**Toxin Overlap in *Crotalus* Snake Genus: Analyzing Venom Composition**

1. **Research Question(s)**
   1. **How much toxin overlap exists between *Crotalus* snake genus?**
      1. What are the most common venom toxins across the genus?
      2. How similar or different are venom compositions between snakes within the genus?
2. **Objective(s)**
   1. Provide a framework for analyzing venom toxin composition in *Crotalus* snakes.
   2. Develop R scripts to import, visualize, and compare toxin composition data.
   3. Summarize toxin distribution across snakes within the genus using graphical representation.
   4. Identify which toxins are most prevalent across the genus in an effort to identify which toxins should be the primary targets when thinking of creating universal or generic antivenoms.
3. **Approach**
   1. I used the -omics data from several publications to create a dataset representing venom toxin composition across various *Crotalus* snakes. The dataset contains binary presence/absence values for major snake venom toxin types. Using R, we will:
      1. Load and clean the dataset.
      2. Visualize toxin distribution using heatmaps.
      3. Summarize toxin diversity across snakes within the genus.
   2. **R Code for Analysis**
      1. **Data Import & Cleaning**

# Load necessary libraries

# install.packages("tidyverse")

# install.packages(“ggplot2”)

# library(tidyverse)

# library(ggplot2)

# Load the dataset

setwd() # Insert relevant working directory

venom\_data <- read.csv("venom\_composition.csv")

# View first few rows

head(venom\_data)

# Check for missing values

sum(is.na(venom\_data))

1. **Exploratory Data Analysis**

# Transform data to long format for visualization

venom\_long <- venom\_data %>%

pivot\_longer(cols = -Species, names\_to = "Toxin", values\_to = "Presence") %>%

mutate(Toxin = gsub("\\.", " ", Toxin)) # Remove periods in toxin names

# Plot heatmap

ggplot(venom\_long, aes(x = Species, y = Toxin, fill = factor(Presence))) +

geom\_tile(width = 0.9) + # Makes each column wider

scale\_fill\_manual(values = c("0" = "white", "1" = "darkgreen"),

labels = c("0" = "Absent", "1" = "Present")) +

scale\_x\_discrete(expand = expansion(mult = 0.1)) + # Increase column spacing

theme\_minimal() +

labs(title = "Venom Toxin Presence Across \*Crotalus\* Genus", fill = "Toxin Presence") +

theme(

axis.text.x = element\_text(angle = 45, hjust = 1), # Tilt x-axis labels

plot.title = element\_text(hjust = 0.5), # Center title

aspect.ratio = 1.5 # Adjust aspect ratio to spread columns

)

1. **Selected References**
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