

# A Comparative Analysis of Colony Counts at Measured Intervals Along the Indian and Banana Rivers Extending to Dragon Point



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## Introduction

Water quality is a critical factor in supporting healthy ecosystems and ensuring public safety. One common method for assessing water quality is measuring bacterial colony counts, which can indicate levels of contamination from environmental or human sources.

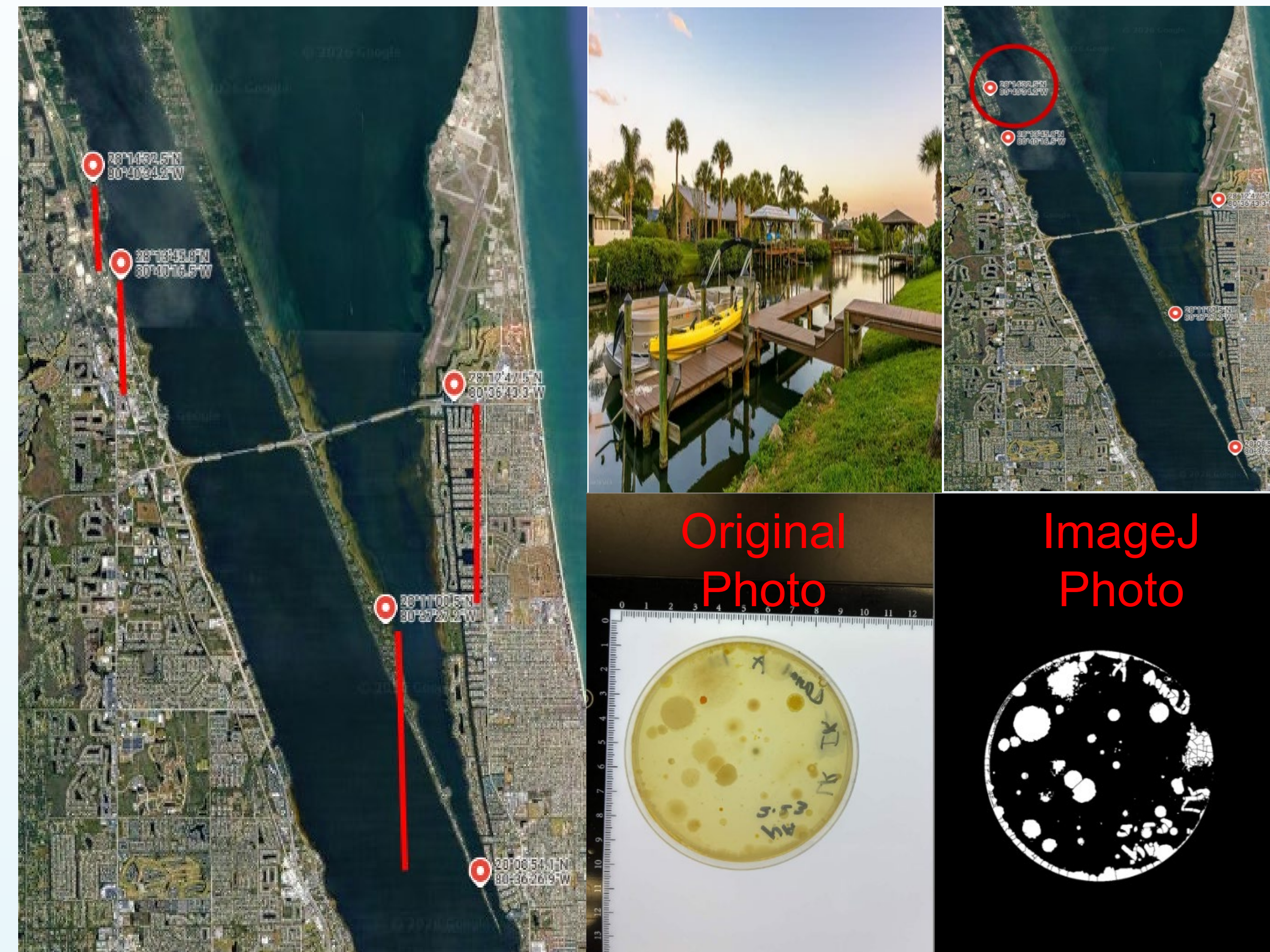
The Indian River and Banana River are part of a connected estuarine system in Florida that experiences varying levels of human activity, runoff, and water flow. These factors can influence microbial populations in the water.

This study investigates how bacterial colony counts vary across multiple locations along these waterways, moving southward toward Dragon Point. By comparing colony counts at measured distances, this research aims to find spatial patterns and potential environmental influences on bacterial concentration.

## Methodology and Material

Water samples were collected from five locations along the Indian and Banana Rivers: Indian River Canal, Indian River Beach, PSFB Marina, Banana River Property, and Dragon Point, spanning approximately 6.55 miles southward. Each sample was prepared by adding 100  $\mu\text{L}$  of the original water sample to 900  $\mu\text{L}$  of sterile water, creating a 1:10 dilution. The diluted samples were then plated onto agar plates and incubated under controlled conditions to allow bacterial colonies to grow. After incubation, colonies were counted both visually and using ImageJ software to improve accuracy and consistency. ImageJ works by converting images of the plates into high-contrast, threshold-based representations, allowing individual colonies to be distinguished from the background and automatically counted based on size and shape parameters. This reduces human error and helps account for overlapping or faint colonies. Because all samples were diluted prior to plating, the observed colony counts were multiplied by 10 to estimate the bacterial concentration in the original water samples.

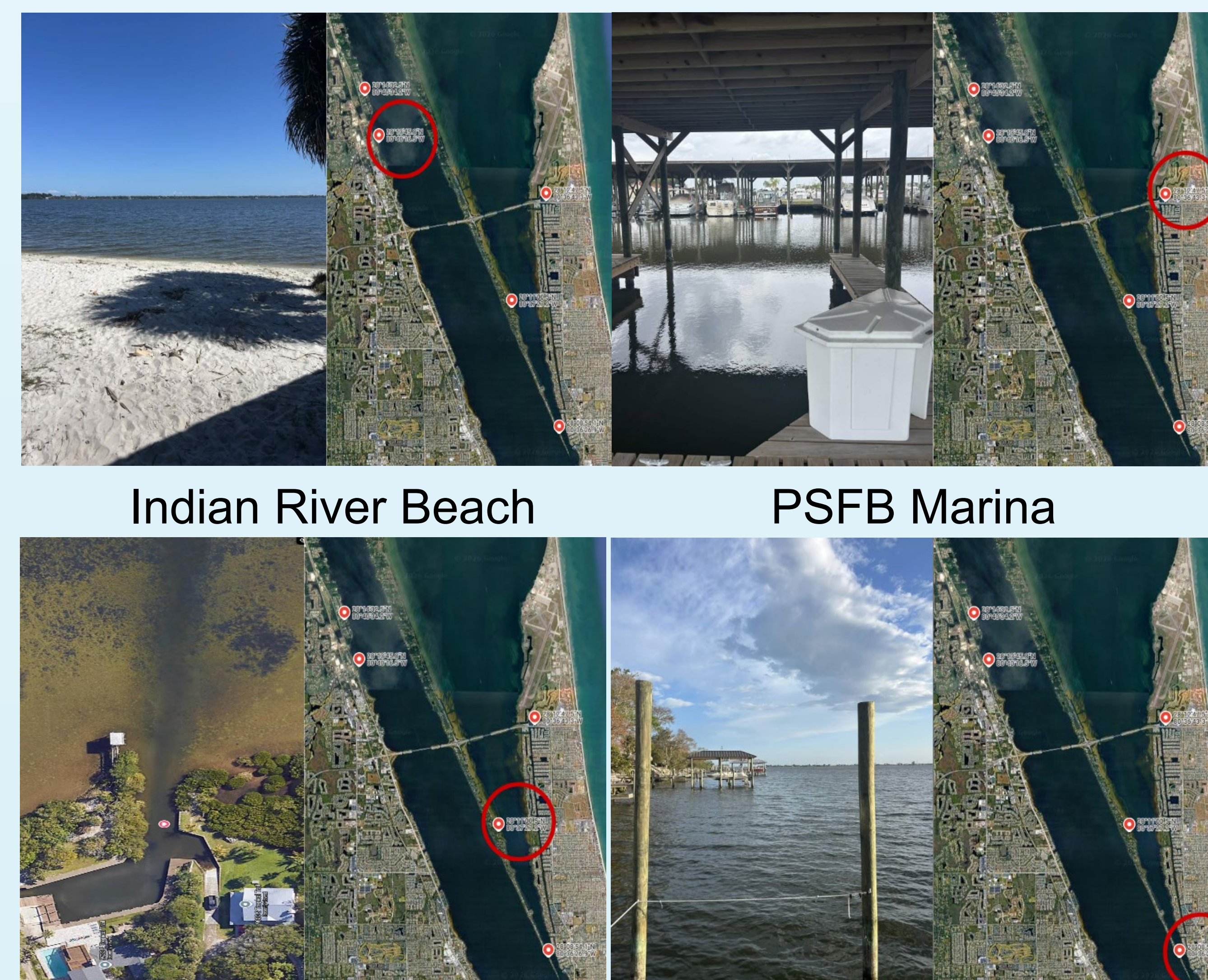
## Images



Locations

Indian River Canal  
Analysis Example

## Other 4 Sites



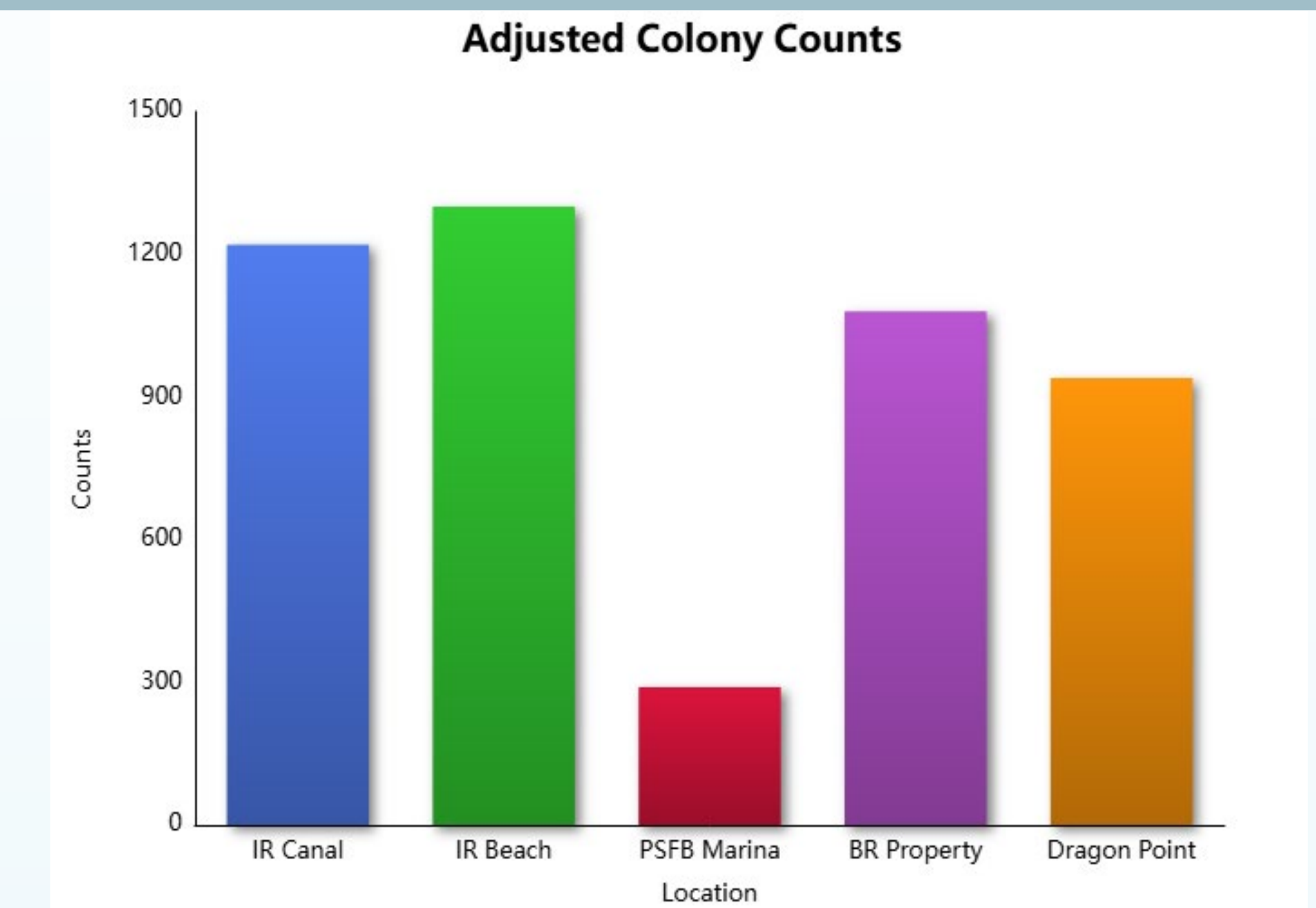
Indian River Beach

PSFB Marina

Banana River Property

Dragon Point

## Results



The graph above displays the estimated bacterial colony counts at each sampling location after adjusting for the 1:10 dilution. Indian River Beach had the highest colony count at approximately 1300, followed by Indian River Canal at approximately 1220. Banana River Property and Dragon Point had counts of approximately 1080 and 940, respectively. PSFB Marina had the lowest colony count at approximately 290. Overall, the data shows a range of colony counts across the five sampling locations.

## Discussion and Conclusion

The results demonstrate clear variation in bacterial colony counts across the sampled locations, with the highest concentrations observed at Indian River Beach and Indian River Canal, and the lowest at PSFB Marina. When adjusted for dilution, these differences become even more pronounced, highlighting the variability in microbial presence across relatively short geographic distances. However, the data does not show a consistent increase or decrease in colony counts moving southward, indicating that distance alone is not the primary factor influencing bacterial concentration. Instead, localized environmental conditions likely play a larger role. These may include differences in human activity, such as residential runoff or marina usage, as well as natural factors like water flow, mixing, and surrounding land use. This study is limited by a single sampling time and a small number of locations, which may not fully represent conditions across the entire river system. Additionally, only total colony counts were measured, without identifying specific bacterial species. Future research could include repeated sampling over time, additional locations, and the measurement of other water quality factors such as pH, salinity, and nutrient levels to provide a more comprehensive understanding of environmental influences on bacterial distribution.

## Acknowledgements

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