



# microshades: An R package for improving color accessibility and organization of microbiome data



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## Background

### Color Vision Deficiency (CVD)

- CVD, commonly known as colorblindness, affects 1 in 12 men and 1 in 200 women - approximately 300 million people worldwide<sup>1</sup>.
- Individuals with CVD do not experience complete loss of color vision, but have reduced ability to distinguish different colors.
- There are three common types of CVD: Deutanopia (red-green colorblindness), Protanopia (red-colorblindness), and Tritanopia (blue-yellow colorblindness).

### Challenges

- Despite the high number of individuals who experience CVD, many scientific figures rely on color to convey information.
- There are several CVD-friendly color palettes available<sup>2-5</sup>, however they are typically limited to 8 – 15 distinct colors or may not be accessible for all forms of CVD.
- Even with these resources, it can be challenging to apply these schemes to scientific figures. For example, when visualizing microbiome data, it is common to represent tens to hundreds of bacterial taxa in one figure, for which the current available CVD color palettes are insufficient.

### References

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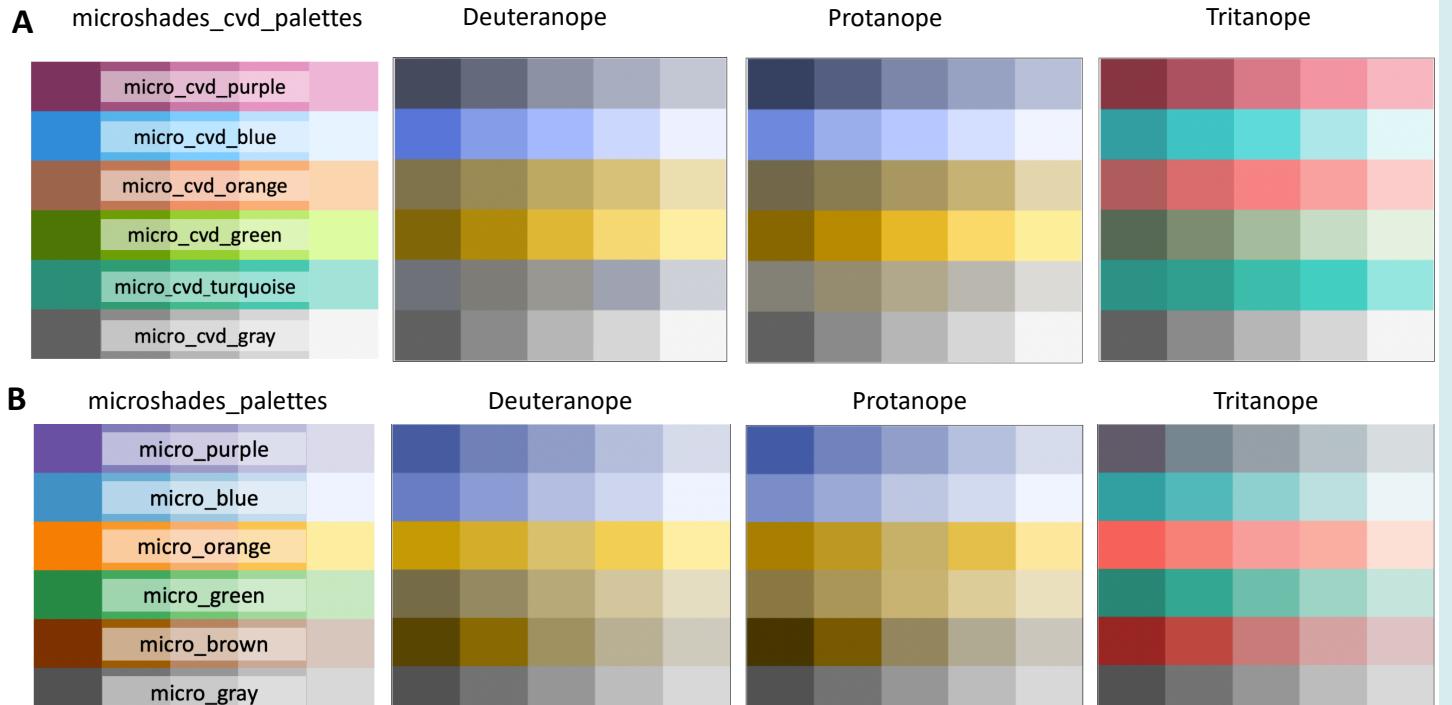
### Acknowledgements

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## Methods

### Color Palette

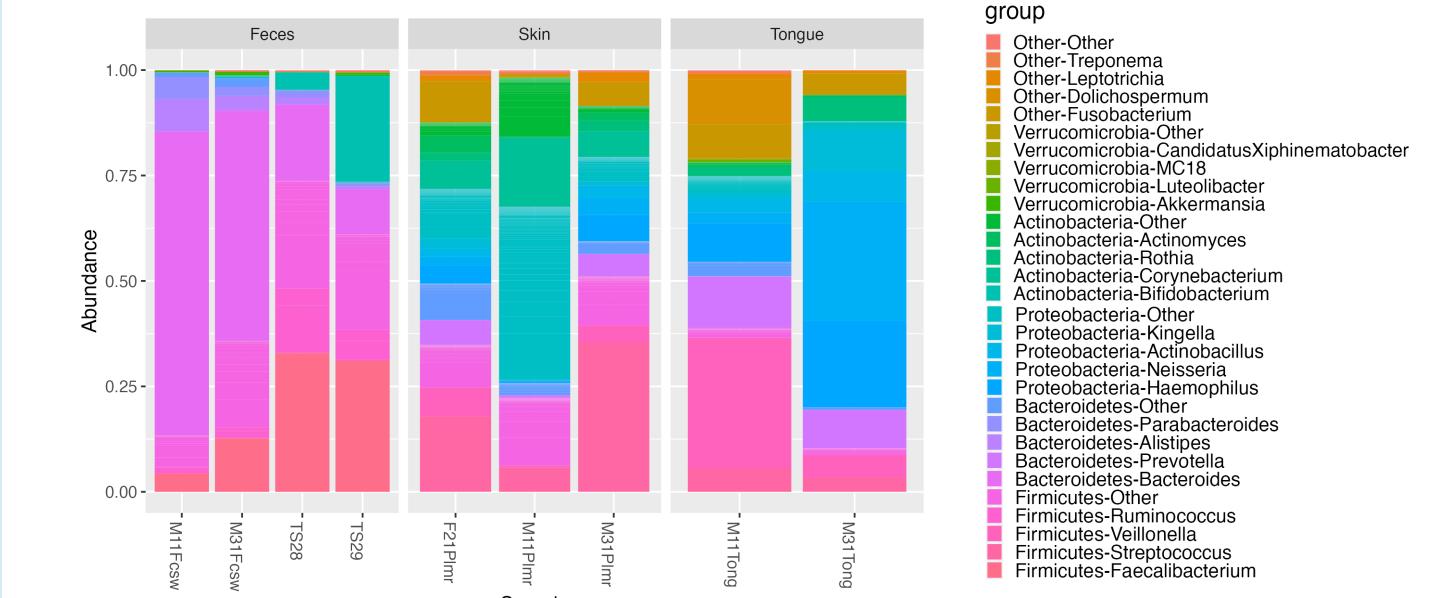
- We developed the *microshades* R package, which provides custom color shading palettes to improve CVD accessibility and data organization. The *microshades* package includes two color palettes: *microshades\_cvd\_palettes* and *microshades\_palettes* (**Figure 1**).
- To construct these palettes, hue (type of color), chroma (colorfulness), and luminance (brightness) were adjusted for optimal visual distinction and CVD accessibility.
- Each color palette contains six hues with five sequential variations of chroma and luminance per hue, for a total of 30 available colors per palette.
- All shades have been tested with a CVD simulator, *cvdemulator*<sup>3</sup> for Deutanope, Protanope, and Tritanope accessibility (**Figure 1**).



**Figure 1.** The *microshades* CVD friendly color palettes (left) and CVD emulations (right) for (A) *microshades\_cvd\_palettes*, and (B) *microshades\_palettes*.  
CVD Emulator: [hclwizard.org:3000/cvdemulator/](http://hclwizard.org:3000/cvdemulator/)  
*microshades*: [bit.ly/microshades](http://bit.ly/microshades)

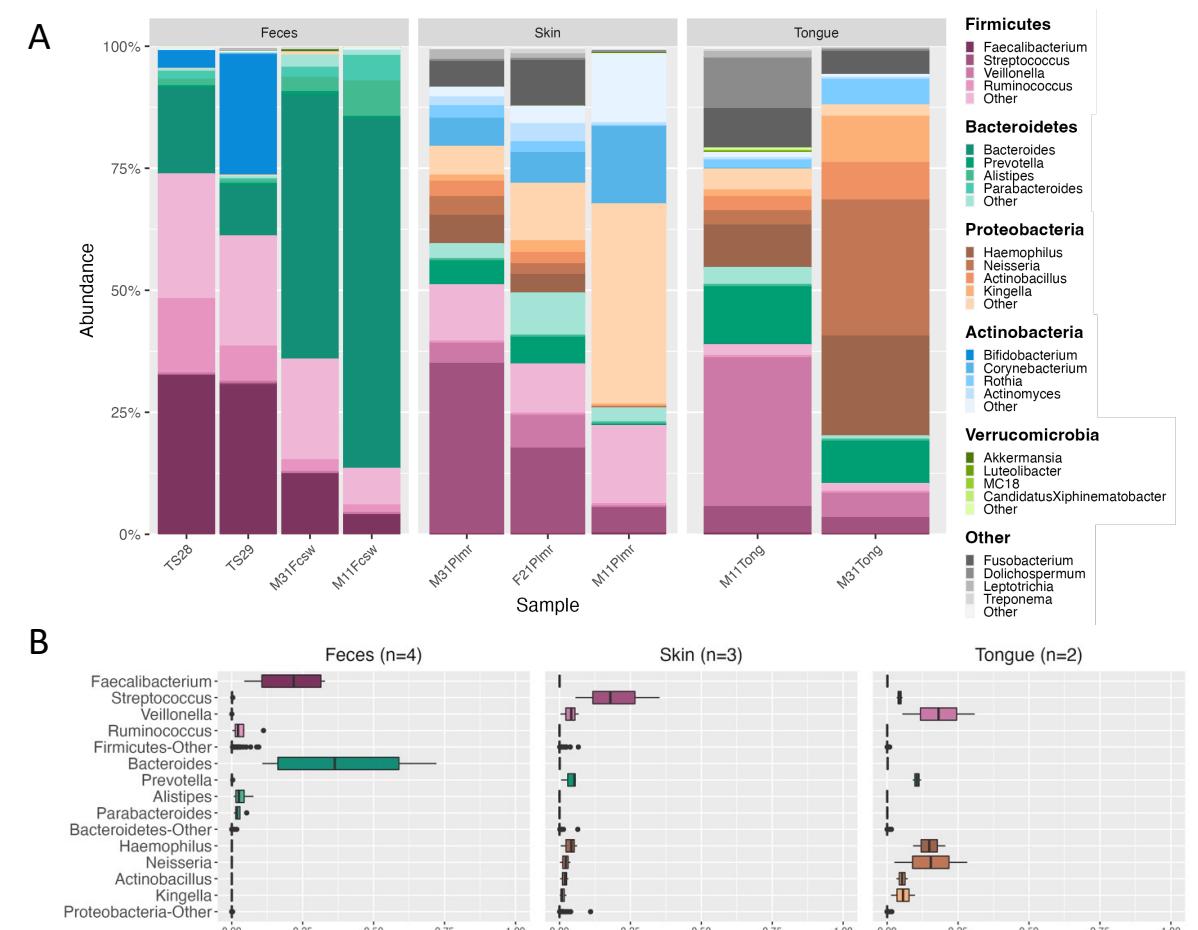
## Results

### Default Colors



**Figure 2.** Stacked barplot of the Global Patterns dataset<sup>6</sup> visualized with *phyloseq*<sup>7</sup> using default colors. Due to the number of different types of bacteria, a continuous palette is used. However, this makes it difficult to distinguish between bacteria.

### microshades Application



**Figure 3.** The Global Patterns dataset<sup>6</sup> visualized with *microshades*. (A) Stacked barplots using the *microshades\_cvd\_palettes* and organization functions. (B) Contribution plots aid in visualizing differences between sampling sites.

## Summary

The *microshades* R package is a visualization tool for microbiome researchers. The package contains two CVD accessible palettes, along with several organization features. The *microshades* package can be used in conjunction with common microbiome R packages, such as *phyloseq*<sup>7</sup>, to enhance microbiome data visualization. Download *microshades* at [bit.ly/microshades](http://bit.ly/microshades) along with microbiome and non-microbiome examples.