

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

1. Research Question(s)

a. How much toxin overlap exists between *Crotalus* snake genus?

- i. What are the most common venom toxins across the genus?
- ii. How similar or different are venom compositions between snakes within the genus?

2. Objective(s)

- a. Provide a framework for analyzing venom toxin composition in *Crotalus* snakes.
- b. Develop R scripts to import, visualize, and compare toxin composition data.
- c. Summarize toxin distribution across snakes within the genus using graphical representation.
- d. 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

- a. 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:
 - i. Load and clean the dataset.
 - ii. Visualize toxin distribution using heatmaps.
 - iii. Summarize toxin diversity across snakes within the genus.

b. R Code for Analysis

i. 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))
```

i. 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
  )

```

4. Selected References

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basiliscus) venom and its immunological relatedness with the venom of Central American rattlesnake (*Crotalus simus*). *Journal of Proteomics*, 158, 62-72.

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