Subject__15

Type	Your Average	Total Average
CALORIES	1760.42	2080.11
PROTEIN	74.55	88.57
TOTAL FAT	63.45	89.97
CARBS	228.95	225.55
FIBER	16.4	21.96

MicroNutrients
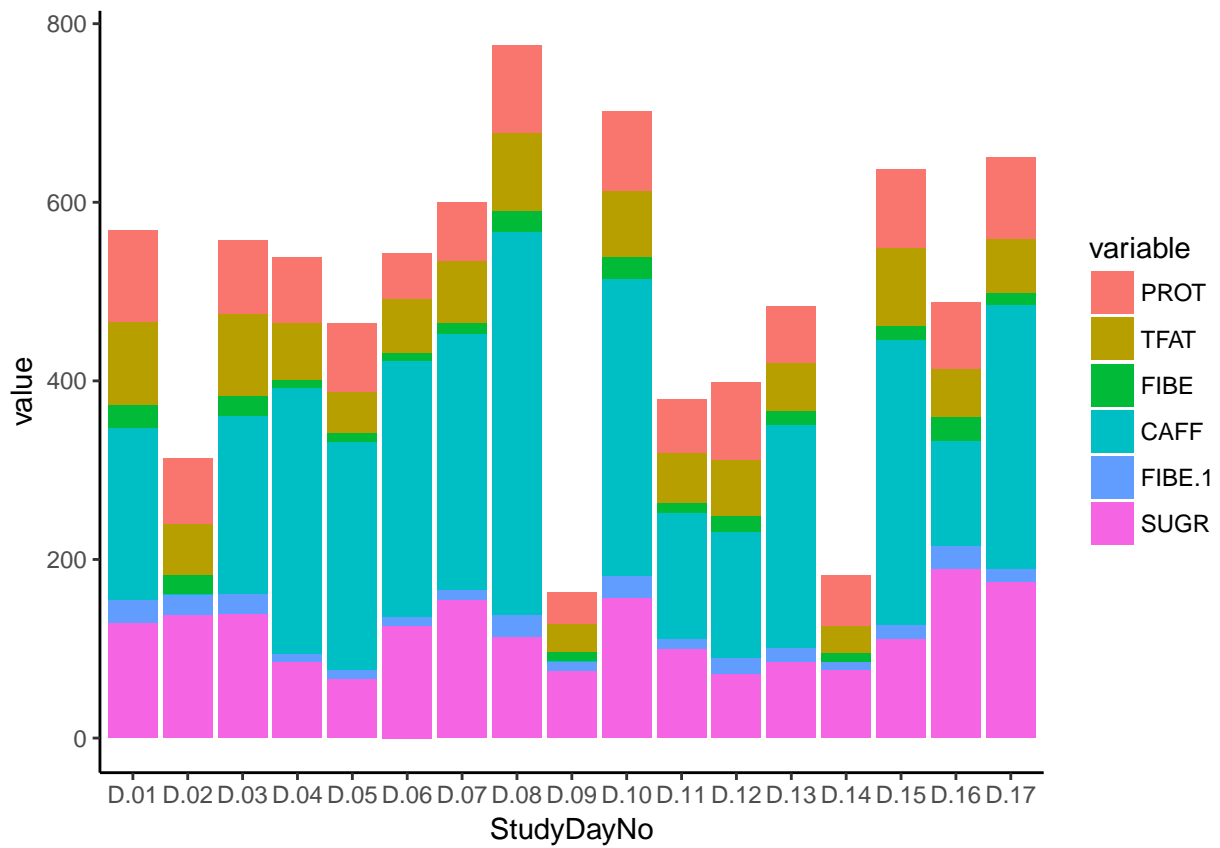
Daily Calorie Intake
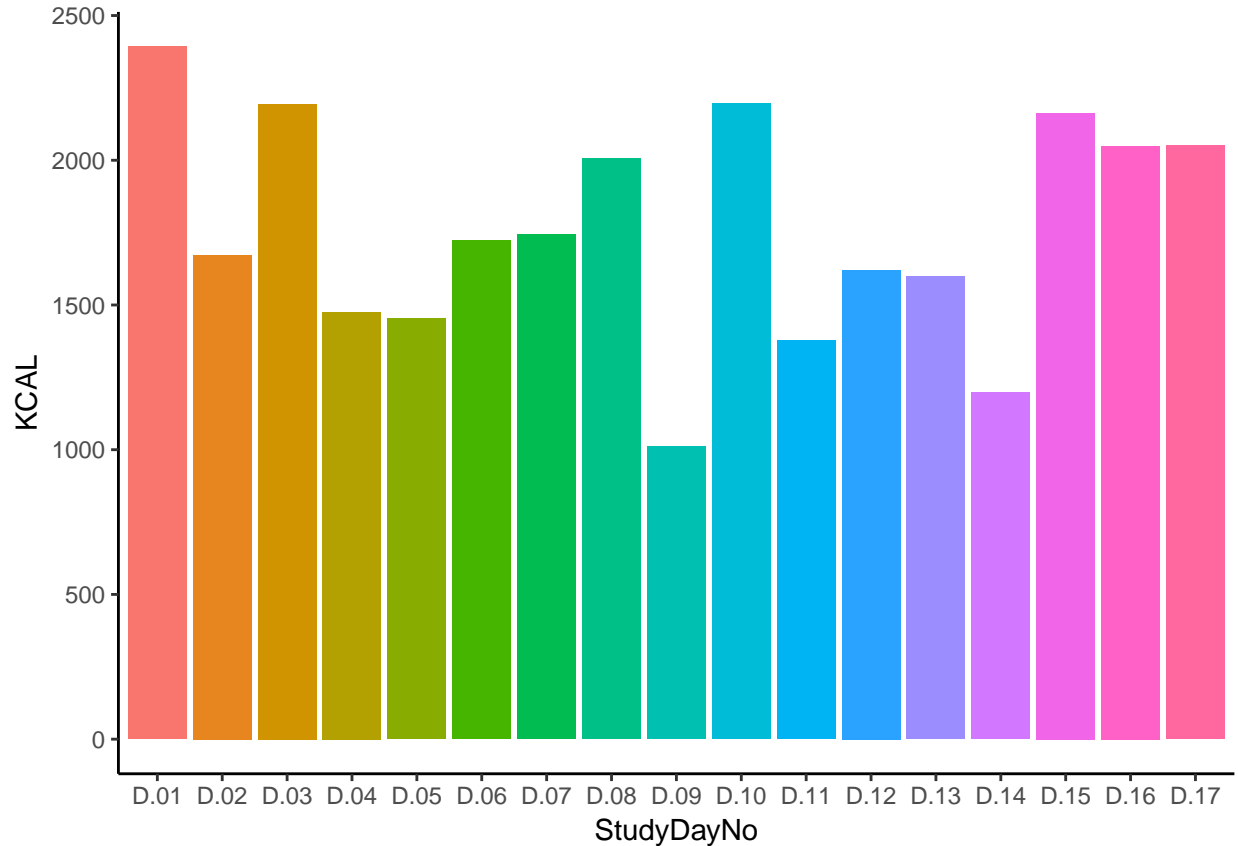
Microbiome Daily Relative Abundance

```
# make ggplot bar chart of top 10 most abundant species per day
#melt subtaxasp to get our dataframe in the long format for future usage
  meltdf<- melt(subtaxasp)
```

```
## Warning in melt.data.table(subtaxasp): To be consistent with reshape2's
## melt, id.vars and measure.vars are internally guessed when both are 'NULL'.
## All non-numeric/integer/logical type columns are conisdered id.vars, which
## in this case are columns [rn]. Consider providing at least one of 'id' or
## 'measure' vars in future.
```

```
  #merge to get access to Day var
  mergedf<- merge(x=meltdf, y=map, by.x = "variable", by.y= "X.SampleID", all.x=TRUE)

  #convert our dataframe species (rn) column to a character
  mergedf$rn <- as.character(mergedf$rn)

  #series of gsub commands meant to neaten and clarify legend content
  mergedf$rn <- gsub(".*s__", "", mergedf$rn)
  mergedf$rn <- gsub("\\[", "",mergedf$rn)
```

```r
mergedf$rn <- gsub("\\]", "",mergedf$rn)
mergedf$rn <- gsub("_", " ",mergedf$rn)


#create <10% abundance category
mergedf$rn[mergedf$value < 0.1] <- "<10% abundance"


ggplot(mergedf, aes(x = StudyDayNo, y = value, fill = rn)) +
  geom_bar(stat = "identity") +
  scale_x_discrete(drop = FALSE) +
  theme_classic() +
  theme(strip.text.y = element_text(angle = 0, size = 8, face = "italic"),
        axis.text.x = element_text(angle = 45, hjust = 1),
        axis.title.x = element_blank(),
        plot.title = element_text(hjust = 0.5),
        strip.background = element_rect(color = "grey")) +
  guides(fill = guide_legend(reverse = TRUE,
                             keywidth = 1,
                             keyheight = 1,
                             ncol = 1)) +
  ylab("Relative Abundance\n") +
  ggtitle("Main species within your gut per day")
```
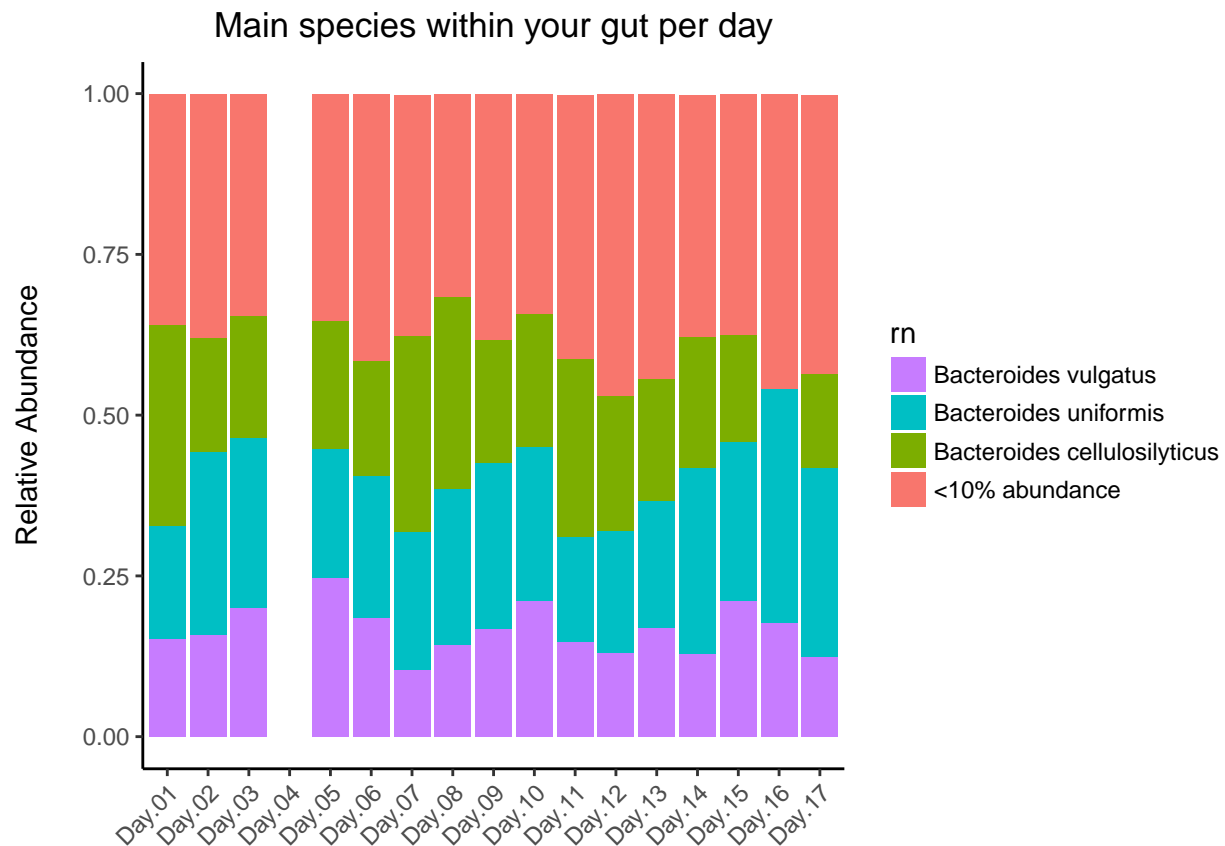


```
## `geom_smooth()` using method = 'loess'
```
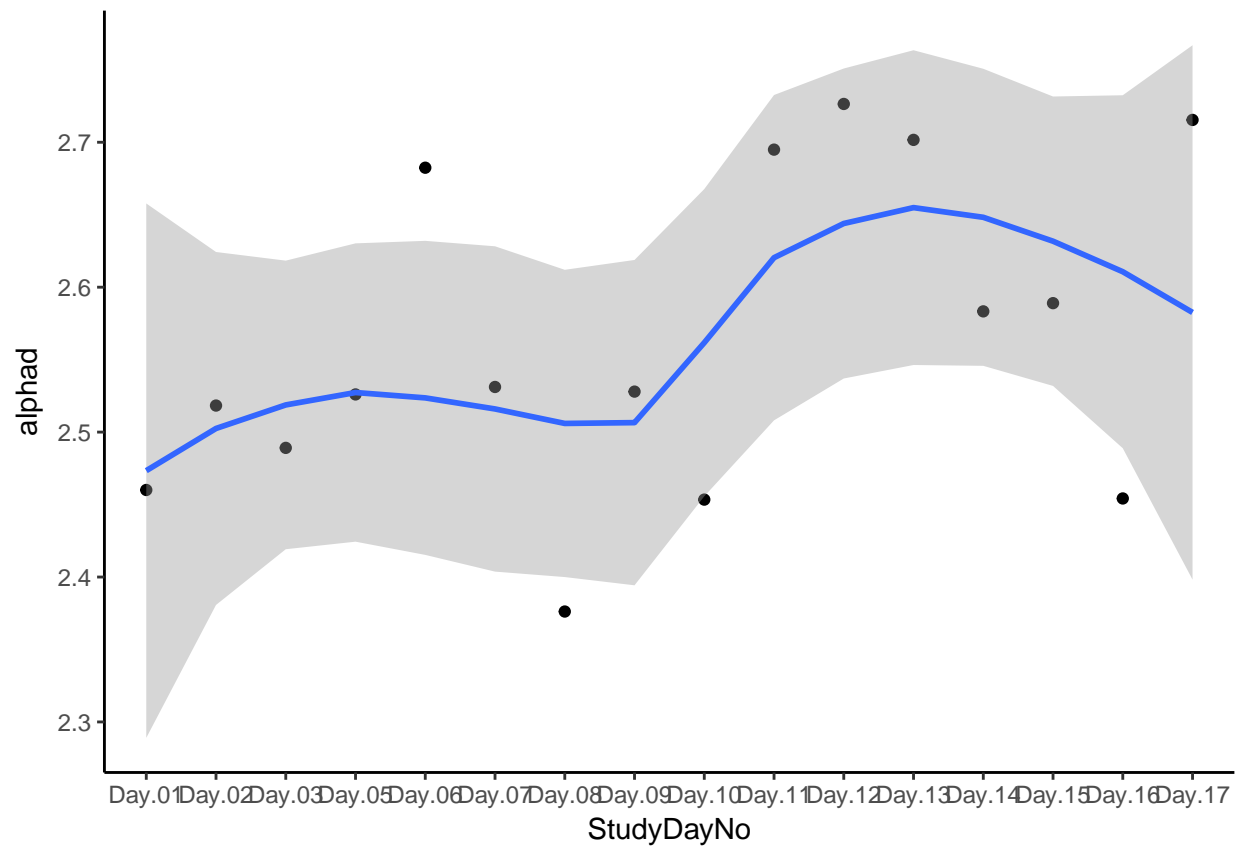
```
#create PCOA plot of beta diversities of pertinent subjects
#
# ggplot(PCOA) +
#   geom_point(aes(x=PC1,y=PC2, col=UserName, shape=UserName, size=4)) + #gives axes and item of focus
#   labs(title="PCOA plot") +
#   scale_shape_manual(values=shape_pal3) +
#   theme_classic()
```