

Test MCTs with CLR-adjusted taxonomy

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```
## named numeric(0)

##          k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroidia
##
## k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides
##
##          k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae
##
##          k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroidia
##
## k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides
##
##          k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae
##

plot.baseline <- baseline[rownames(baseline) %in% names(sigs),]
plot.baseline.t <- as.data.frame(t(plot.baseline))
plot.baseline.t$timepoint <- "baseline"
plot.baseline.t <- rownames_to_column(plot.baseline.t, var = "UserName")

plot.final <- final[rownames(final) %in% names(sigs),]
plot.final.t <- as.data.frame(t(plot.final))
plot.final.t$timepoint <- "final"
plot.final.t <- rownames_to_column(plot.final.t, var = "UserName")

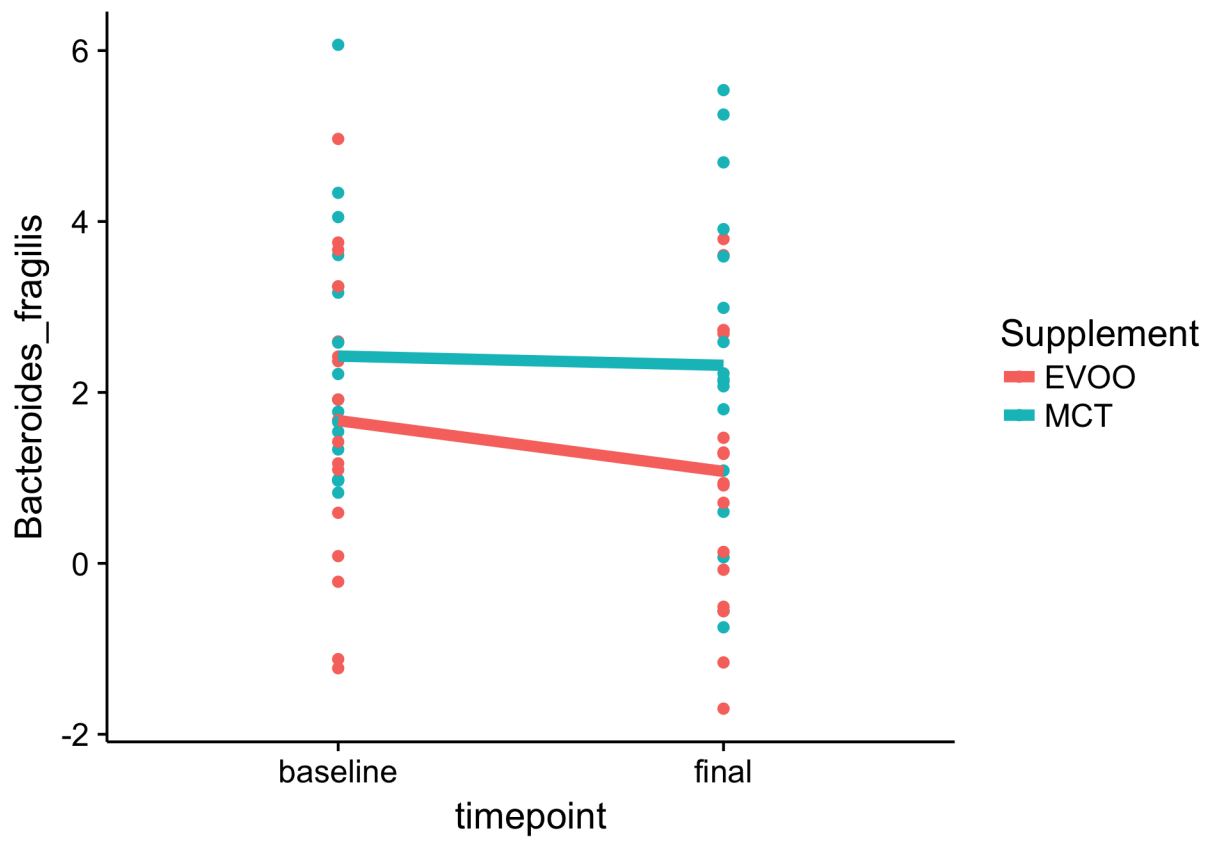
plot <- rbind(plot.final.t, plot.baseline.t)
plot <- inner_join(plot, tax_smry_map)

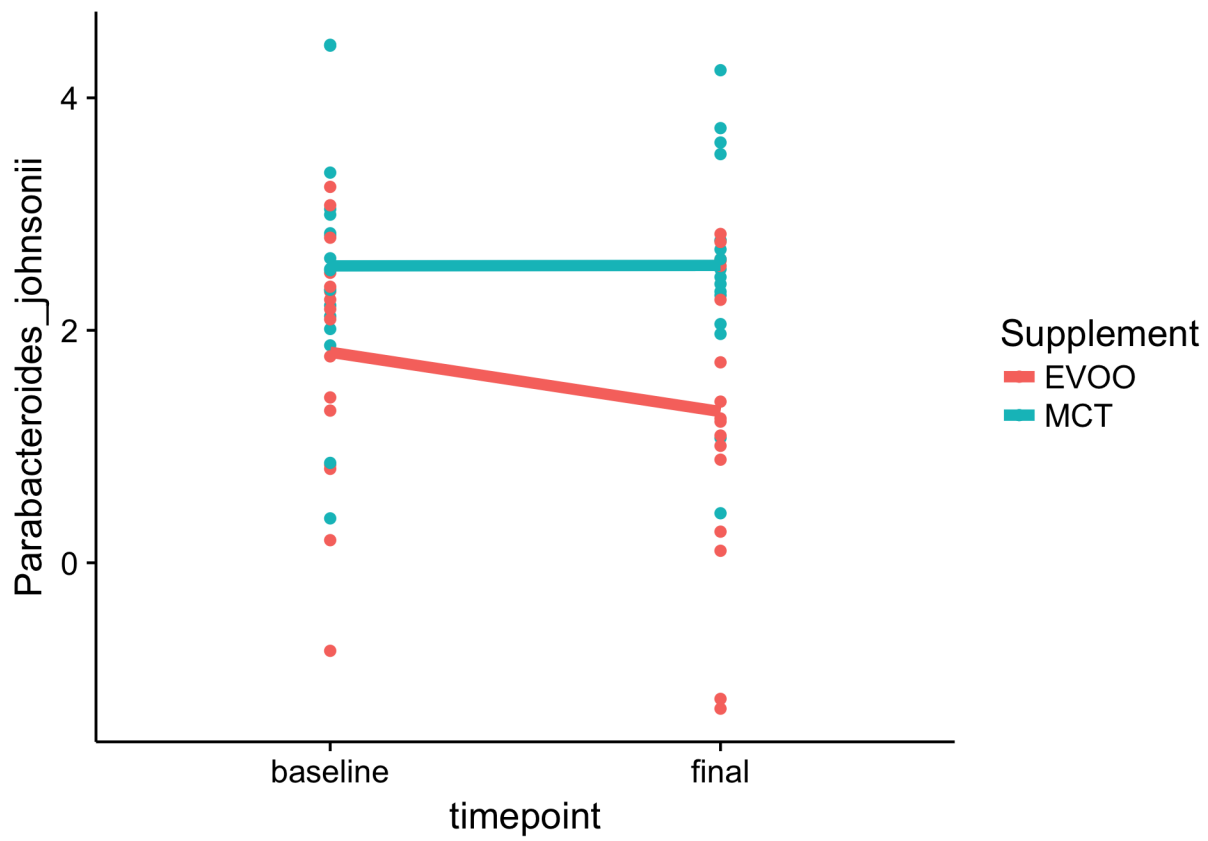
## Joining, by = "UserName"

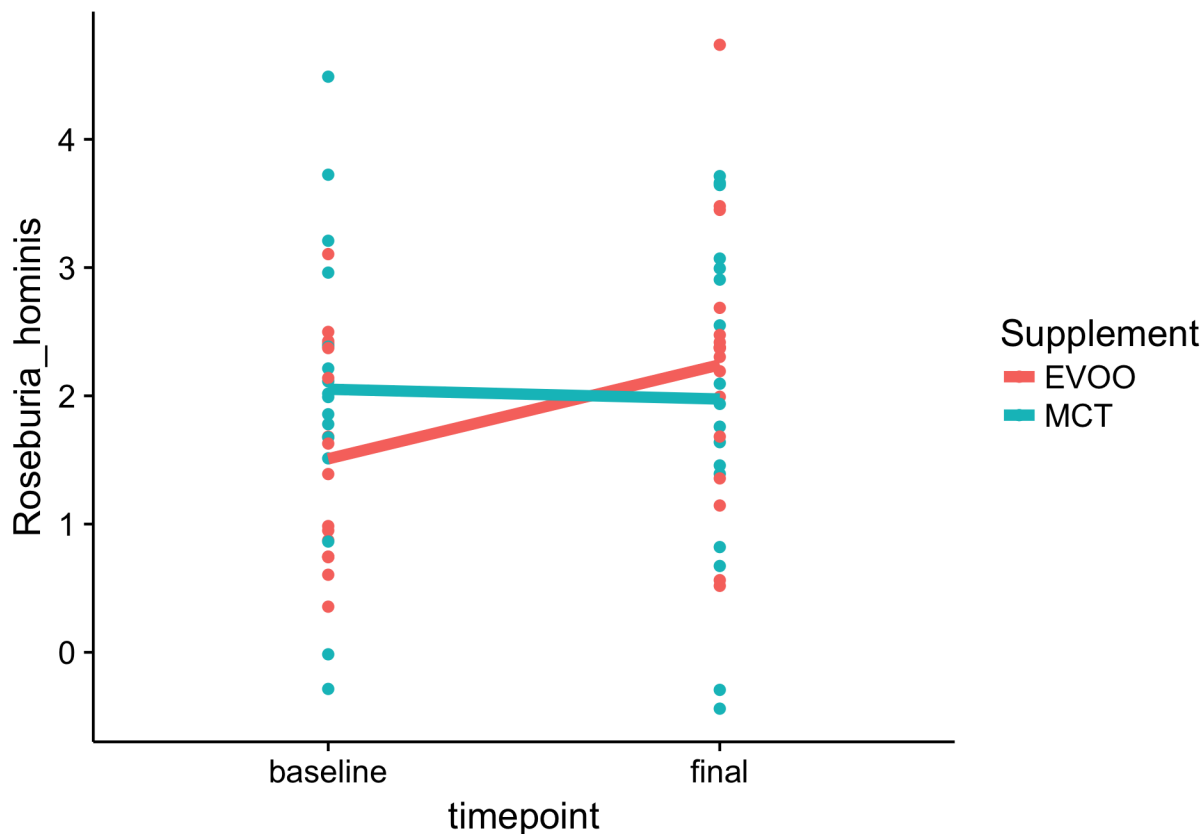
## Warning: Column `UserName` joining character vector and factor, coercing
## into character vector

names(sigs) <- gsub(".*s__", "", names(sigs))
colnames(plot) <- gsub(".*s__", "", colnames(plot))
names(sigs) <- gsub("]", "", names(sigs))
colnames(plot) <- gsub("]", "", colnames(plot))
names(sigs) <- gsub("\\[", "", names(sigs))
colnames(plot) <- gsub("\\[", "", colnames(plot))

for (i in names(sigs)) {
  print(ggplot(plot, aes_string(x = "timepoint", y = i, color = "Supplement")) +
    geom_point() +
    geom_smooth(aes(group = Supplement), size = 2, method = "lm", se = FALSE)
  )
}
```







```
##
## Spearman's rank correlation rho
##
## data: plot$Bacteroides_fragilis[plot$Supplement == "EVOO"] and plot$LDL.Final[plot$Supplement == "EVOO"]
## S = 7157.7, p-value = 0.08224
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.3119038

##
## Spearman's rank correlation rho
##
## data: plot$Parabacteroides_johnsonii[plot$Supplement == "EVOO"] and plot$LDL.Final[plot$Supplement == "EVOO"]
## S = 6223.7, p-value = 0.4424
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.1407057

##
## Spearman's rank correlation rho
##
## data: plot$Roseburia_hominis[plot$Supplement == "EVOO"] and plot$LDL.Final[plot$Supplement == "EVOO"]
## S = 5997.2, p-value = 0.5891
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
```

```
##          rho
## -0.09919201
## Warning: Removed 4 rows containing non-finite values (stat_smooth).
## Warning: Removed 4 rows containing missing values (geom_point).
```

