

Univariate Graphing Assignment

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Describing Distribution

Load necessary libraries needed.

```
# Load libraries
library(sjPlot); library(ggplot2); library(ggpubr); library(here);library(gtsummary)

# Import data
load(here("data/environmental_impact_clean.Rdata"))
```

Environmental_impacts_freshwater_use

“environmental_impacts_freshwater_use” variable represents environmental impact of using freshwater (use in km3) on diet and nutrition in certain regions.

```
summary(region$environmental_impacts_freshwater_use)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0003	0.4669	2.3623	30.6096	11.1830	1699.1279

```
IQR(region$environmental_impacts_freshwater_use)
```

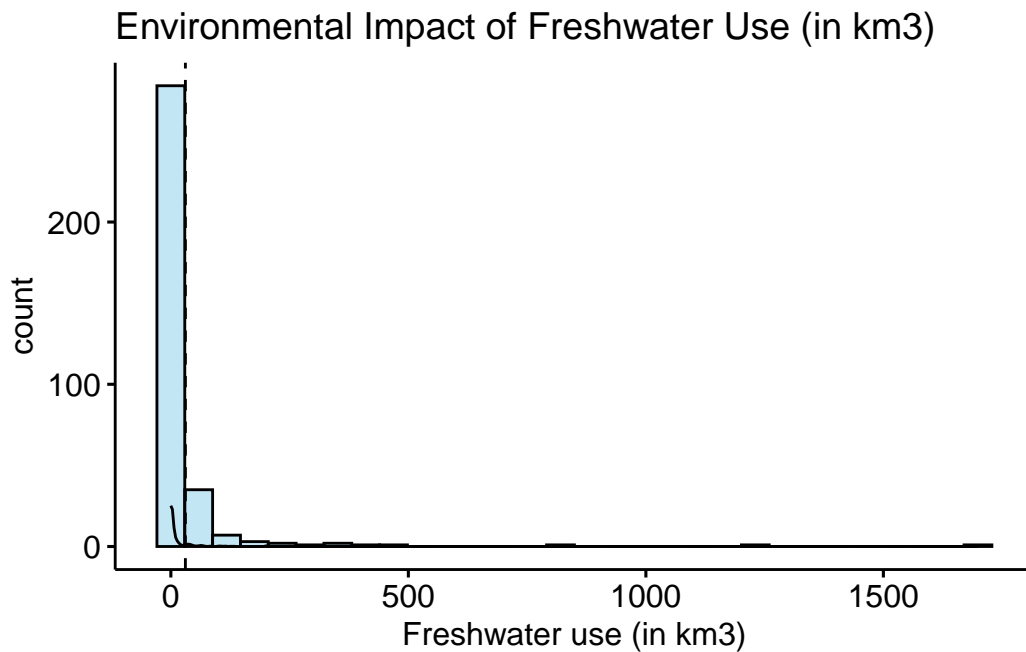
```
[1] 10.71601
```

```
sd(region$environmental_impacts_freshwater_use)
```

```
[1] 133.1164
```

Histogram for variable “environmental_impacts_freshwater_use” in km3 units.

```
# this function is from the ggpubr package
gghistogram(data=region, x = "environmental_impacts_freshwater_use", add = "mean",
            fill = "skyblue", add_density = TRUE,
            xlab = "Freshwater use (in km3)",
            title = "Environmental Impact of Freshwater Use (in km3)")
```



The histogram titled “Environmental Impact of Freshwater Use (in km³)” depicts the distribution of impact of freshwater use on diet and nutrition in various regions with 351 observations and . The data seems to be right-skewed, indicating more frequent lower values with a long tail of higher values. The mean of environmental impact of freshwater use is around 30.6096 km³, with the median of 2.3623 km³. The interquartile range (IQR) is 10.71601 which spans from 0.4669 km³ to 11.1830 km³, showing where the middle 50% of the data lies that is middle of data from variable. The range of the data is huge with a standard deviation of 133.1164 km³. There seem some outliers that are values outside this range or due to data entry errors.

Environmental_impacts_land_use

“environmental_impacts_land_use” variable represents environmental impact of land (use in Mkm²) on diet and nutrition in certain regions.

```
summary(region$environmental_impacts_land_use)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.00	10.12	57.97	1035.65	410.46	58062.30

```
IQR(region$environmental_impacts_land_use, na.rm = TRUE)
```

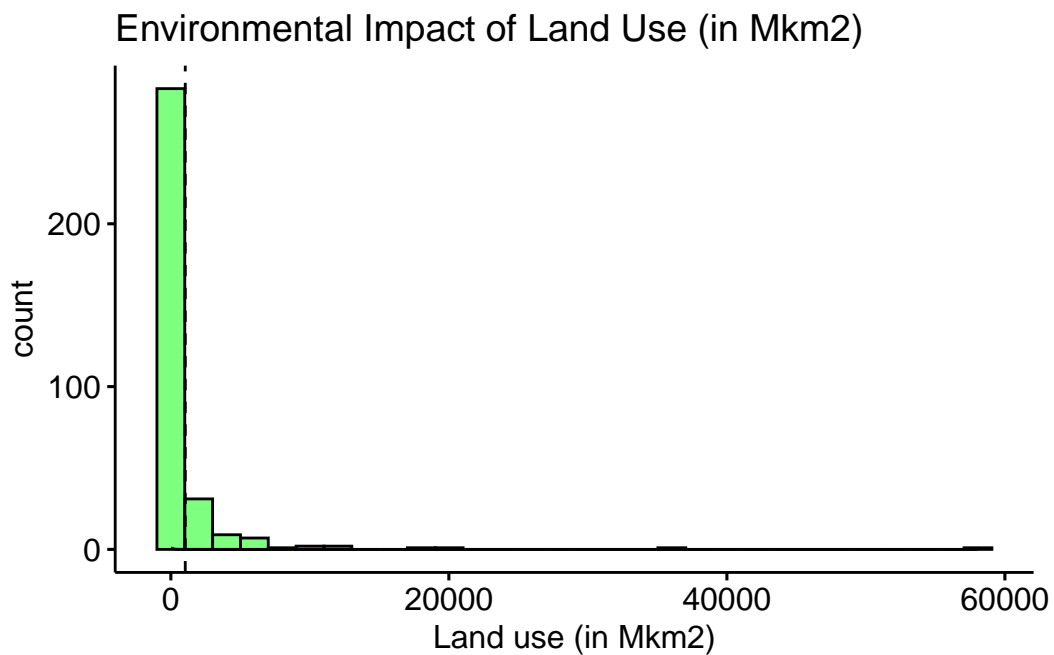
```
[1] 400.3397
```

```
sd(region$environmental_impacts_land_use, na.rm = TRUE)
```

```
[1] 4220.845
```

Histogram for variable “environmental_impacts_land_use” in Mkm2

```
# this function is from the ggpubr package
gghistogram(data=region, x = "environmental_impacts_land_use",
  add = "mean",
  fill = "green", add_density = TRUE,
  xlab = "Land use (in Mkm2)",
  title = "Environmental Impact of Land Use (in Mkm2)")
```



The histogram titled “Environmental Impact of Land Use (in Mkm²)” illustrates how impact of land use on diet and nutrition is distributed in million square kilometers (Mkm²). The data appears to be right-skewed, suggesting that lower values are more common, with a long tail extending towards higher values. The average land use is approximately 1035.65 Mkm², while the median is slightly lower at 57.97 Mkm². The interquartile range (IQR) is 400.3397 which spans from 10.12 Mkm² to 410.46 Mkm², indicating where the middle 50% of the data falls. The overall range of the data is quite large with a standard deviation of 4220.845 Mkm². There are some outliers present, which could be values that fall outside this range or may result from data entry mistakes.

Region

“region” variable represents regions or places for analyzing impact of it by environmental factors on diet and nutrition.

```
table(region$region, useNA = "always")
```

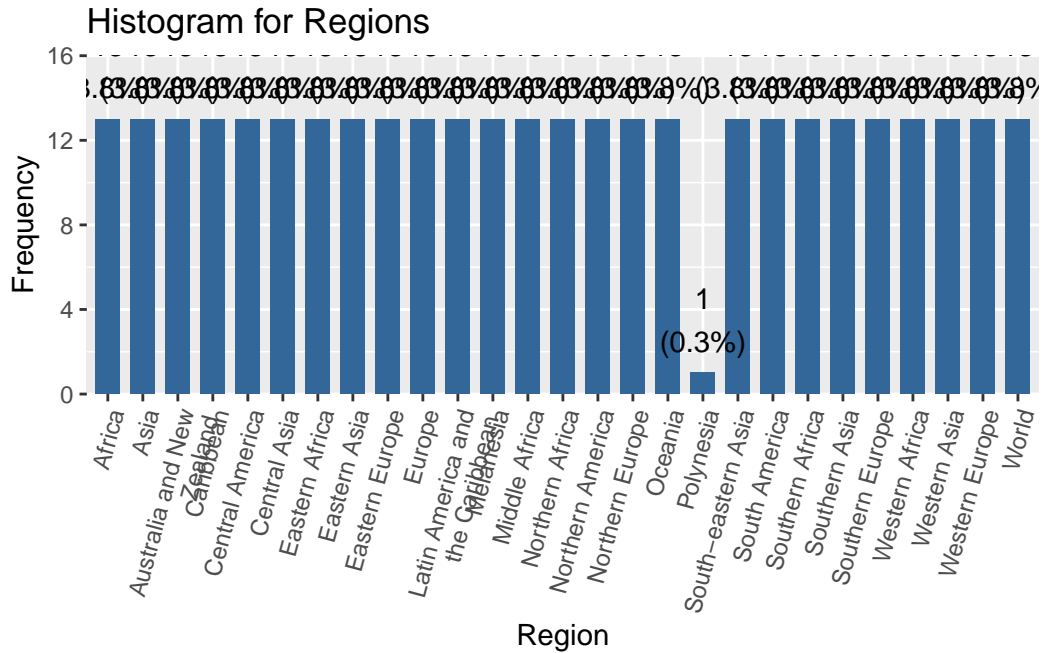
Africa	Asia
13	13
Australia and New Zealand	Caribbean
13	13
Central America	Central Asia
13	13
Eastern Africa	Eastern Asia
13	13
Eastern Europe	Europe
13	13
Latin America and the Caribbean	Melanesia
13	13
Middle Africa	Northern Africa
13	13
Northern America	Northern Europe
13	13
Oceania	Polynesia
13	1
South-eastern Asia	South America
13	13
Southern Africa	Southern Asia
13	13
Southern Europe	Western Africa

13	13
Western Asia	Western Europe
13	13
World	<NA>
13	0

```
prop.table(table(region$region))
```

Africa	Asia
0.038348083	0.038348083
Australia and New Zealand	Caribbean
0.038348083	0.038348083
Central America	Central Asia
0.038348083	0.038348083
Eastern Africa	Eastern Asia
0.038348083	0.038348083
Eastern Europe	Europe
0.038348083	0.038348083
Latin America and the Caribbean	Melanesia
0.038348083	0.038348083
Middle Africa	Northern Africa
0.038348083	0.038348083
Northern America	Northern Europe
0.038348083	0.038348083
Oceania	Polynesia
0.038348083	0.002949853
South-eastern Asia	South America
0.038348083	0.038348083
Southern Africa	Southern Asia
0.038348083	0.038348083
Southern Europe	Western Africa
0.038348083	0.038348083
Western Asia	Western Europe
0.038348083	0.038348083
World	
0.038348083	

```
plot_frq(region$region) + labs(title = "Histogram for Regions", x = "Region",
                               y = "Frequency") +
  theme(axis.text.x = element_text(angle = 75, vjust = 1, hjust = 1))
```



The histogram titled “Histogram for Regions” illustrates how often different regions appear in the dataset. It reveals that almost all regions have same frequency count than Polynesia that has 1 count only. The data for region “Asia” is standing out as the leading region. Every region make 7% of data (i.e. number of observations (N=13)) besides Polynesia which makes 0.3% of data (i.e. number of observations (N=1))

Disagg_value

“disagg_value” variable represents diet items(fruits,vegetables,beef,etc) in particular region.

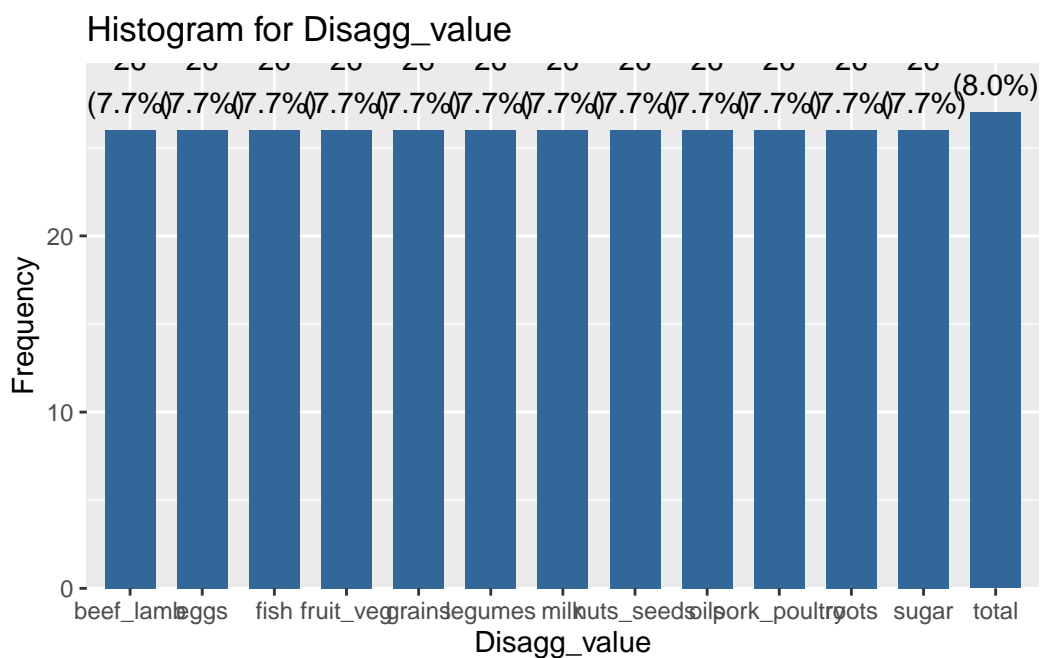
```
table(region$disagg_value,useNA = "always")
```

beef_lamb	eggs	fish	fruit_veg	grains	legumes
26	26	26	26	26	26
milk	nuts_seeds	oils	pork_poultry	roots	sugar
26	26	26	26	26	26
total	<NA>				
27	0				

```
prop.table(table(region$disagg_value))
```

beef_lamb	eggs	fish	fruit_veg	grains	legumes
0.07669617	0.07669617	0.07669617	0.07669617	0.07669617	0.07669617
milk	nuts_seeds	oils	pork_poultry	roots	sugar
0.07669617	0.07669617	0.07669617	0.07669617	0.07669617	0.07669617
total					
0.07964602					

```
plot_frq(region$disagg_value) + labs(title = "Histogram for Disagg_value", x = "Disagg_value")
```



The plot illustrates how often different disagg_value (i.e. diet) appear in the dataset. It reveals that almost all disagg_value have same frequency count than total which contains all other disagg_values that are there in that region having 27 which is higher than other. The data for region “total” is standing out as the leading value. Every value makes 7.7% of data (i.e. number of observations (N=26)) besides total which makes 8.0% of data (i.e. number of observations (N=27)).