Untitled

```r
library(tidyverse)
library(SummarizedExperiment)
theme_set(theme_bw())



load("species_tse.rda")
focus_taxa <- c("Slackia isoflavoniconvertens",
        "Streptococcus gordonii", "Klebsiella variicola
        CAG:634")

abundances <- t(assay(species_tse)) |>
  as_tibble() |>
  select(focus_taxa)

species_data <- abundances |>
  bind_cols(as_tibble(colData(species_tse))) |>
  pivot_longer(-colnames(colData(species_tse)))



species_data |>
  ggplot(aes(age, value, col = BMI)) +
  geom_point(size = 0.5, alpha = 0.8) +
  stat_smooth(method = "lm", se = FALSE, col = "black") +
  facet_grid(name ~ reorder(study_name, value, mean),
        scales = "free_y") +
  scale_y_log10()
```