Final project

Annie Cohen

3/26/2022

```r
cancerdata <- data %>%
  mutate(prop_infiltrated = infiltration_count/tile_count)

long_data <- cancerdata %>%
  pivot_longer(-colnames(cancerdata[,c(1:8,34)]), names_to = "gene", values_to = "exp")

genes <- c("TLR4","CIITA","KLRD1","MC3R","NAMPT")

long_data %>%
  filter(gene %in% genes) %>%
  ggplot(aes(x = exp, y = prop_infiltrated, col = gender)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = 'lm', formula = 'y~x', se = FALSE) +
  facet_wrap(~gene) +
  scale_color_manual(values = c("cornflowerblue","darkgoldenrod2")) +
  theme_classic()
```