SIMILARITY MEASURE IN THE SPACE OF COLOR PALETTES

Color exploration with Emil Hvitfeldt Hansen

Twitter: @Emil_Hvitfeldt

Github: EmilHvitfeldt

github.com/EmilHvitfeldt/OCRUG-color-talk bit.ly/OCRUG-Color-Talk

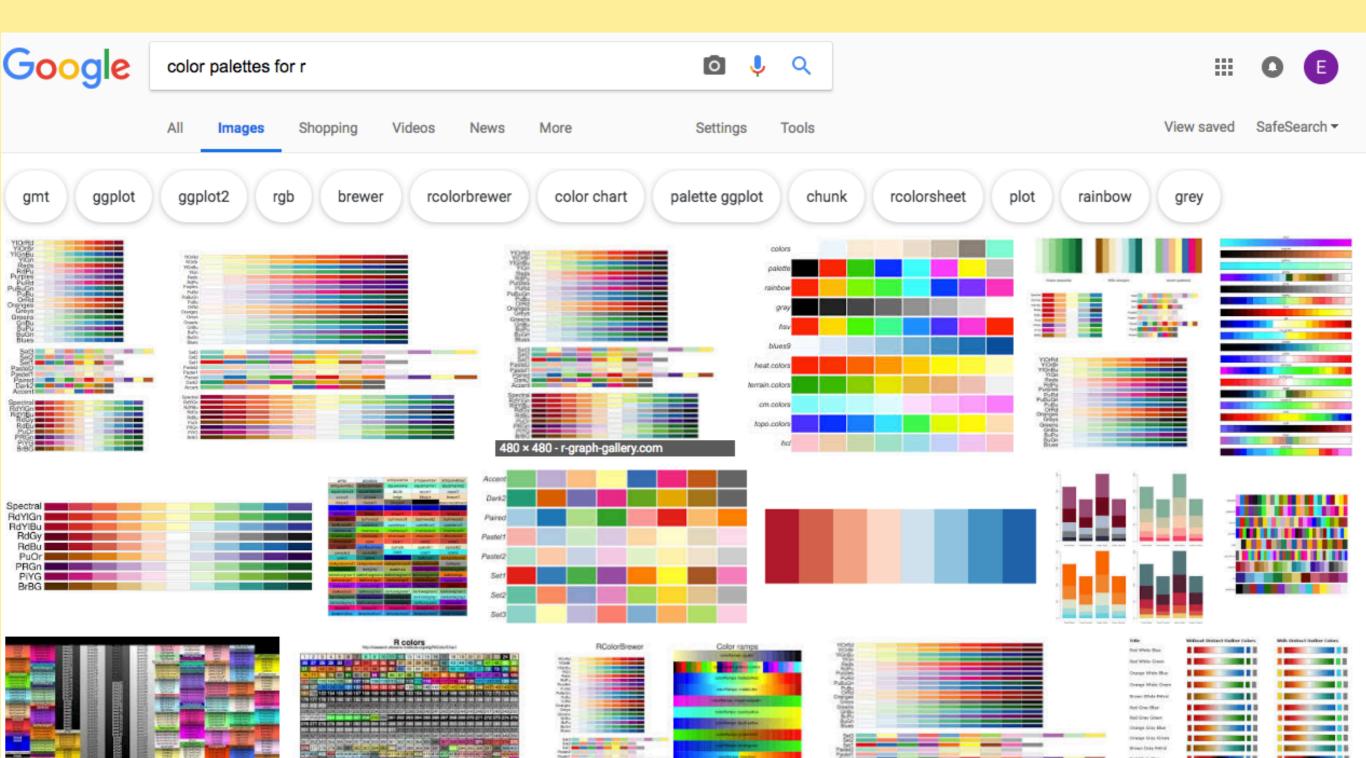
OVERVIEW

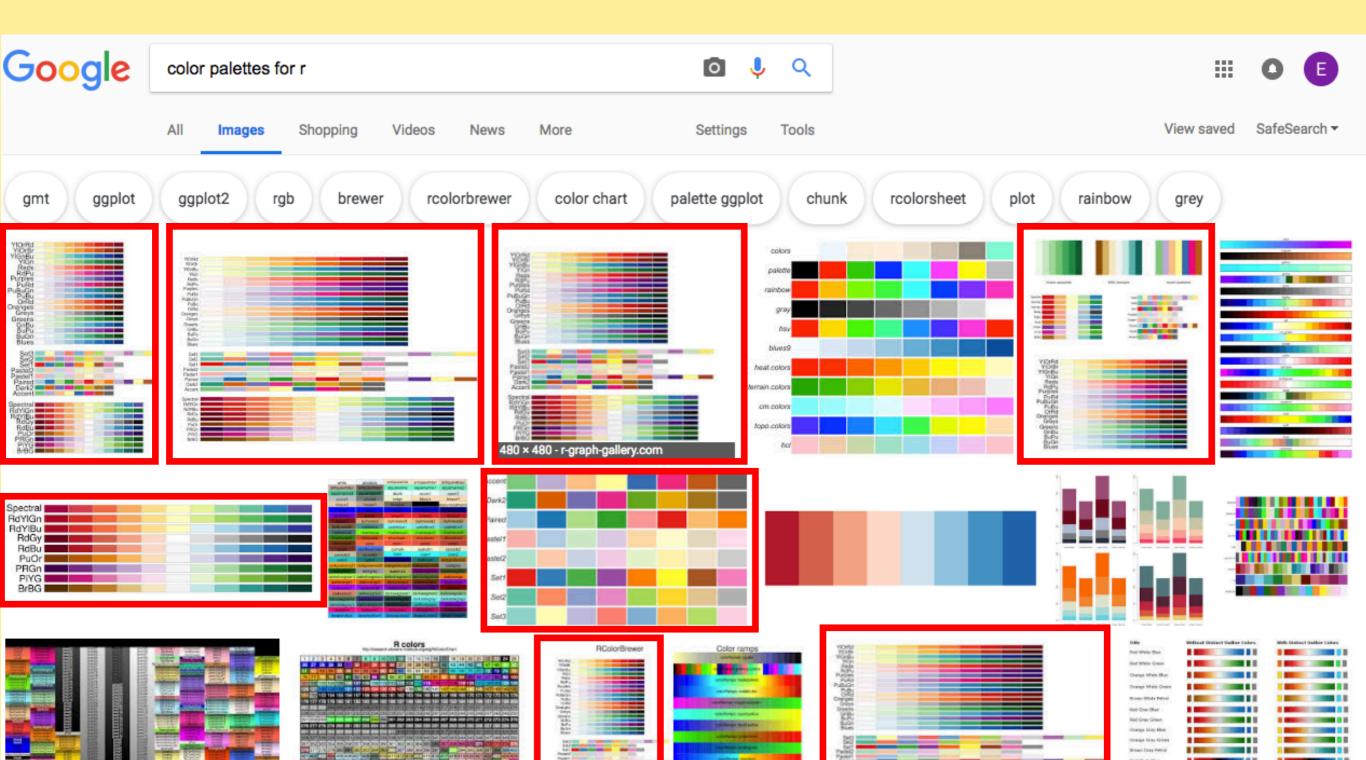
Overview

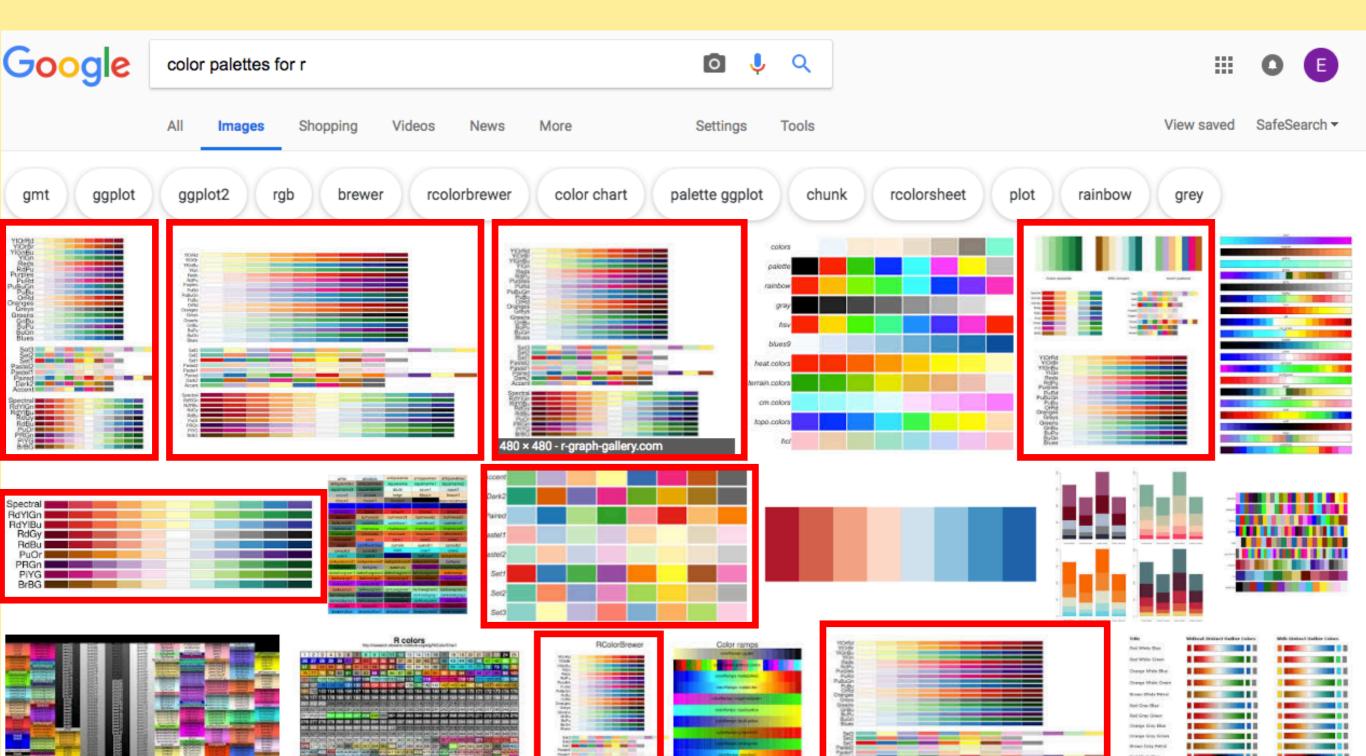
Motivation

Method

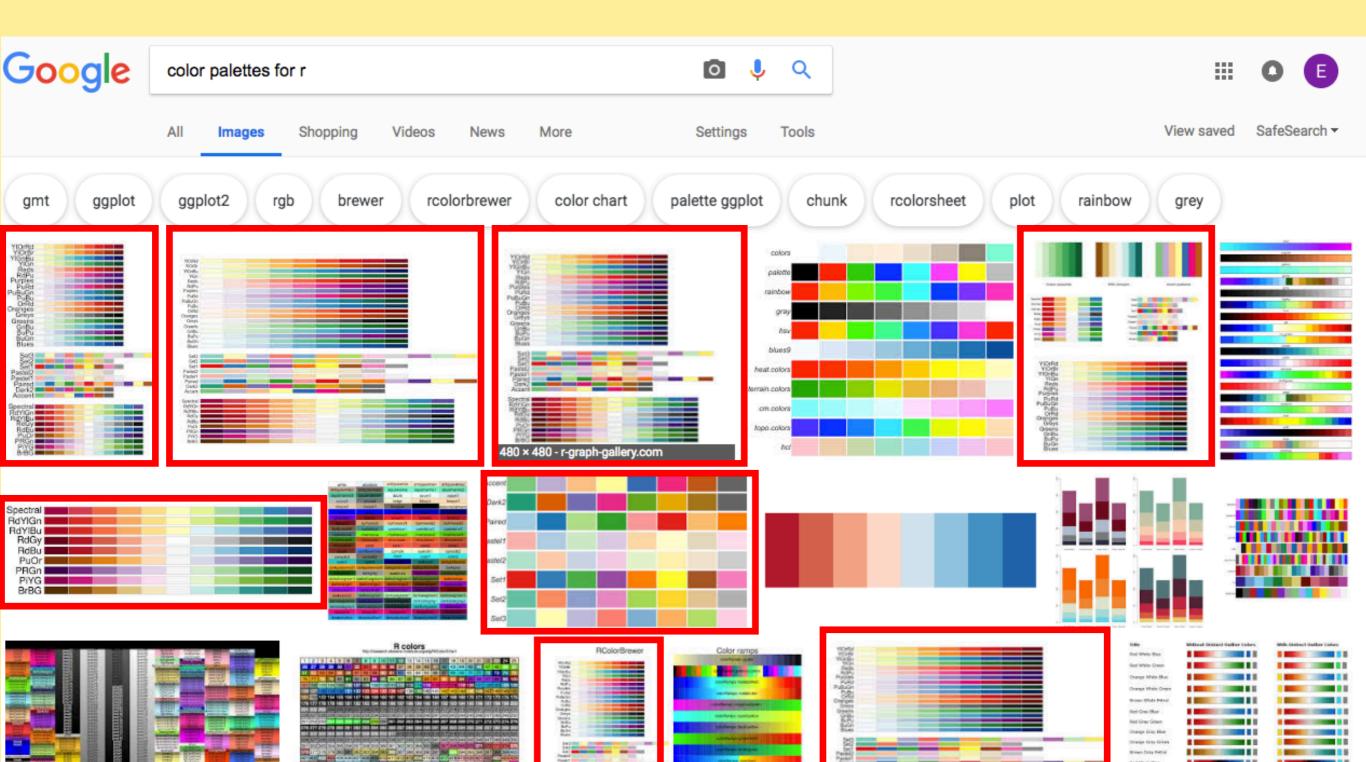
Results





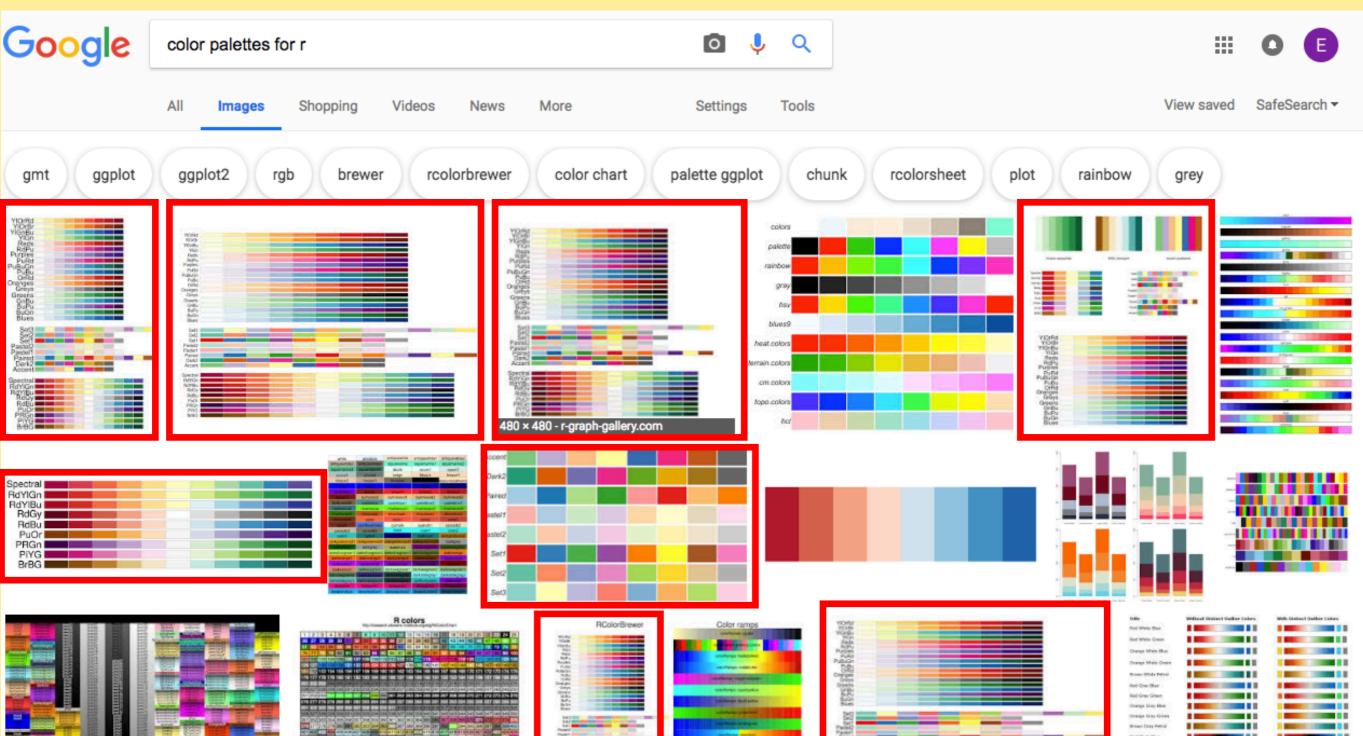


AVAILABLE COLOR PALETTES



AVAILABLE COLOR PALETTES

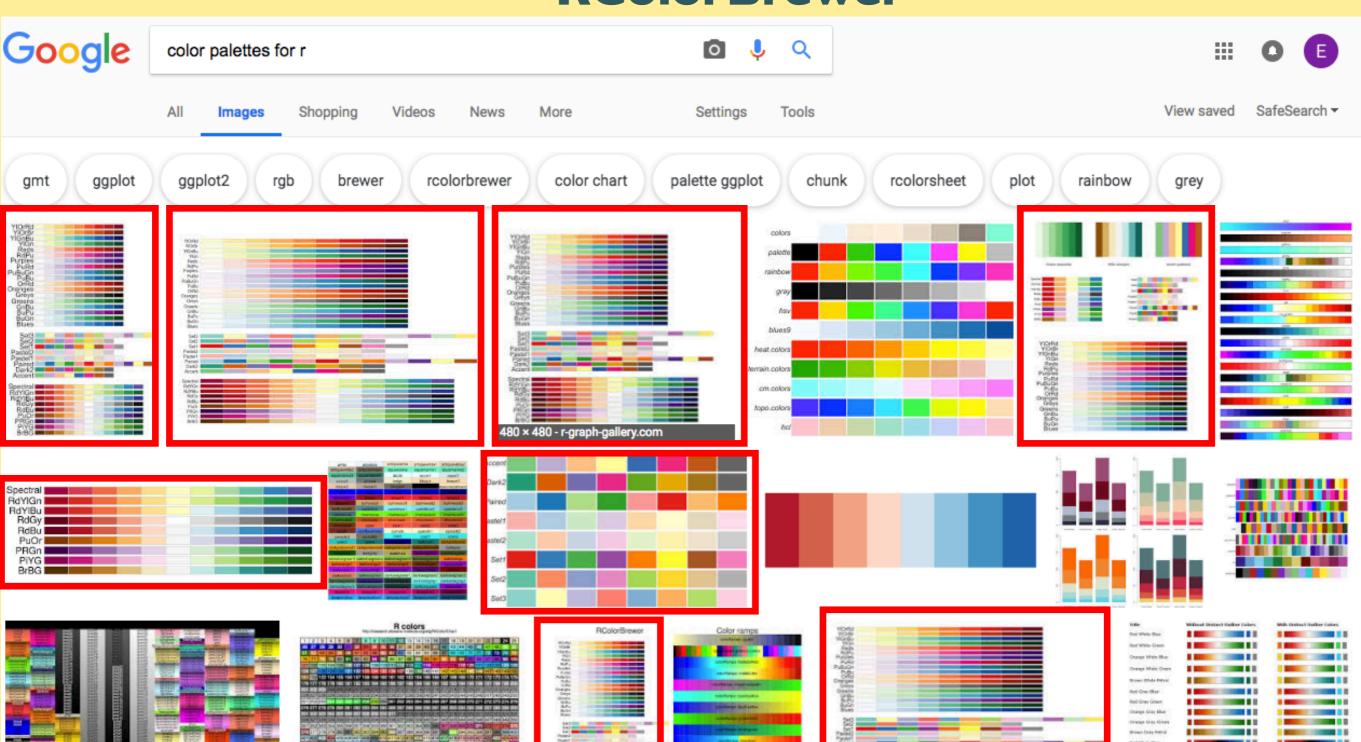
RColorBrewer



RColorBrewer

AVAILABLE COLOR PALETTES

RColorBrewer

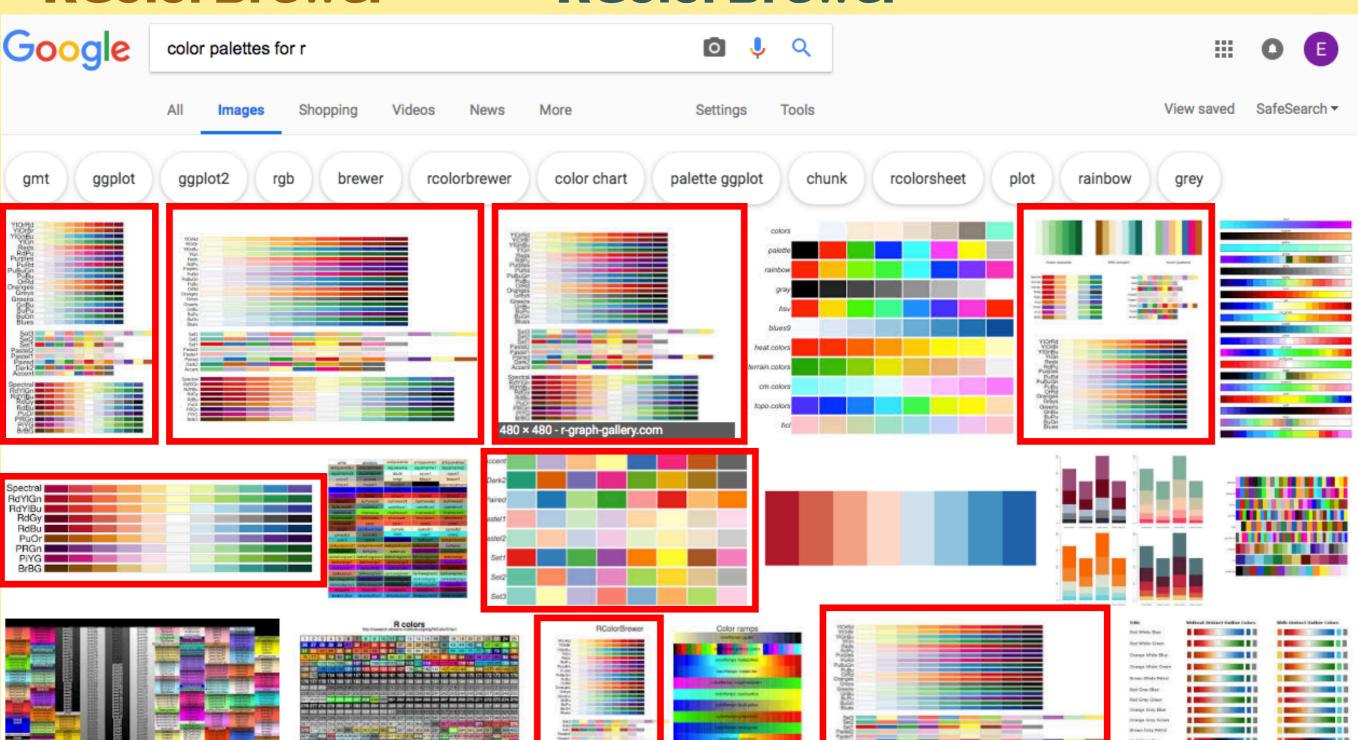


RColorBrewer

AVAILABLE COLOR PALETTES

RColorBrewer

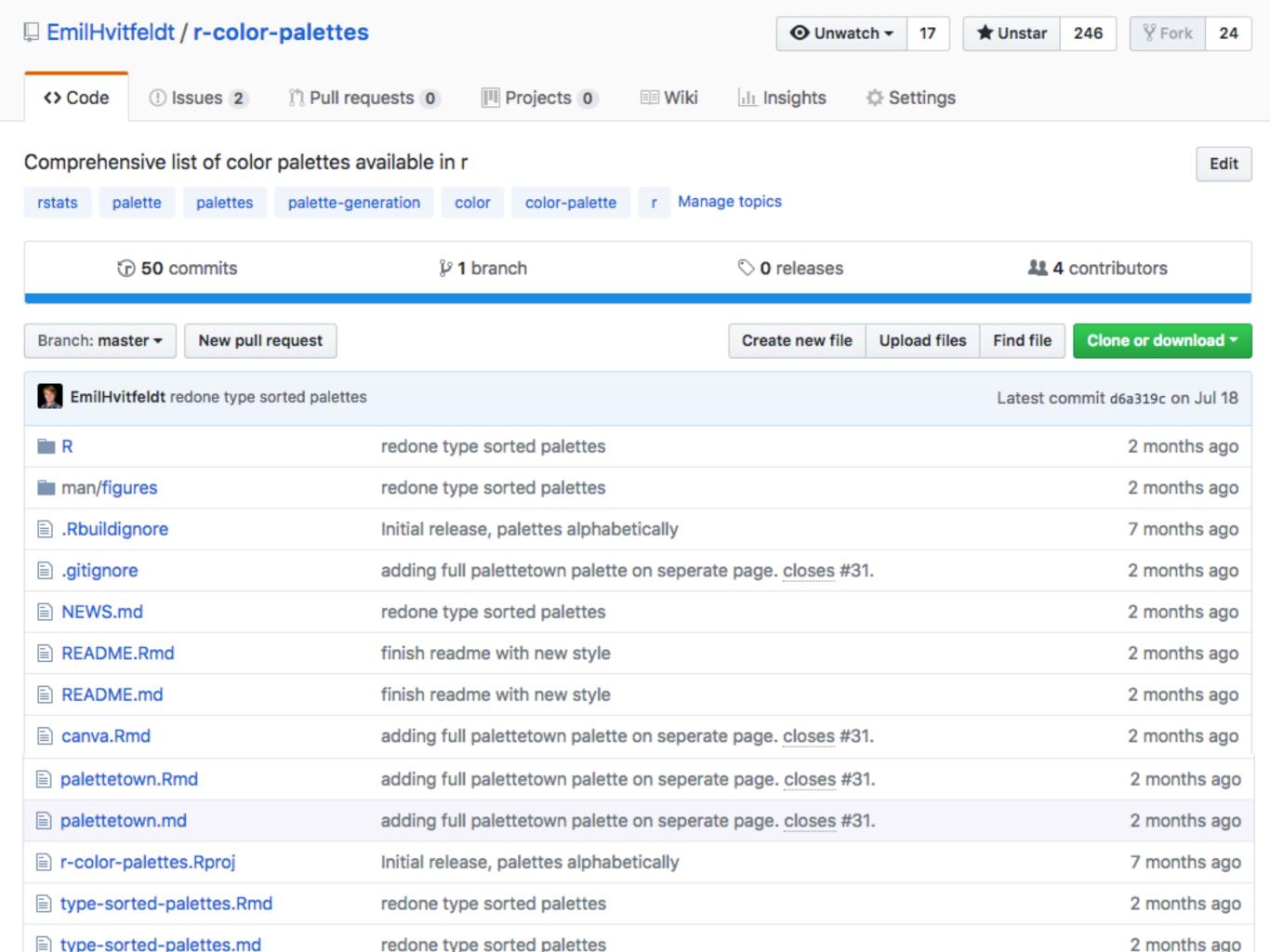
RColorBrewer



SOMETHING IS MISSING

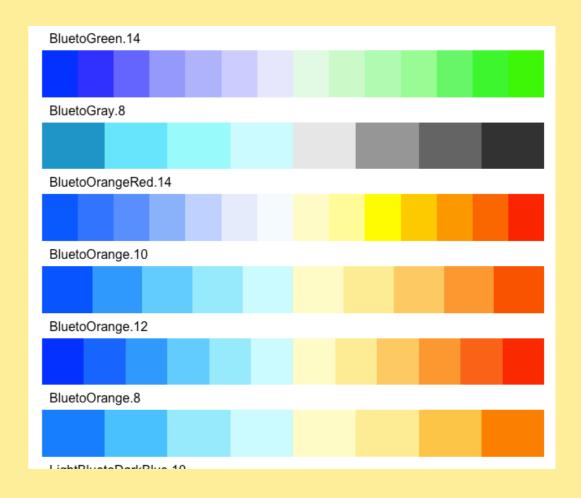
- Where is the viridis palettes?
- Where is the scico palettes?
- Where is the nord palettes?
- Where is the ochRe palettes?

•



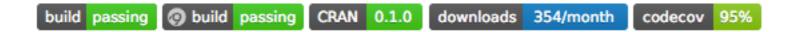
958 palettes from 28 packages







paletteer





The goal of **paletteer** is to be a comprehensive collection of color palettes in R using a common interface. Think of it as the "caret of palettes".

```
paletteer_c(package = "scico", palette = "berlin", n = 10)
#> [1] "#9EB0FF" "#5AA3DA" "#2D7597" "#194155" "#11181D" "#270C01" "#501802"
#> [8] "#8A3F2A" "#C37469" "#FFACAC"
paletteer_d("nord", "frost")
#> [1] "#8FBCBB" "#88C0D0" "#81A1C1" "#5E81AC"
paletteer_dynamic("cartography", "green.pal", 5)
#> [1] "#B8D9A9" "#8DBC80" "#5D9D52" "#287A22" "#17692C"
```

```
paletteer_c(scico, berlin, 10)
#> [1] "#9EB0FF" "#5AA3DA" "#2D7597" "#194155" "#11181D" "#270C01" "#501802"
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paletteer

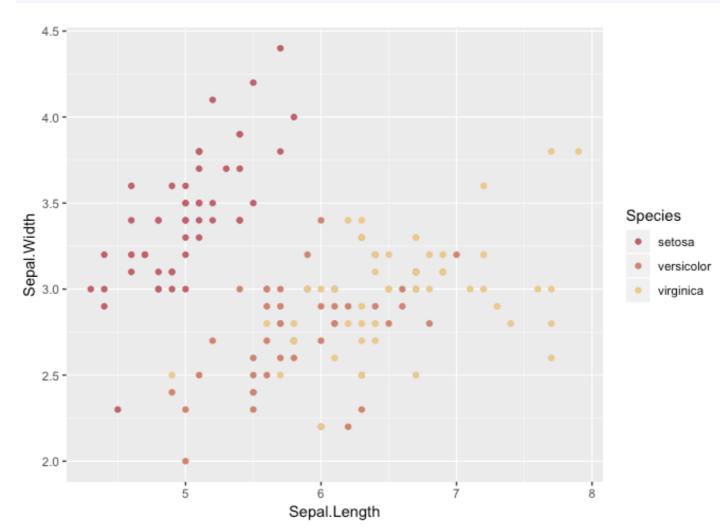




The goal of **paletteer** is to be a comprehensive collection of color palettes in R using a common interface. Think of it as the "caret of palettes".

```
library(ggplot2)

ggplot(iris, aes(Sepal.Length, Sepal.Width, color = Species)) +
   geom_point() +
   scale_color_paletteer_d(nord, aurora)
```







New problem with discoverability



New problem with discoverability

• 100s of palettes, hard to find a new one without using r-color-

palettes



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• 100s of palettes, hard to find a new one without using r-color-

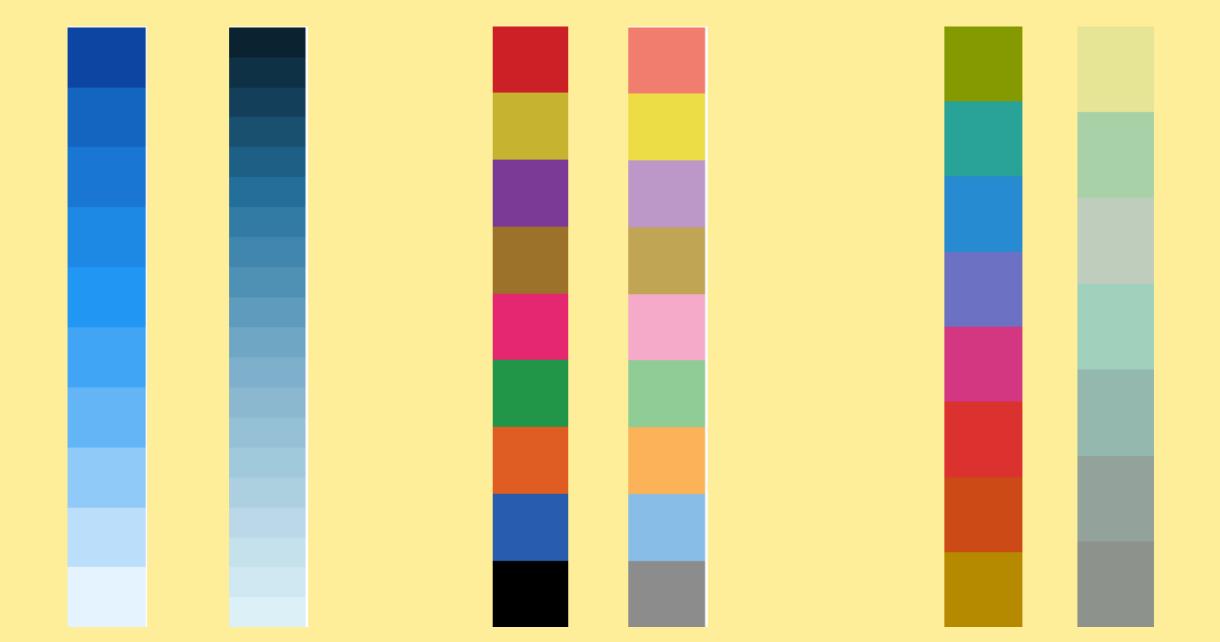
palettes

Still using same palettes



PLAN

• Develop tool to find palette that "looks like" palette you present.



THE INPUT

	l I		ı
#8E938D	red	green	blue
#93A39C [1,]	142	147	141
#95B8AF [2,]	147	163	156
→ #9FD1BE → [3,]	149	184	175
[4,]	159	209	190
#BFCDBD [5,]	191	205	189
#A9D1A7 [6,]	169	209	167
#E6E496 [7,]	230	228	150

NOTRIVIALTRANSFORMATION

Interpolation to fit max length would leads to trouble with palettes of the same scale but different lengths, and qualitative palettes.

Padding with zeroes would not work with diverging palettes.

HAND CRAFTING FEATURES

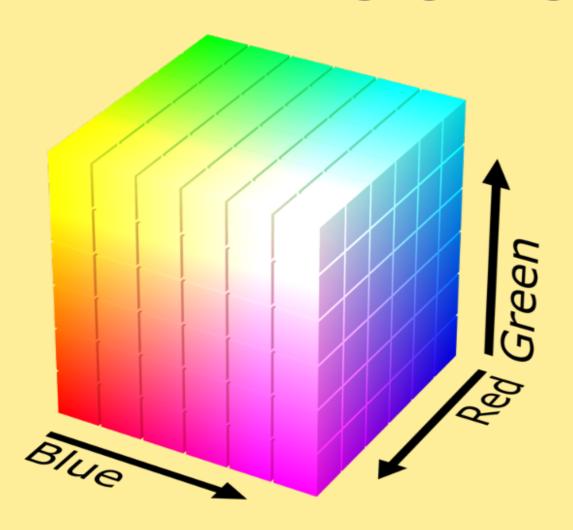
• similar to early image classification

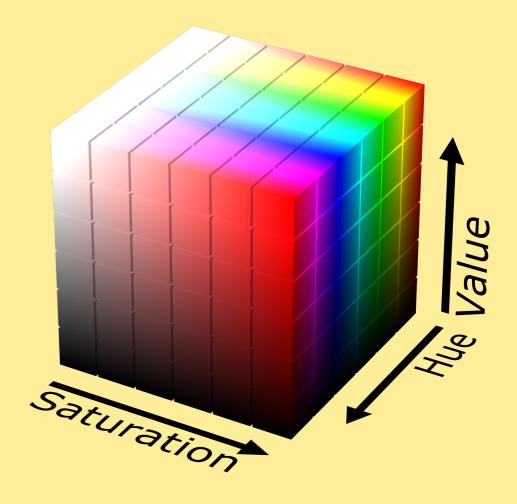
FEATURE LIST

- Includes a certain color
- All a certain color
- Length
- Type (sequential, divergent, qualitative. hardcoded)
- Linearity
- Twice linear (to identify divergent palettes)
- Colorblindness
- Minimal distance between points
- Maximal distance between points

Continuous palettes are taken with 20 points

COLORSPACES





Also CIELAB color space

Create a tibble with a list column of the colors

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- •
- Profit?

CREATINGTIBBLE

R/data_list.R

```
##
  package
                palette
                            type length group
                                                  colors
## 1 ggthemes
                                            c <chr [20]>
                   Red sequential
                                      20
                                            c <chr [20]>
                Green sequential
                                     20
## 2 ggthemes
## 3 ggthemes
                   Blue sequential
                                      20
                                            c <chr [20]>
## 4 ggthemes
             Orange sequential
                                      20
                                            c <chr [20]>
## 5 ggthemes
            Gray sequential
                                      20
                                            c <chr [20]>
## 6 ggthemes Blue Light sequential
                                      20
                                            c <chr [20] >
```

934 rows in total

FEATURE FUNCTIONS

```
color_contains <- function(pal, color, space) {
   spectrum1 <- convert_colour(t(col2rgb(pal)), "rgb", space)
   spectrum2 <- convert_colour(t(col2rgb(color)), "rgb", space)

   compare_colour(spectrum1, spectrum2, space, method = "cie2000") %>%
        min()
}
```

convert_colour() and compare_colour() from farver package

FEATURE FUNCTIONS

```
linear <- function(pal, space) {
  colors <- convert_colour(t(col2rgb(pal)), "rgb", space) %>%
    as.data.frame() %>%
    mutate(x = row_number())

out <- lm(x ~ ., colors) %>%
    summary() %>%
    .$adj.r.squared

if(is.nan(out))
    return(0)

out
}
```

convert_colour() and compare_colour() from farver package

```
data_num <- data_list %>%
  mutate(# contains all a certain color
         contains yellow = map dbl(colors, ~ color contains(.x, "yellow", "hsv")),
         contains orange = map dbl(colors, ~ color contains(.x, "orange", "hsv")),
         contains red = map dbl(colors, ~ color contains(.x, "red", "hsv")),
         contains_purple = map_dbl(colors, ~ color_contains(.x, "purple", "hsv")),
         contains blue = map dbl(colors, ~ color contains(.x, "blue", "hsv")),
         contains green = map dbl(colors, ~ color contains(.x, "green", "hsv")),
         contains brown = map dbl(colors, ~ color contains(.x, "brown", "hsv")),
         contains_white = map_dbl(colors, ~ color_contains(.x, "white", "hsv")),
         contains_black = map_dbl(colors, ~ color_contains(.x, "black", "hsv")),
         # All a certain color
         all contains yellow = map dbl(colors, ~ color all contains(.x, "yellow", "hsv")),
         all contains orange = map dbl(colors, ~ color all contains(.x, "orange", "hsv")),
         all_contains_red = map_dbl(colors, ~ color_all_contains(.x, "red", "hsv")),
         all_contains_purple = map_dbl(colors, ~ color_all_contains(.x, "purple", "hsv")),
         all_contains_blue = map_dbl(colors, ~ color_all_contains(.x, "blue", "hsv")),
         all_contains_green = map_dbl(colors, ~ color_all_contains(.x, "green", "hsv")),
         all_contains_brown = map_dbl(colors, ~ color_all_contains(.x, "brown", "hsv")),
         all_contains_white = map_dbl(colors, ~ color_all_contains(.x, "white", "hsv")),
         all_contains_black = map_dbl(colors, ~ color_all_contains(.x, "black", "hsv")),
         # Is it linear in a perceptually uniform space
         linear = map_dbl(colors, ~ linear(.x, "hunterlab")),
         linear_deutan = map_dbl(colors, ~ linear(deutan(.x), "hunterlab")),
         linear_protan = map_dbl(colors, ~ linear(protan(.x), "hunterlab")),
         linear tritan = map dbl(colors, ~ linear(tritan(.x), "hunterlab")),
         # Twice linear
         twice_linear = map_dbl(colors, ~ linear_split(.x, "hunterlab")),
         twice_linear_deutan = map_dbl(colors, ~ linear_split(deutan(.x), "hunterlab")),
         twice_linear_protan = map_dbl(colors, ~ linear_split(protan(.x), "hunterlab")),
         twice_linear_tritan = map_dbl(colors, ~ linear_split(tritan(.x), "hunterlab")),
```

```
# Min distance between points
min_distance = map_dbl(colors, ~ min_distance(.x, "hunterlab")),
min_distance_deutan = map_dbl(colors, ~ min_distance(deutan(.x), "hunterlab")),
min_distance_protan = map_dbl(colors, ~ min_distance(protan(.x), "hunterlab")),
min_distance_tritan = map_dbl(colors, ~ min_distance(tritan(.x), "hunterlab")),
# Max distance between points
max_distance = map_dbl(colors, ~ max_distance(.x, "hunterlab")),
max_distance_deutan = map_dbl(colors, ~ max_distance(deutan(.x), "hunterlab")),
max_distance_protan = map_dbl(colors, ~ max_distance(protan(.x), "hunterlab")),
max_distance_tritan = map_dbl(colors, ~ max_distance(tritan(.x), "hunterlab")),
# IQR distance between points
iqr_distance = map_dbl(colors, ~ iqr_distance(deutan(.x), "hunterlab")),
iqr_distance_deutan = map_dbl(colors, ~ iqr_distance(deutan(.x), "hunterlab")),
iqr_distance_tritan = map_dbl(colors, ~ iqr_distance(protan(.x), "hunterlab")),
iqr_distance_tritan = map_dbl(colors, ~ iqr_distance(tritan(.x), "hunterlab")))
)
```

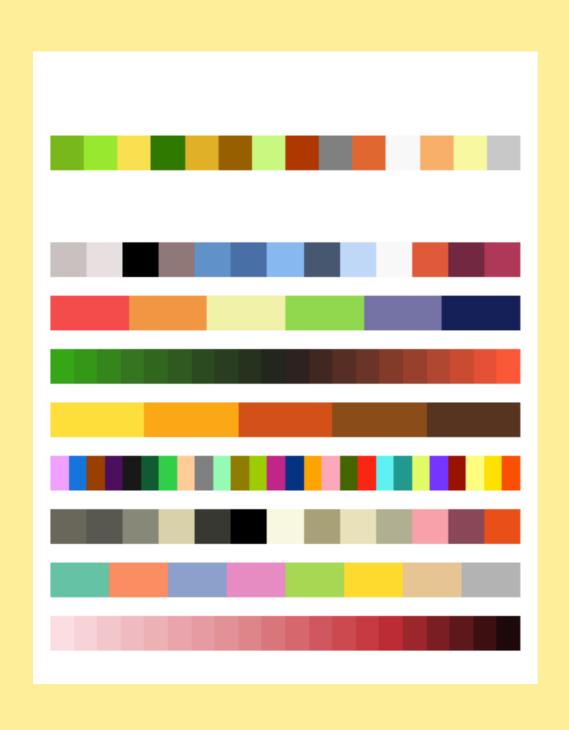
SCALING

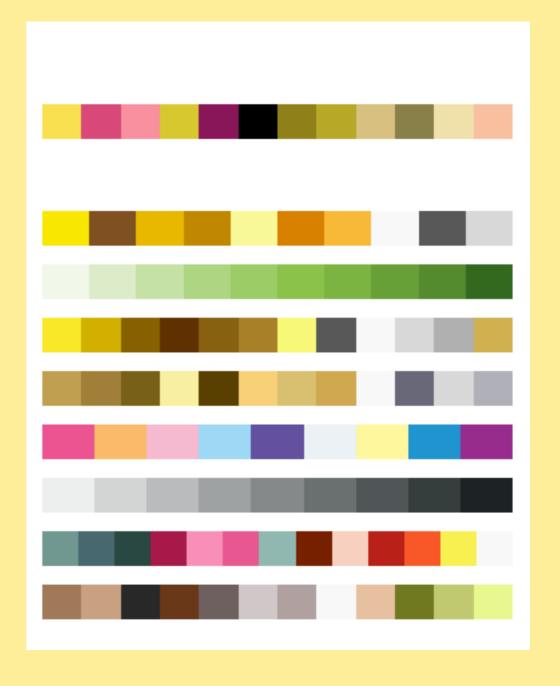
```
data meta <- data num %>%
  mutate(id = as.character(str_glue("{package}-{palette}-{group}")))
data prescaled <- data meta %>%
  select(-package, -palette, -colors) %>%
  mutate_at(vars(type, group), funs(as.factor))
library(recipes)
re <- recipe(id \sim ., data = data prescaled) \%>\%
  step dummy(type, group) %>%
  step_center(all_predictors()) %>%
  step scale(all predictors()) %>%
  prep()
data_scaled <- bake(re, newdata = data_prescaled)</pre>
```

MODELING

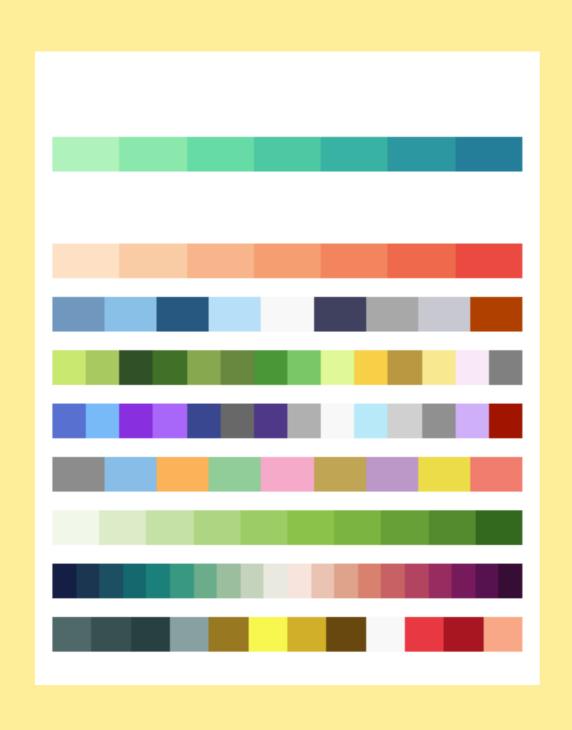
- Simple nearest neighbors method
- Using Euclidean distance
- Same weights for all predictors due to scaling

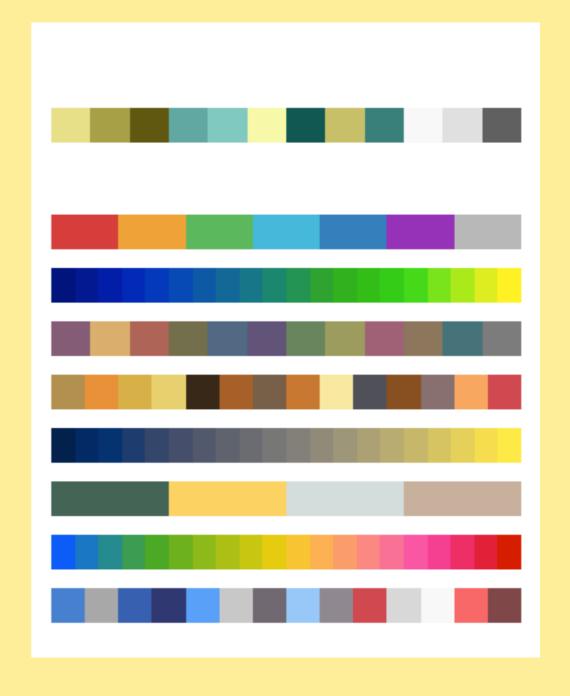
BASELINE



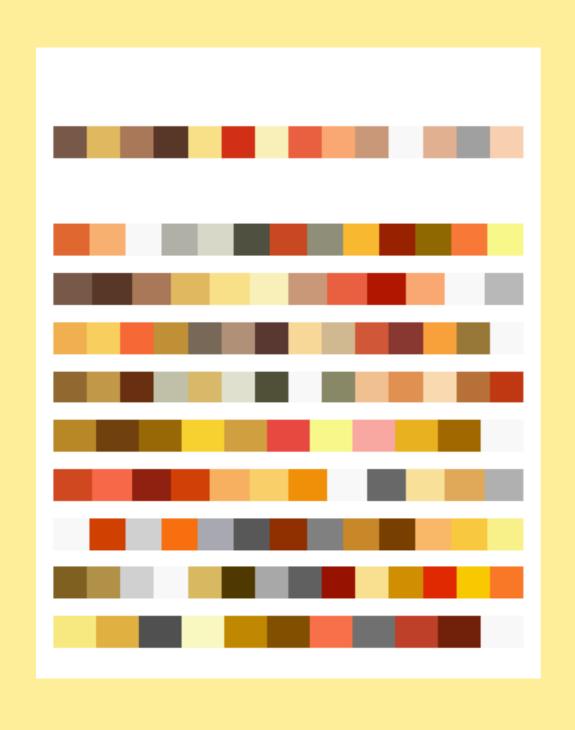


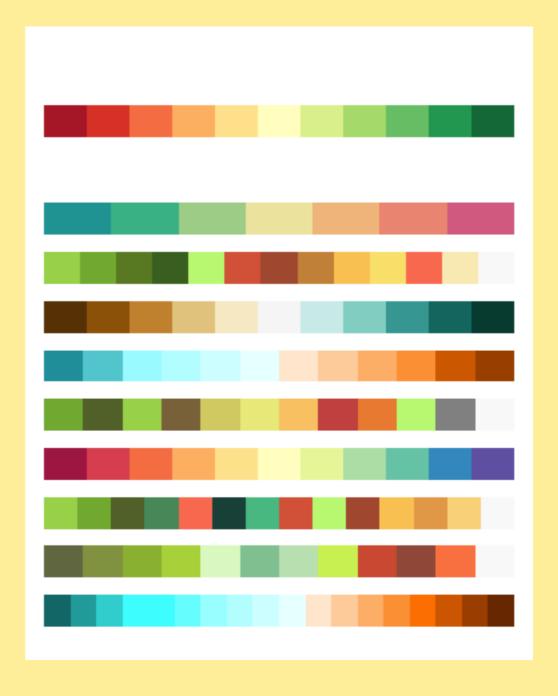
BASELINE





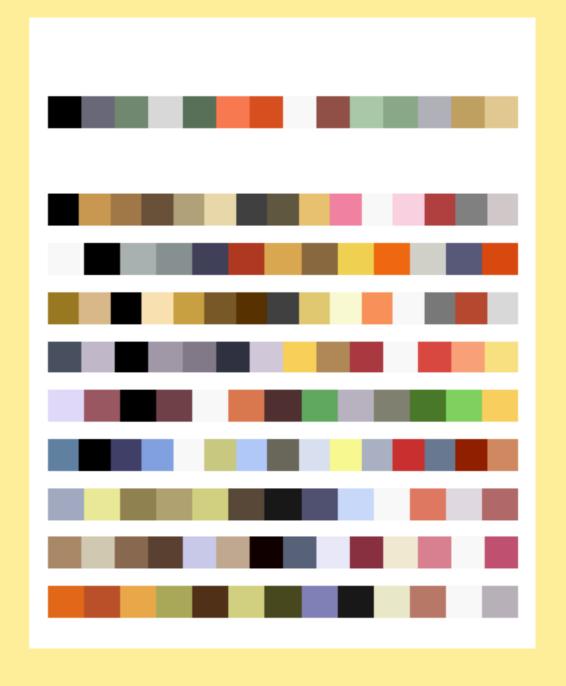
NEAREST NEIGHBORS





NEAREST NEIGHBORS





LIVE DEMO

With audience participation