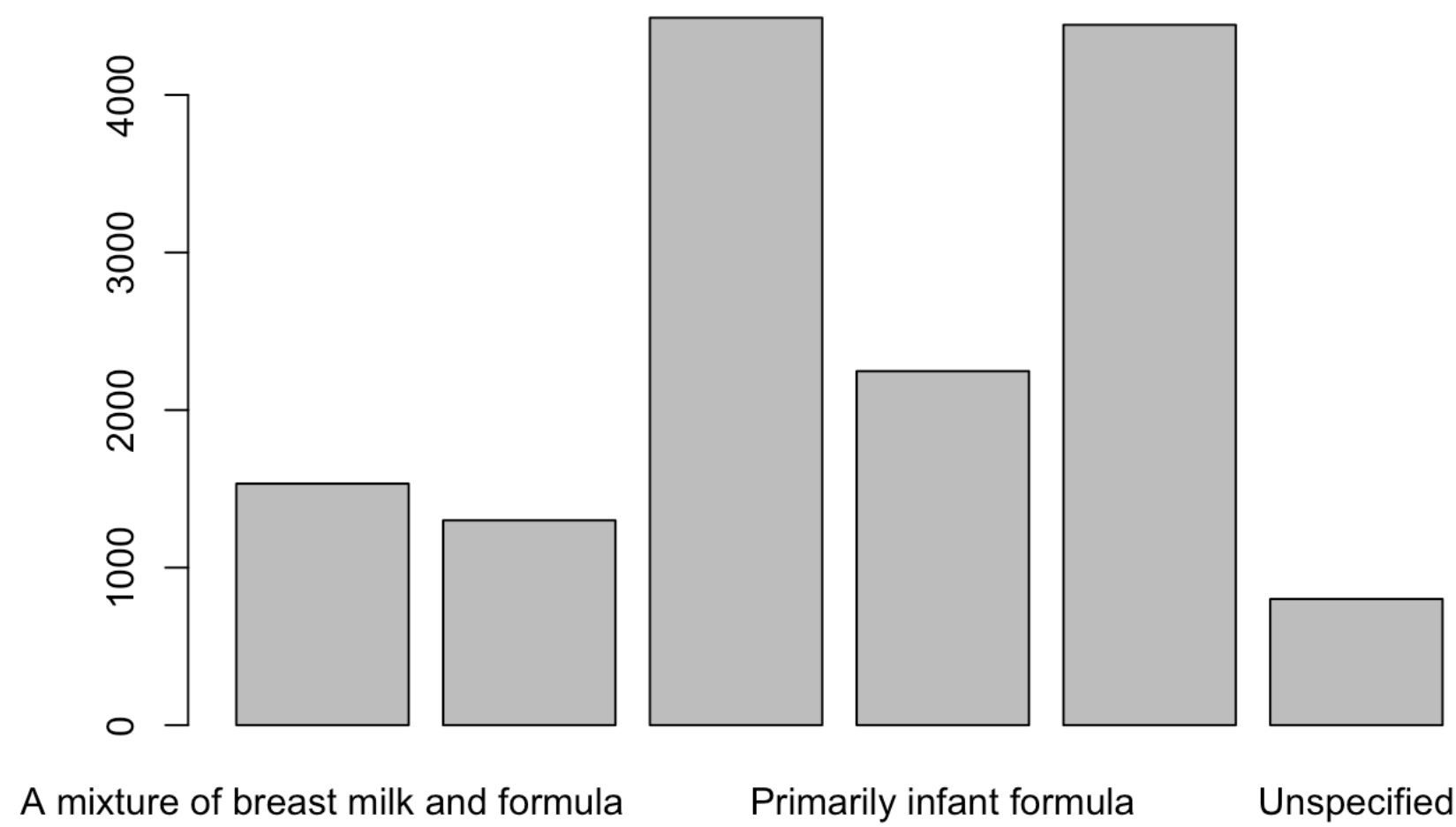
```
barplot(Categ_Delivery) #CSECTION=TRUE
```



```
Categ_Fed<- summary(as.factor(Meta$FED_AS_INFANT))
Categ_Fed
```

```
## A mixture of breast milk and formula          Not sure
##                1533                        1300
##      Primarily breast milk      Primarily infant formula
##                4490                        2247
##                Unknown          Unspecified
##                4445                        801
```

```
barplot(Categ_Fed)
```



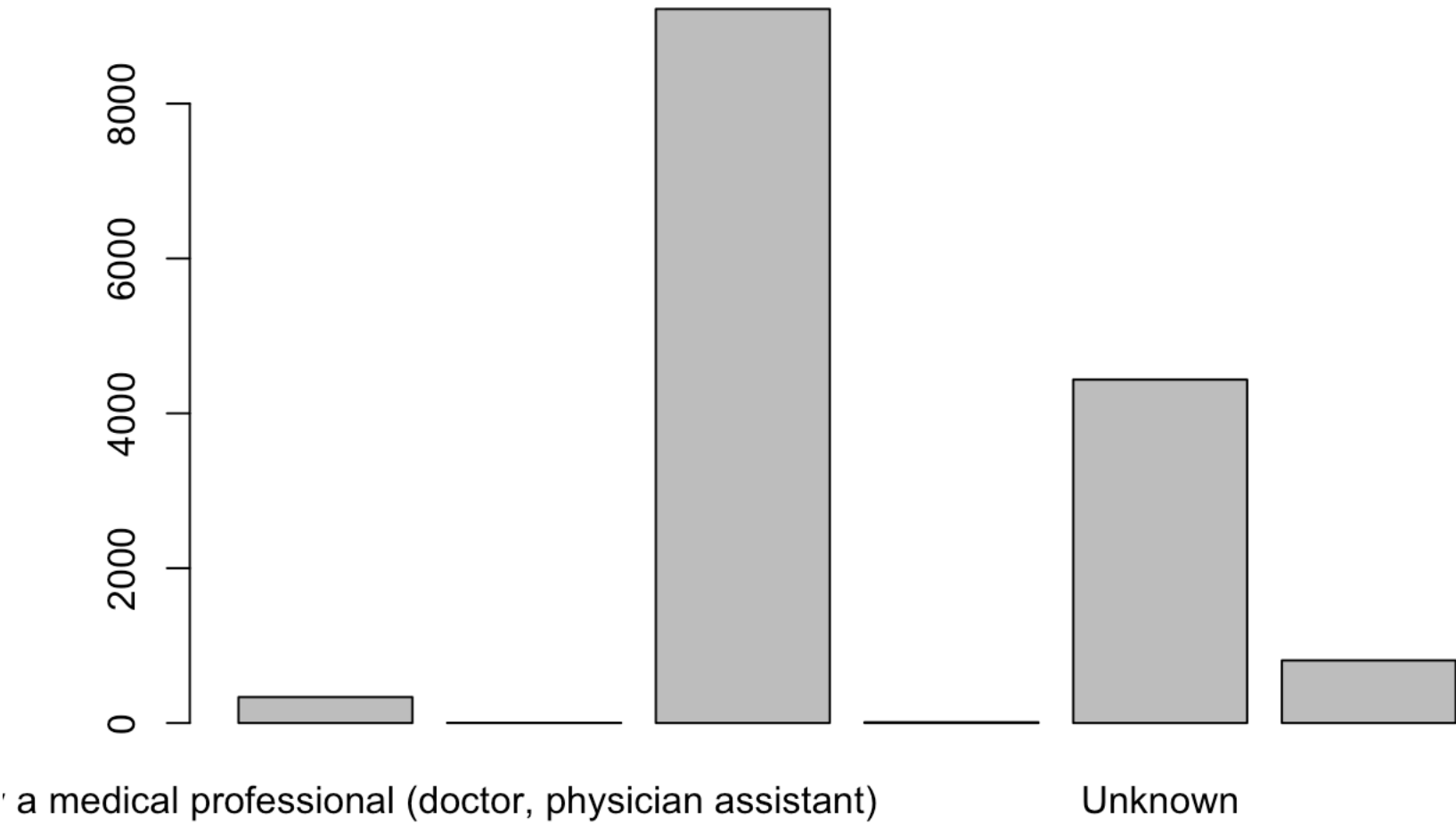
```
Categ_Healthy<- summary(as.factor(Meta$SUBSET_HEALTHY))
Categ_Healthy
```

```
## false False  true  True
##   5566  2995  3842  2413
```

```
Categ_CVD<- summary(as.factor(Meta$CARDIOVASCULAR_DISEASE))
Categ_CVD
```

```
## Diagnosed by a medical professional (doctor, physician assistant)
##                                     335
##           Diagnosed by an alternative medicine practitioner
##                                     3
##           I do not have this condition
##                                     9223
##           Self-diagnosed
##                                     10
##           Unknown
##                                     4436
##           Unspecified
##                                     809
```

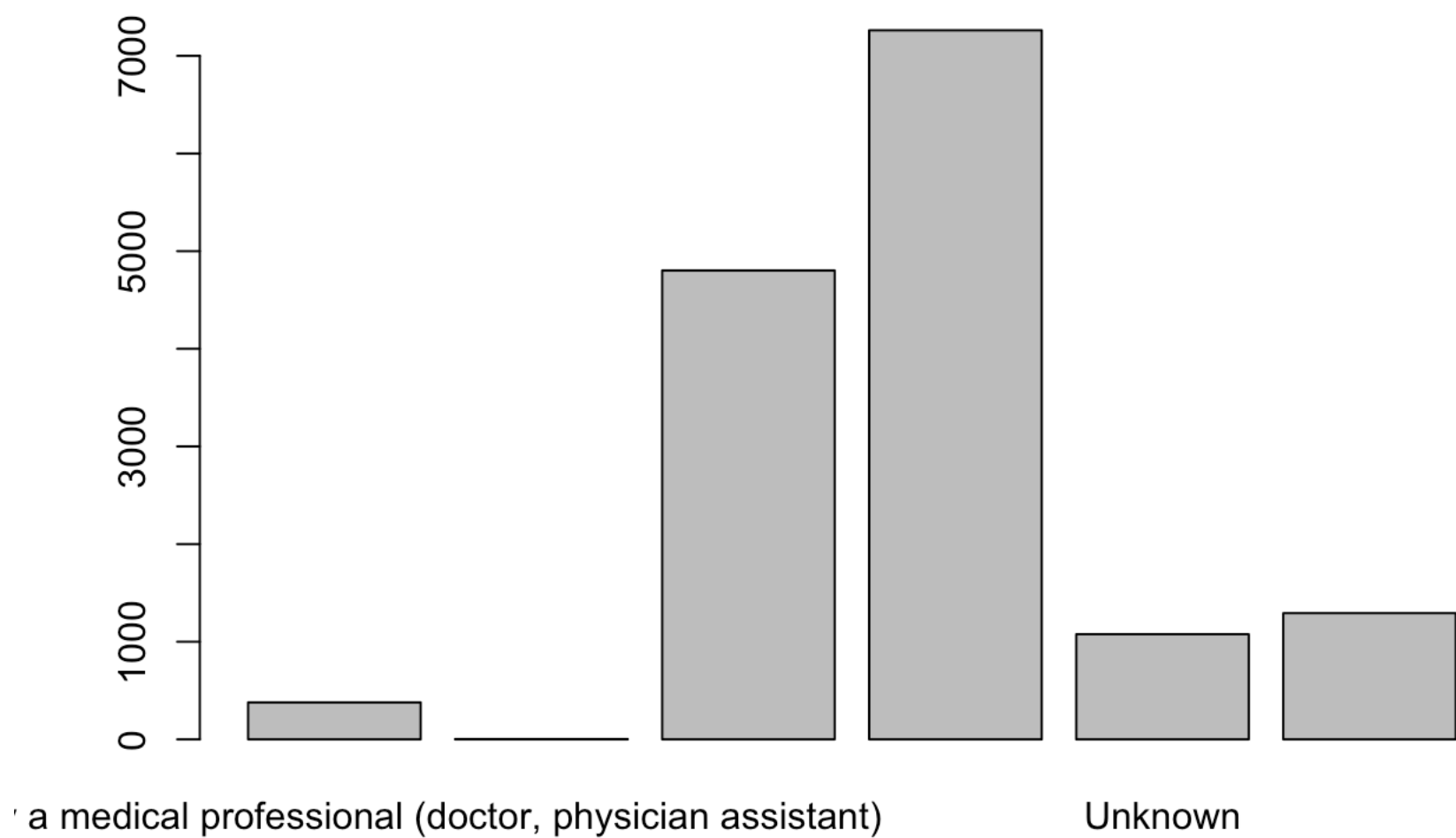
```
barplot(Categ_CVD)
```



```
Categ_Cancer<- summary(as.factor(Meta$CANCER))
Categ_Cancer
```

```
## Diagnosed by a medical professional (doctor, physician assistant)
##                                     379
##           Diagnosed by an alternative medicine practitioner
##                                     3
##           I do not have this condition
##                                     4802
##           no_data
##                                     7262
##           Unknown
##                                     1077
##           Unspecified
##                                     1293
```

```
barplot(Categ_Cancer)
```



```
Categ_Diabetes<- summary(as.factor(Meta$DIABETES))  
Categ_Diabetes
```

```
## Diagnosed by a medical professional (doctor, physician assistant)  
##                                     203  
##           Diagnosed by an alternative medicine practitioner  
##                                     3  
##           I do not have this condition  
##                                13934  
##           Self-diagnosed  
##                                     12  
##           Unknown  
##                                396  
##           Unspecified  
##                                268
```

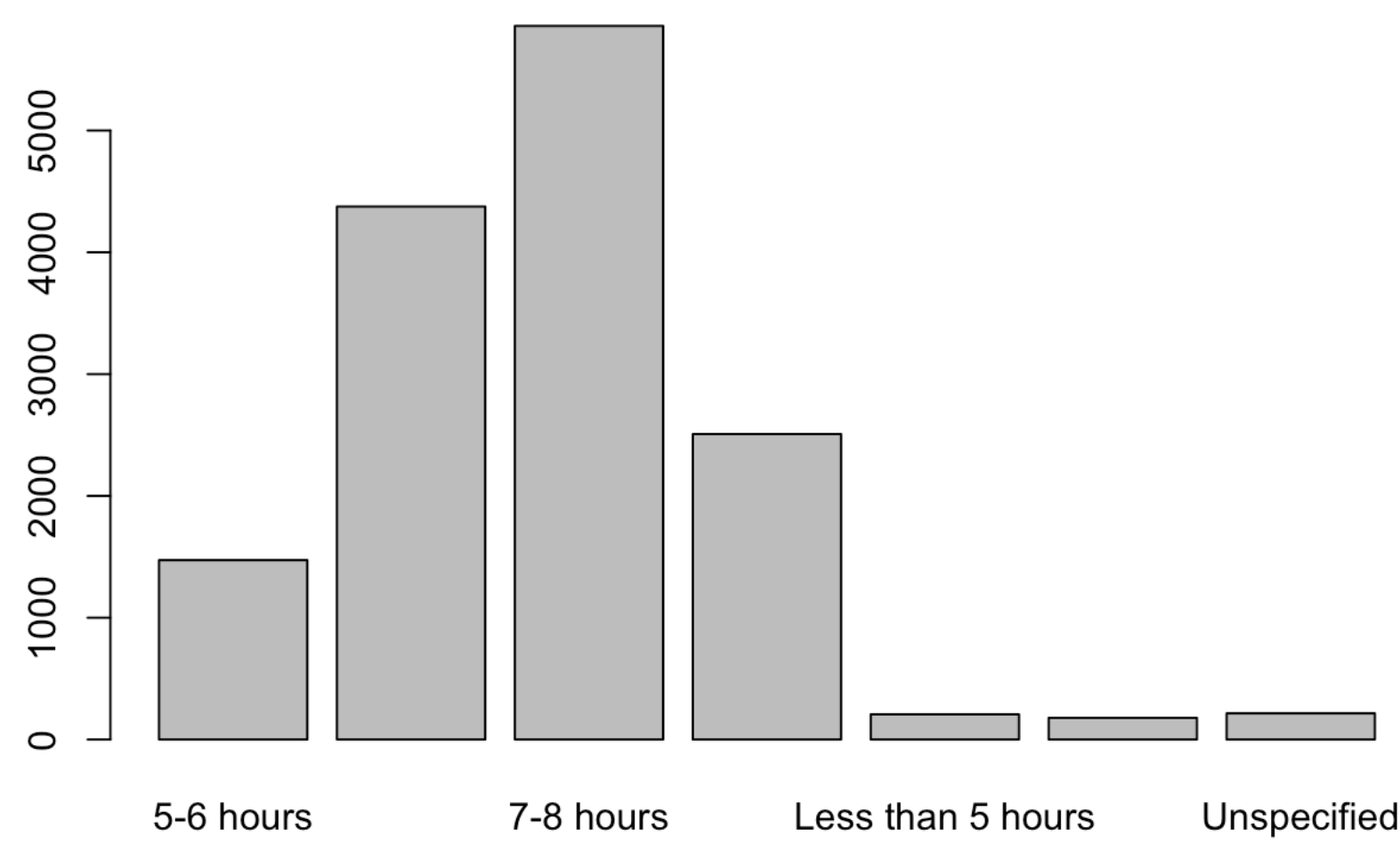
```
barplot(Categ_Diabetes)
```



```
Categ_Sleep<- summary(as.factor(Meta$SLEEP_DURATION))  
Categ_Sleep
```

##	5-6 hours	6-7 hours	7-8 hours	8 or more hours
##	1473	4376	5859	2508
##	Less than 5 hours	Unknown	Unspecified	
##	207	178	215	

```
barplot(Categ_Sleep)
```



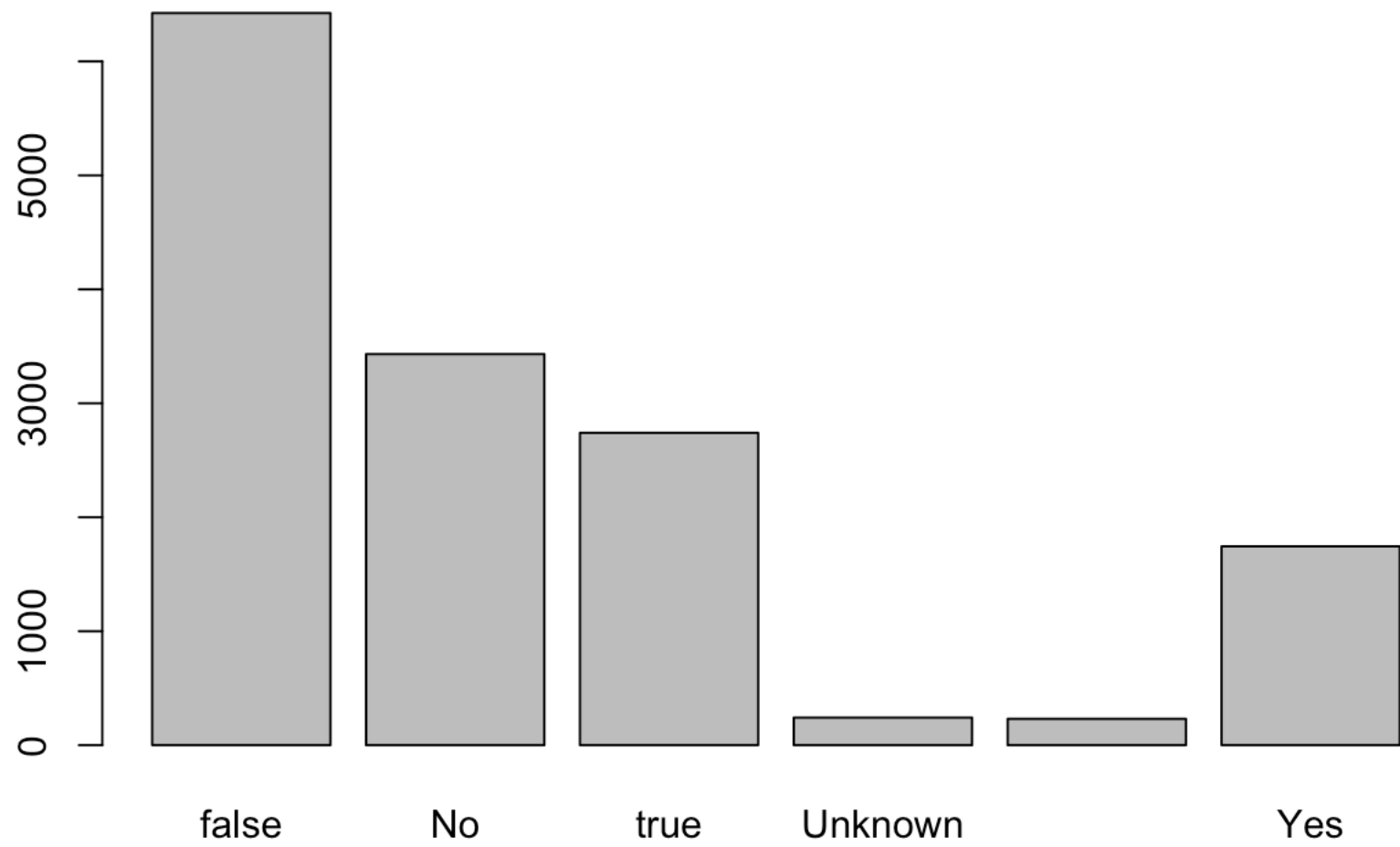
```
Categ_Pet<- summary(as.factor(Meta$PETS_OTHER))
Categ_Pet
```

##	false	No	no_data	true	Unknown	Unspecified
##	1049	3602	7262	142	1077	1254
##	Yes					
##	430					

```
Categ_Dog<- summary(as.factor(Meta$DOG))
Categ_Dog
```

##	false	No	true	Unknown	Unspecified	Yes
##	6425	3432	2741	242	231	1745

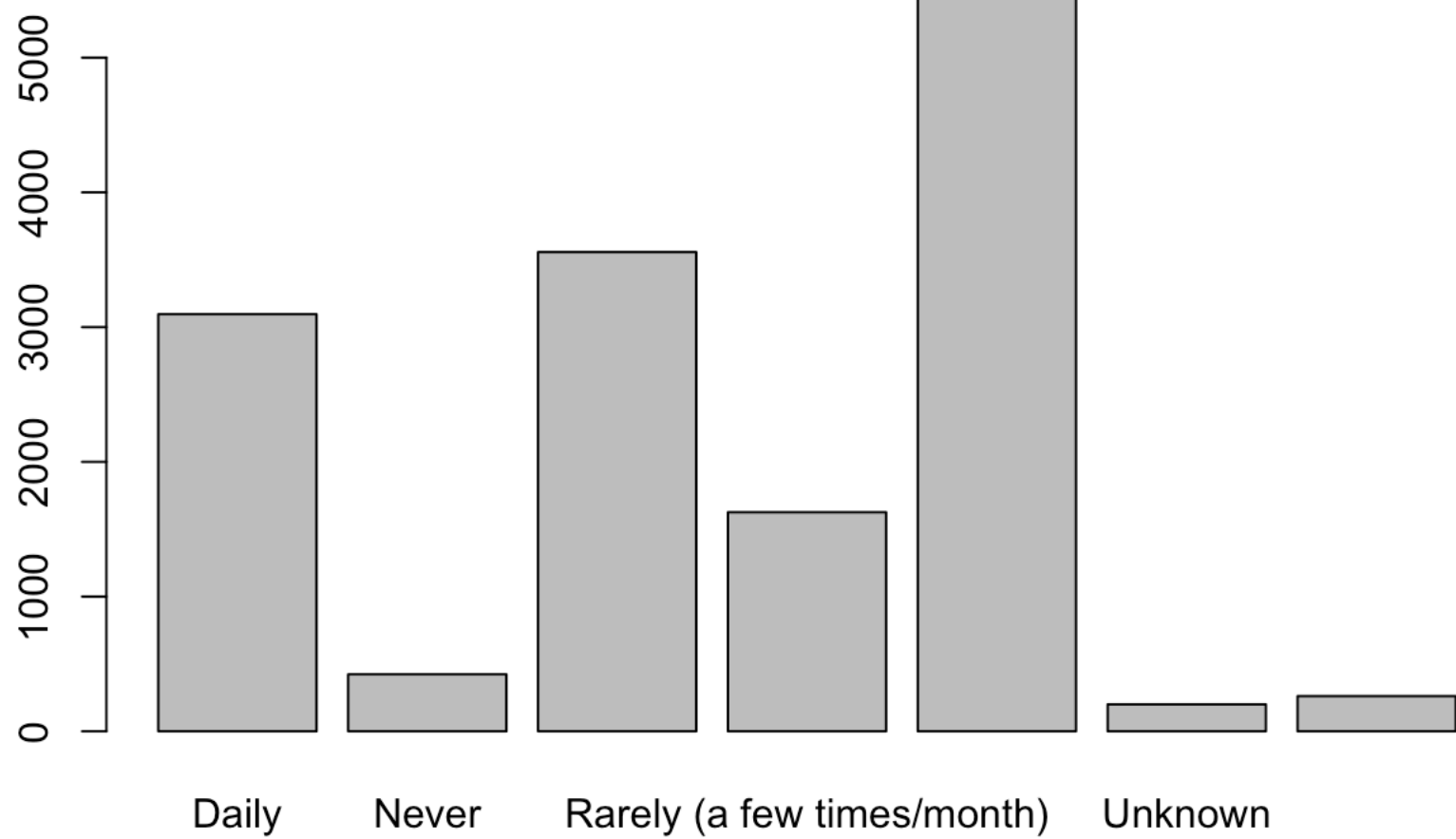
```
barplot(Categ_Dog)
```



```
Categ_Exercise<- summary(as.factor(Meta$EXERCISE_FREQUENCY))
Categ_Exercise
```

```
##           Daily           Never
##           3096           423
## Occasionally (1-2 times/week) Rarely (a few times/month)
##           3557           1626
## Regularly (3-5 times/week)      Unknown
##           5653           200
##           Unspecified
##           261
```

```
barplot(Categ_Exercise)
```



Breakdown by Age Split

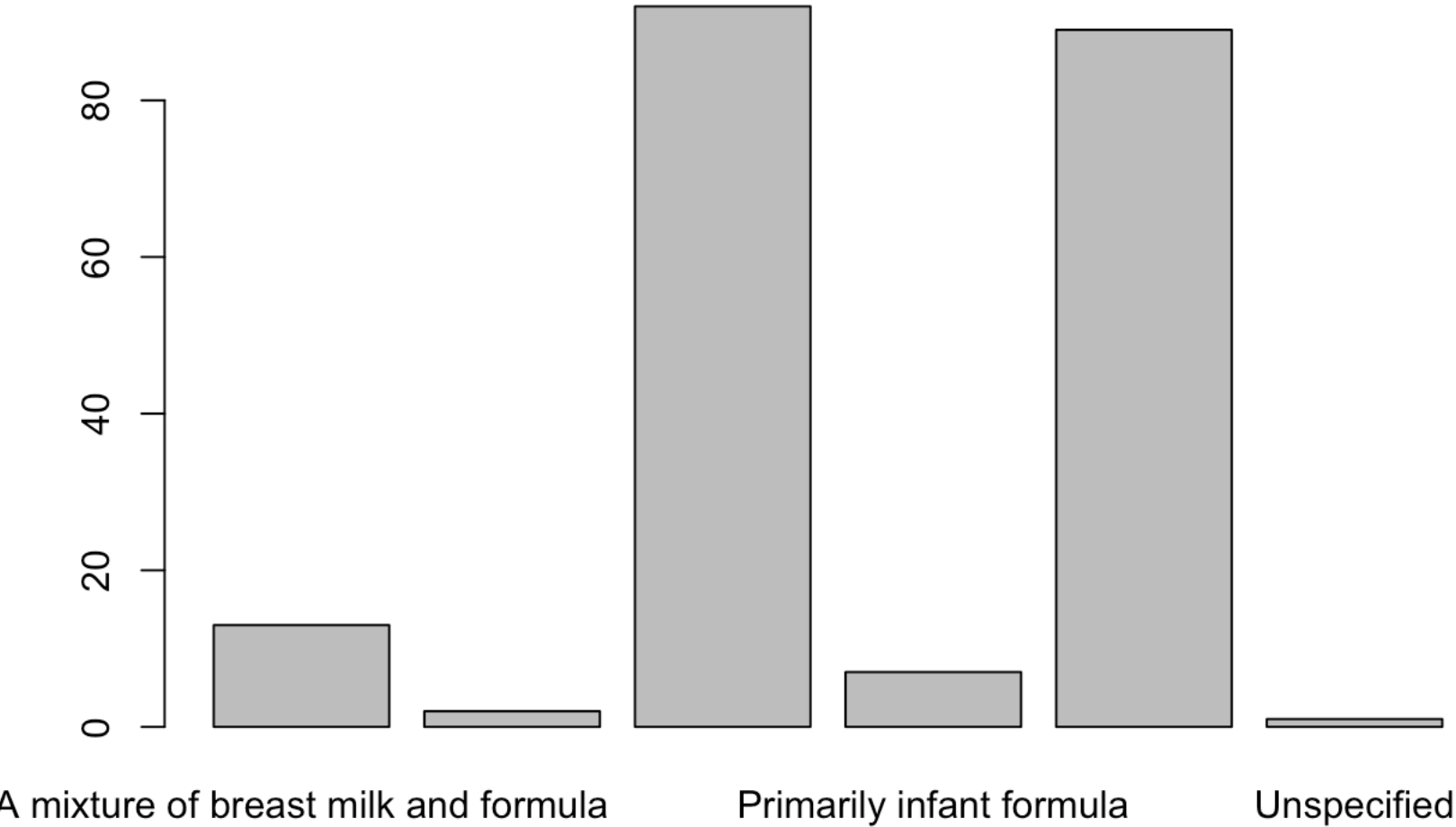
```
#Split Meta for Under age 3
Meta3 <-subset(Meta, AGE_YEARS<3)
summary(Meta3$AGE_YEARS)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.000   1.000   2.000   1.662   2.000   2.000
```

```
#Under 3 and what they are fed
Categ_Fed3<- summary(as.factor(Meta3$FED_AS_INFANT))
Categ_Fed3
```

```
## A mixture of breast milk and formula                Not sure
##                      13                      2
##      Primarily breast milk      Primarily infant formula
##                      92                      7
##                      Unknown      Unspecified
##                      89                      1
```

```
barplot(Categ_Fed3)
```



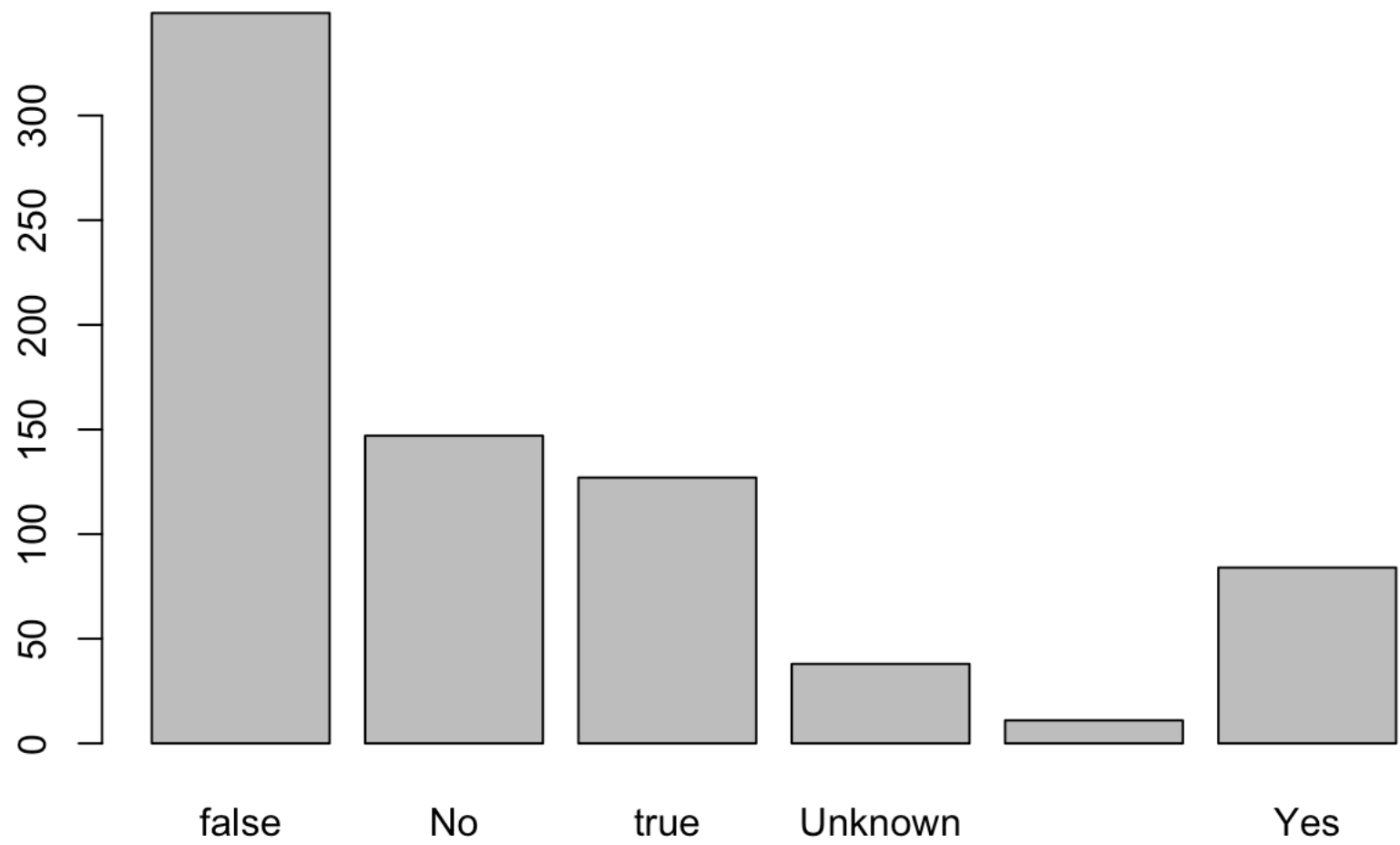
```
#Split Meta for Under age 12
Meta12 <-subset(Meta, AGE_YEARS<12)
summary(Meta12$AGE_YEARS)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.000   2.000   5.000   5.386   8.000  11.000
```

```
#Under 12 with Allergies
Categ_Allergies12<- summary(as.factor(Meta12$SEASONAL_ALLERGIES))
Categ_Allergies12
```

```
##      false      No      true      Unknown Unspecified      Yes
##      349      147      127        38         11      84
```

```
barplot(Categ_Allergies12)
```



```
#or
count(Meta12, 'SEASONAL_ALLERGIES')
```

```
## SEASONAL_ALLERGIES freq
## 1 false 349
## 2 No 147
## 3 true 127
## 4 Unknown 38
## 5 Unspecified 11
## 6 Yes 84
```

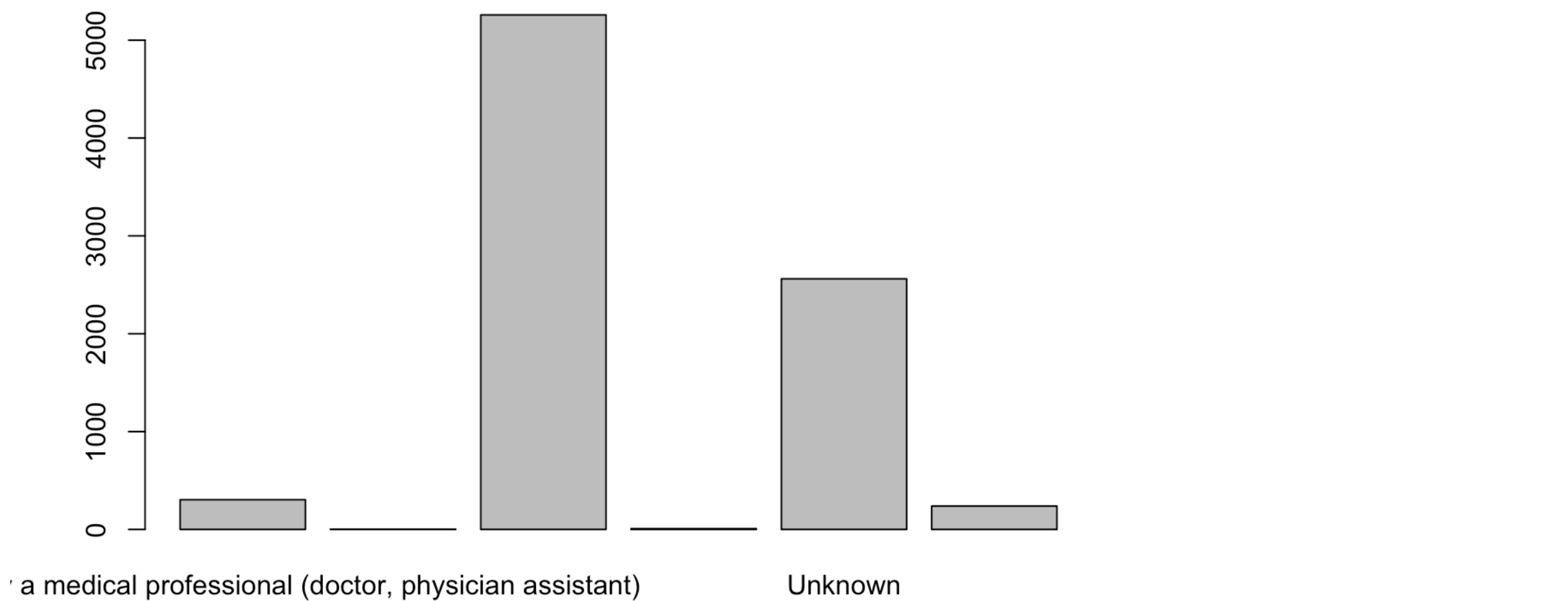
```
#Split Meta Over 40
Meta40 <-subset(Meta, AGE_YEARS>40)
summary(Meta40$AGE_YEARS)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 41.00 49.00 56.00 56.76 64.00 101.00
```

```
#Over 40 and CVD
Categ_CVD40<- summary(as.factor(Meta40$CARDIOVASCULAR_DISEASE))
Categ_CVD40
```

```
## Diagnosed by a medical professional (doctor, physician assistant)
## 304
## Diagnosed by an alternative medicine practitioner
## 2
## I do not have this condition
## 5258
## Self-diagnosed
## 8
## Unknown
## 2561
## Unspecified
## 239
```

```
barplot(Categ_CVD40)
```

BiVariate Exploration

Allergies and _____ in participants under age 12

```
#Seasonal Allergies and Dogs
knitr:: kable (count(Meta12, c('SEASONAL_ALLERGIES', 'DOG')))
```

SEASONAL_ALLERGIES	DOG	freq
false	false	255
false	true	91
false	Unknown	3
No	No	119
No	Yes	28
true	false	75
true	true	51
true	Unknown	1
Unknown	false	27
Unknown	true	8
Unknown	Unknown	3
Unspecified	No	8
Unspecified	Yes	3
Yes	No	68
Yes	Yes	16

```
#or
#Meta12 %>% filter(SEASONAL_ALLERGIES=c("true", "Yes")) %>% summary(as.factor('DOG'))

#Seasonal Allergies and Other Pets
knitr:: kable (count(Meta12, c('SEASONAL_ALLERGIES', 'PETS_OTHER')))
```

SEASONAL_ALLERGIES	PETS_OTHER	freq
false	false	28
false	no_data	276
false	true	10
false	Unknown	35
No	No	113

No	Unknown	2
No	Unspecified	5
No	Yes	27
true	false	12
true	no_data	106
true	true	1
true	Unknown	8
Unknown	false	2
Unknown	no_data	32
Unknown	Unknown	4
Unspecified	No	7
Unspecified	Unspecified	1
Unspecified	Yes	3
Yes	No	74
Yes	Unknown	2
Yes	Unspecified	5
Yes	Yes	3

```
#Seasonal Allergies and Delivery Method
knitr:: kable (count(Meta12, c('SEASONAL_ALLERGIES', 'CSECTION')))
```

SEASONAL_ALLERGIES	CSECTION	freq
false	false	4
false	No	216
false	Not sure	1
false	Unknown	3
false	Yes	125
No	No	108
No	Yes	39
true	No	94
true	Not sure	2
true	Yes	31
Unknown	No	20
Unknown	Unknown	6
Unknown	Yes	12
Unspecified	No	7
Unspecified	Unspecified	2
Unspecified	Yes	2
Yes	No	58
Yes	Not sure	1
Yes	Yes	25

```
#Seasonal Allergies and Food as Infant
knitr:: kable (count(Meta12, c('SEASONAL_ALLERGIES', 'FED_AS_INFANT')))
```

SEASONAL_ALLERGIES	FED_AS_INFANT	freq
false	A mixture of breast milk and formula	39
false	Primarily breast milk	121
false	Primarily infant formula	14
false	Unknown	175

No	A mixture of breast milk and formula	19
No	Primarily breast milk	111
No	Primarily infant formula	16
No	Unspecified	1
true	A mixture of breast milk and formula	18
true	Not sure	2
true	Primarily breast milk	28
true	Primarily infant formula	21
true	Unknown	58
Unknown	A mixture of breast milk and formula	8
Unknown	Primarily breast milk	11
Unknown	Primarily infant formula	1
Unknown	Unknown	18
Unspecified	A mixture of breast milk and formula	2
Unspecified	Primarily breast milk	5
Unspecified	Primarily infant formula	2
Unspecified	Unspecified	2
Yes	A mixture of breast milk and formula	44
Yes	Not sure	1
Yes	Primarily breast milk	34
Yes	Primarily infant formula	5

List of all variables available for further analysis

names (Meta)		
##	[1]	"#SampleID"
##	[2]	"BarcodeSequence"
##	[3]	"LinkerPrimerSequence"
##	[4]	"VIOSCREEN_MANNITOL"
##	[5]	"VIOSCREEN_SFA100"
##	[6]	"NON_FOOD_ALLERGIES_BEESTINGS"
##	[7]	"VIOSCREEN_FINISHED"
##	[8]	"TONSILS_REMOVED"
##	[9]	"WEIGHT_CHANGE"
##	[10]	"VIOSCREEN_SFA170"
##	[11]	"VIOSCREEN_VEGETABLE_SERVINGS"
##	[12]	"VIOSCREEN_SORBITOL"
##	[13]	"COUNTRY_OF_BIRTH"
##	[14]	"PETS_OTHER"
##	[15]	"MASTERMIX_LOT"
##	[16]	"VIOSCREEN_SFA80"
##	[17]	"VIOSCREEN_BETACAR"
##	[18]	"VIOSCREEN_LOW_FAT_DAIRY_SERVING"
##	[19]	"VIOSCREEN_NIACINEQ"
##	[20]	"ORIG_NAME"
##	[21]	"ALLERGIC_TO_OTHER"
##	[22]	"VIOSCREEN_GAMMTOCO"
##	[23]	"SPECIALIZED_DIET_I_DO_NOT_EAT_A_SPECIALIZED_DIET"
##	[24]	"VIOSCREEN_LYSINE"
##	[25]	"VIOSCREEN_ISOMALT"
##	[26]	"LIVER_DISEASE"
##	[27]	"BODY_PRODUCT"
##	[28]	"VIOSCREEN_DATABASE"
##	[29]	"VIOSCREEN_FIBINSO"
##	[30]	"WHOLE_GRAIN_FREQUENCY"
##	[31]	"ARTIFICIAL_SWEETENERS"
##	[32]	"ENV_MATERIAL"
##	[33]	"VIOSCREEN_SUCROSE"
##	[34]	"ENA-BASE-COUNT"
##	[35]	"VIOSCREEN_CLAC9T11"
##	[36]	"SUBSET_HEALTHY"
##	[37]	"VIOSCREEN_FIBER"
##	[38]	"VIOSCREEN_LACTITOL"

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## [39] "VIOSCREEN_HEI_NON_JUICE_FRT"
## [40] "VIOSCREEN_HEI_SCORE"
## [41] "ALLERGIC_TO_UNSPECIFIED"
## [42] "VIOSCREEN_OXALICM"
## [43] "VIOSCREEN_ALPHACAR"
## [44] "SALTED_SNACKS_FREQUENCY"
## [45] "ALCOHOL_TYPES_UNSPECIFIED"
## [46] "AGE_CAT"
## [47] "VIOSCREEN_QUESTIONNAIRE"
## [48] "VIOSCREEN_LYCOPENE"
## [49] "VIOSCREEN_VEG5_DAY"
## [50] "SUBSET_BMI"
## [51] "MIGRAINE"
## [52] "VIOSCREEN_HEI_MILK"
## [53] "SPECIALIZED_DIET_EXCLUDE_REFINED_SUGARS"
## [54] "VIOSCREEN_CLAT10C12"
## [55] "VIOSCREEN_CARBO"
## [56] "VIOSCREEN_HEI_MEAT_BEANS"
## [57] "VIOSCREEN_HEI_SOL_FAT_ALC_ADD_SUG"
## [58] "AGE_YEARS"
## [59] "VIOSCREEN_GLUCOSE"
## [60] "VIOSCREEN_HEI2010_REFINED_GRAINS"
## [61] "LIBRARY_CONSTRUCTION_PROTOCOL"
## [62] "VIOSCREEN_LUTZEAX"
## [63] "EXERCISE_FREQUENCY"
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## [68] "VIOSCREEN_SALAD_VEGETABLE_SERVINGS"
## [69] "BOWEL_MOVEMENT_FREQUENCY"
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## [76] "VIOSCREEN_FIBH2O"
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## [79] "VIOSCREEN_PHENYLAL"
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## [90] "HOMECOOKED_MEALS_FREQUENCY"
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## [92] "VIOSCREEN_D_MILK"
## [93] "HEIGHT_UNITS"
## [94] "VIOSCREEN_M_ORGAN"
## [95] "VIOSCREEN_M_POULT"
## [96] "VIOSCREEN_M_MPF"
## [97] "VIOSCREEN_WHOLE_GRAIN_SERVINGS"
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## [103] "VIOSCREEN_NCCGLGR"
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## [105] "VIOSCREEN_HEI_FRUIT"
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## [107] "VITAMIN_D_SUPPLEMENT_FREQUENCY"
## [108] "ADD_ADHD"
## [109] "READY_TO_EAT_MEALS_FREQUENCY"
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## [111] "VIOSCREEN_SATOCO"
## [112] "VIOSCREEN_RIBOFLA"
## [113] "VIOSCREEN_STARCH"
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## [134] "DIABETES"
## [135] "CDIFF"
## [136] "VIOSCREEN_SODIUM"
## [137] "RUN_CENTER"
## [138] "VIOSCREEN_BETATOCO"
## [139] "HEIGHT_CM"
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## [141] "VIOSCREEN_FISH_SERVINGS"
## [142] "CHICKENPOX"
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## [150] "VIOSCREEN_BETAINE"
## [151] "VIOSCREEN_ALCOHOL_SERVINGS"
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## [153] "FLOSSING_FREQUENCY"
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## [170] "VIOSCREEN_F_NJ_TOTAL"
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## [193] "DEPRESSION_BIPOLAR_SCHIZOPHRENIA"
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## [207] "ROOMMATES"
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## [209] "VIOSCREEN_SACCHAR"
## [210] "VIOSCREEN_ERYTHR"
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## [222] "VIOSCREEN_PFA225"
## [223] "VIOSCREEN_HEI2010_WHOLE_FRUIT"
## [224] "ALCOHOL_FREQUENCY"
## [225] "POULTRY_FREQUENCY"
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## [228] "VIOSCREEN_PROLINE"
## [229] "VIOSCREEN_M_MEAT"
## [230] "ROOMMATES_IN_STUDY"
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## [252] "VIOSCREEN_VITA_RE"
## [253] "COLLECTION_TIME"
## [254] "VIOSCREEN_VEGSUMM"
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## [256] "VIOSCREEN_SFA60"
## [257] "COLLECTION_MONTH"
## [258] "VITAMIN_B_SUPPLEMENT_FREQUENCY"
## [259] "TM300_8_TOOL"
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## [261] "SUBSET_IBD"
## [262] "VIOSCREEN_HEI_SAT_FAT"
## [263] "VIOSCREEN_TOTFOLAT"
## [264] "VIOSCREEN_ARGININE"
## [265] "VIOSCREEN_HEI2010_FATTY_ACIDS"
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## [272] "VIOSCREEN_ALPHTOCO"
## [273] "VIOSCREEN_GLTC"
## [274] "VIOSCREEN_MULTI_CALCIUM_DOSE"
## [275] "ALLERGIC_TO"
## [276] "VIOSCREEN_VITA_IU"
## [277] "MENTAL_ILLNESS_TYPE_PTSD_POSTTRAUMATIC_STRESS_DISORDER"
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## [279] "VIOSCREEN_CALCIUM_FREQ"
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[293] "VIOSCREEN_PROTVEG"
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[511] "SEQUENCING_METH"
[512] "VIOSCREEN_JOULES"
[513] "VIOSCREEN_FORMONTN"
[514] "VIOSCREEN_SWEET_SERVINGS"
[515] "EXPERIMENT_CENTER"
[516] "POOL_FREQUENCY"
[517] "VIOSCREEN_FOL_DEQV"
[518] "PKU"
[519] "VIOSCREEN_ASH"
[520] "VIOSCREEN_METHHIS3"
[521] "AGE_CORRECTED"
[522] "SPECIALIZED_DIET_OTHER_RESTRICTIONS_NOT_DESCRIBED_HERE"
[523] "VIOSCREEN_NATOCO"
[524] "Description"

```
## [525] "SIMPLE_BODY_SITE"
## [526] "TITLE_ACRONYM"
## [527] "TITLE_BODY_SITE"
## [528] "HMP_SITE"
```

Interactive Data Widget

Here is an intereactive and searchable version of the dataset. The same could also be done by exporting it to an excel file.

```
library(DT)
datatable(Meta, options = list(pageLength = 25))
```

Show

10

 entries

Search:

	#SampleID	BarcodeSequence	LinkerPrimerSequence	VIOSCREEN_MANNITOL	VIOSCREEN_SFA100	NON_FOOD_
1	10317.000027826	no_data	no_data	0.496931478	0.88257555	false
2	10317.000027827	no_data	no_data			false
3	10317.000027824	ATATTGGCAGCC	GTGTGCCAGCMGCCGCGGTAA			No
4	10317.000027825	no_data	no_data			false
5	10317.000027822	GGCTTCGGAGCG	GTGTGCCAGCMGCCGCGGTAA	0.289205452	0.432219205	No
6	10317.000014400	no_data	no_data			false
7	10317.000027820	no_data	no_data			false
8	10317.000065774	GAGCGCCGAACA	GTGTGCCAGCMGCCGCGGTAA			No

9	10317.000065776	GTAAACGACTTG	GTGTGCCAGCMGCCGCGGTAA				No
10	10317.000065777	ACATAGCGGTTC	GTGTGCCAGCMGCCGCGGTAA				No
11	10317.000065770	GTCACCAATCCG	GTGTGCCAGCMGCCGCGGTAA				No
12	10317.000065771	GAGTCCGTTGCT	GTGTGCCAGCMGCCGCGGTAA				No
13	10317.000027828	no_data	no_data		0.203397254	0.040273975	false
14	10317.000027829	no_data	no_data				false
15	10317.000001386	no_data	no_data				false
16	10317.000001384	no_data	no_data				false
17	10317.000001380	no_data	no_data				false
18	10317.000001389	no_data	no_data				false
19	10317.000030085	GGACAAGTGCGA	GTGTGCCAGCMGCCGCGGTAA				No
20	10317.000030086	no_data	no_data		0.248109582	0.777780778	false

21	10317.000030087	no_data	no_data				false
22	10317.000030080	no_data	no_data				false
23	10317.000030081	no_data	no_data				false
24	10317.000030082	no_data	no_data		0.269287674	0.656739703	false
25	10317.000030083	no_data	no_data		0.115671236	0.296684934	false

Input OTU/Taxonomy

Create a phyloseq object to work with inside of the phyloseq package. To do this we will upload the “.biom” file then merge the metadata, OTU, taxonomy, and tree file. This will allow us to explore the diversity of the sample. Again check your file names and paths in order to use this code. (Note: “.biom” file is found in the “OTU” folder of the “latest” data. The “meta” folder appears to be missing the “.biom” file associated with the previously used metadata within the “Meta” folder)

```
##Import OTU file
#Data originally downloaded from <ftp://ftp.microbio.me/AmericanGut/latest>
#Make sure to pull the correct biom file to match the meta data down for analysis.

# To read in original .biom file use command below
file_path<- ("~/Desktop/otu_table.biom")
dat <- import_biom(file_path)

#To fix error saying "input string 1 is invalid in this locale" run command "Sys.setlocale(locale="C")" in consol
e and run command chunk again

#Make Phyloseq values for separate pieces of the biom file
#Taxonomy
taxonomy <- tax_table(dat)
#OTU
OTU_table<- otu_table(dat)

#MetaData
#Create Phyloseq object for sample data so it can be merged
SampleData<- sample_data(Meta)
SD<-sample_data(Meta)

#Import the tree corresponding to this data ### Will Not work
tree<-read_tree_greengenes("~/Desktop/97_otus.tree")

#Merge OTU, Taxonomy, and metadata into one phyloseq object called "ps"that can be used for analysis
Sample_data <- (SD)
sam_cov <- as.data.frame(Sample_data)
rownames(sam_cov) <- sam_cov$"#SampleID"
sd <- sample_data(sam_cov)
sample_names(sd) #Previous steps fix error in naming of SampleIds
otus <- otu_table(OTU_table, taxa_are_rows = TRUE)
sample_names(otus)
tt <- tax_table(taxonomy)
ps <- phyloseq(otus, sd, tt,tree) #Step to merge OTU,Taxonomy, and metadata
ps #View object and make sure it has all 3 parts
```

Summary of OTU

```
#Summary of OTU
ntaxa(ps)
rank_names(ps)
nsamples(ps)
sample_names(ps)[1:5]
otu_table(ps)[1:5, 1:5]
tax_table(ps)[1:5, 1:4]
taxa_names(ps)[1:10]
```