

Mixture Effect Index

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```
library(phyloseq)
library(readr)
library(tidyverse)
library(Rmisc)
```

Mixture Effect Index

$$MEI_{otuX} = \frac{A_{observed} - A_{expected}}{A_{expected}} = \frac{A_{c+a} - \left(\frac{A_a + A_c}{2}\right)}{\frac{A_a + A_c}{2}}$$

Aobserved = OTU X abundance of what you observed in the mixed treatment (i.e. Ac+a) Aexpected = OTU X abundance of what you expect to find in the mixed treatment based on adding both INDIVIDUAL effects together and dividing by two. Ac+a = abundance of OTU X in Compost+Alfalfa amendment Ac = abundance of OTU X in Compost ONLY amendment Aa = abundance of OTU X in Alfalfa ONLY amendment

How to interpret... MEI ~ 1 for an OTU = non-additive effect, or not interaction

MEI » 1 for an OTU = synergistic effect of adding Compost & Alfalfa together

MEI « 1 for an OTU = antagonistic effect of adding Compost & Alfalfa together

It would be neat to see what bacteria species/clades have strong positive, or negative, MEI's.

It would be cool to look at this MEI through time (for inorganic N and MBC too). I think you could make a PCA or nmDS of MEI scores too and look at how it relates to other things you measured (nitrate, pH, etc...)!

For more information on MEI see... Wardle, D. A., Bonner, K. I., & Nicholson, K. S. (1997). Biodiversity and plant litter: experimental evidence which does not support the view that enhanced species richness improves ecosystem function. *Oikos*, 247-258. Meier, C. L., & Bowman, W. D. (2010). Chemical composition and diversity influence non-additive effects of litter mixtures on soil carbon and nitrogen cycling: implications for plant species loss. *Soil Biology and Biochemistry*, 42(9), 1447-1454. McDaniel, M. D., Grandy, A. S., Tiemann, L. K., & Weintraub, M. N. (2016). Eleven years of crop diversification alters decomposition dynamics of litter mixtures incubated with soil. *Ecosphere*, 7(8), e01426.

Incubation data and taxonomy

```
### Scale color for phyla, consistent phyla colors across plots
#Function to make all phyla colors consistent
phylalist <- data.frame(tax_table(inc), row.names = NULL) %>%
  select(Phylum) %>%
```

```

unique()
phylalist$Phylum <- as.character(phylalist$Phylum)
phylalist$Phylum[is.na(phylalist$Phylum)] <- "Unclassified"
# this package will generate a palette based on number and desired colors
library(colorspace)
colors <- sequential_hcl(n_distinct(phylalist), palette = "viridis") %>%
  sample() %>%
  setNames(phylalist$Phylum)

```

MEI function

First start out by looking at all samples, later we will do calculation for early and late groups

```

MEI <- function(phy, taxa){
  OTU <- taxa
  Aca <- subset_samples(phy, treatment %in% "Mix") %>%
    transform_sample_counts(function(x) {x/sum(x)}) %>%
    prune_taxa(taxa = OTU) %>%
    sample_sums() %>%
    mean()
  Aa <- subset_samples(phy, treatment %in% "Alfalfa") %>%
    transform_sample_counts(function(x) {x/sum(x)}) %>%
    prune_taxa(taxa = OTU) %>%
    sample_sums() %>%
    mean()
  Ac <- subset_samples(phy, treatment %in% "Compost") %>%
    transform_sample_counts(function(x) {x/sum(x)}) %>%
    prune_taxa(taxa = OTU) %>%
    sample_sums() %>%
    mean()
  MEI <- (Aca - ((Aa + Ac)/2))/((Aa + Ac)/2)
  return(MEI)
}

```

```

resp_table <- read_csv("../Data/resp_table.csv")

```

```
## Warning: Missing column names filled in: 'X1' [1]
```

```

##
## -- Column specification -----
## cols(
##   X1 = col_character(),
##   Alfalfa_Early = col_double(),
##   Alfalfa_Late = col_double(),
##   Compost_Early = col_double(),
##   Compost_Late = col_double(),
##   Mix_Early = col_double(),
##   Mix_Late = col_double()
## )

```

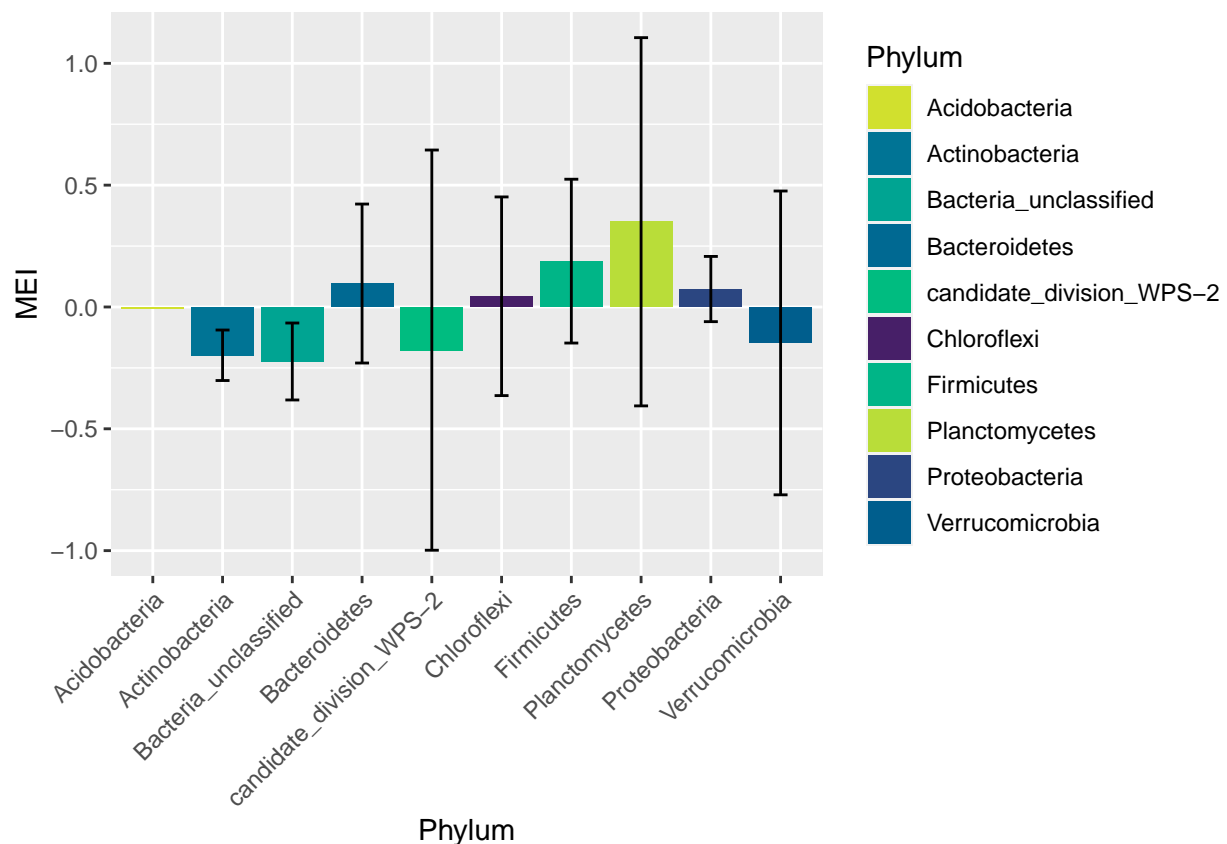
```
MEI_responder <- resp_table$X1 %>%
  map( ~ MEI(inc, taxa = .))

resp_table$MEI <- unlist(MEI_responder)
```

```
Taxa_responders <- prune_taxa(resp_table$X1, inc) %>%
  tax_table()
```

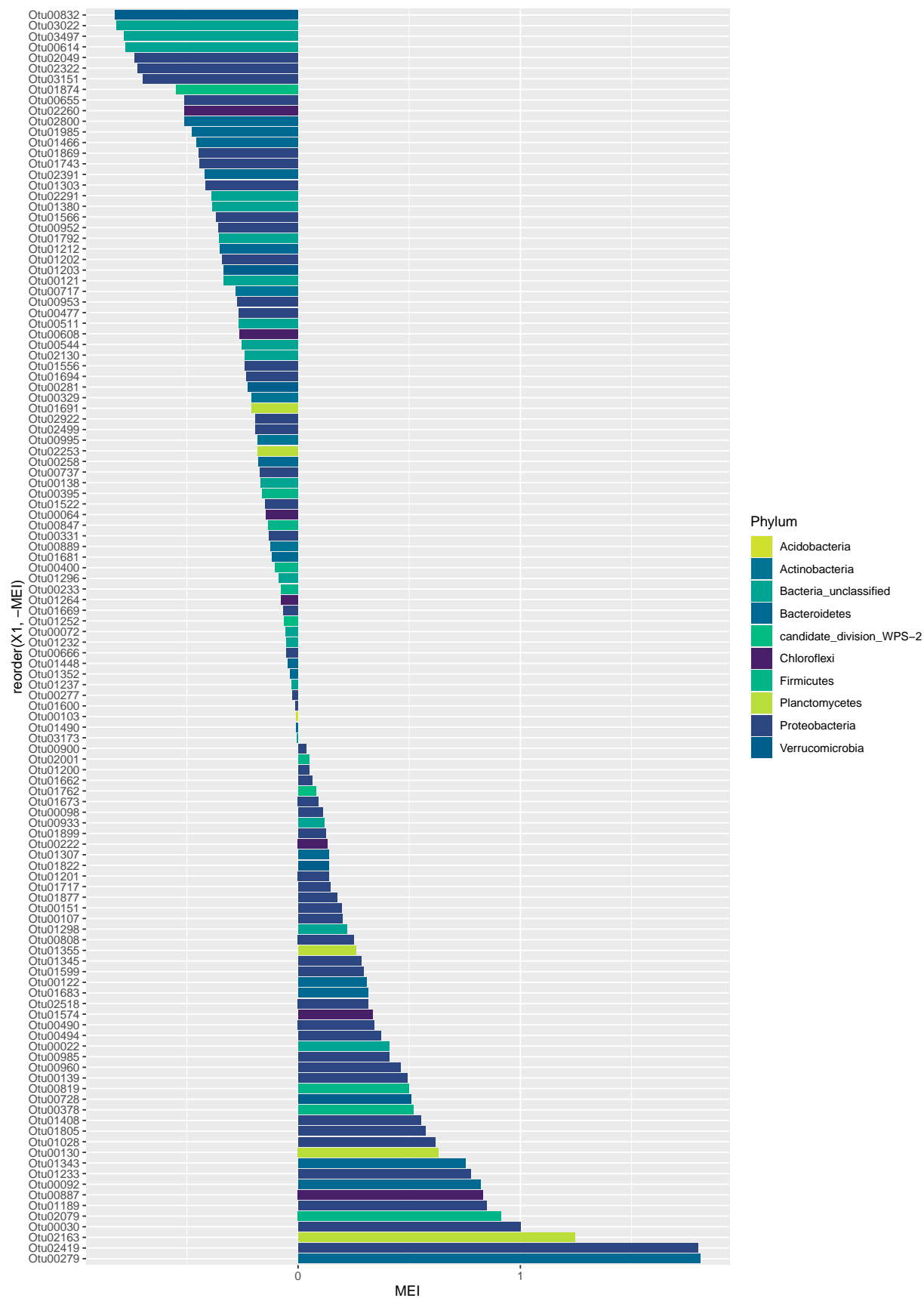
```
resp_table <- cbind(resp_table, as.data.frame(Taxa_responders))
summarySE(resp_table, measurevar = "MEI", groupvars = "Phylum") %>%
  ggplot(aes(x = Phylum, y = MEI, fill = Phylum)) +
  geom_bar(position=position_dodge(), stat="identity") +
  geom_errorbar(aes(ymin = MEI - ci, ymax = MEI + ci),
    width=.2, position=position_dodge(.9)) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  scale_color_manual(aesthetics = "fill", values = colors)
```

```
## Warning in qt(conf.interval/2 + 0.5, datac$N - 1): NaNs produced
```



All responding OTUs

```
ggplot(resp_table, aes(x = reorder(X1, -MEI), y = MEI, fill = Phylum)) +  
  geom_bar(stat = "identity") + coord_flip() +  
  scale_color_manual(aesthetics = "fill", values = colors)
```



Ammendment responding OTUs

```
alf_OTUS <- readRDS("../Data/LFC_alf_OTUs.RDS")
comp_OTUS <- readRDS("../Data/LFC_comp_OTUs.RDS")
mix_OTUS <- readRDS("../Data/LFC_mix_OTUs.RDS")
```

```
alf_MEI <- alf_OTUS$OTU %>%
  map( ~ MEI(inc, taxa = .))

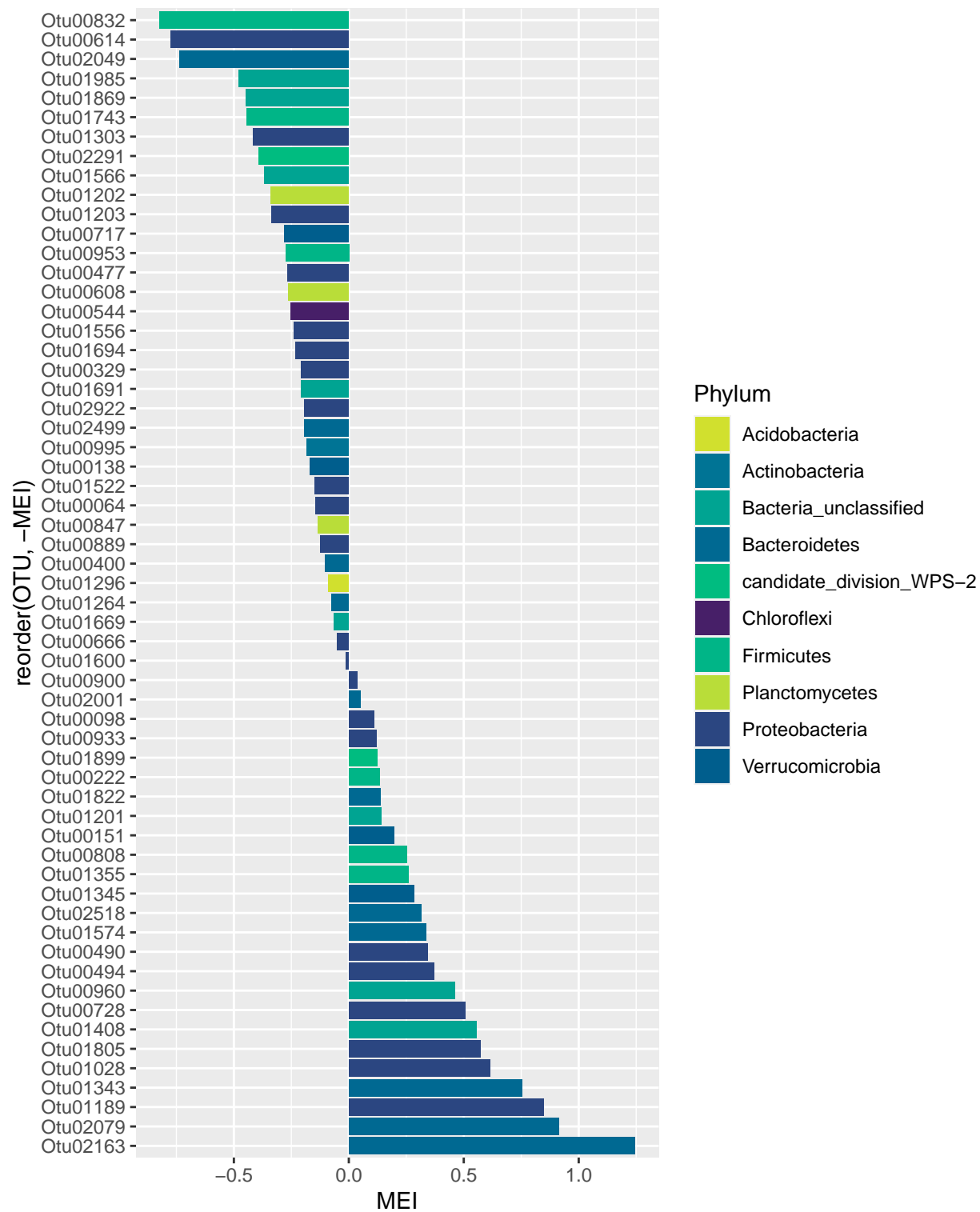
comp_MEI <- comp_OTUS$OTU %>%
  map( ~ MEI(inc, taxa = .))

mix_MEI <- mix_OTUS$OTU %>%
  map( ~ MEI(inc, taxa = .))
```

```
alf_OTUS$MEI <- unlist(alf_MEI)
comp_OTUS$MEI <- unlist(comp_MEI)
mix_OTUS$MEI <- unlist(mix_MEI)
```

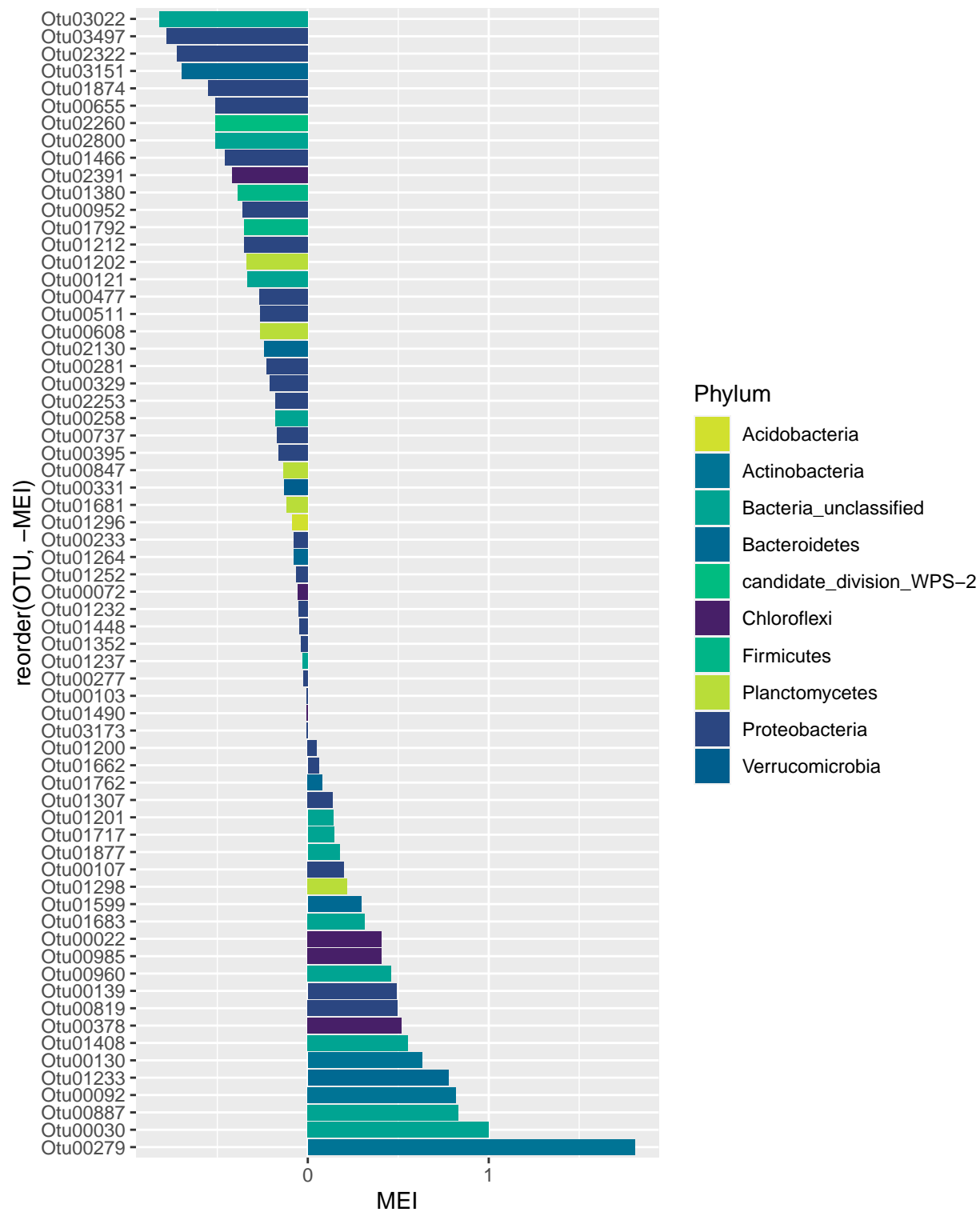
Plot alf responder OTUs' MEI

```
ggplot(alf_OTUS, aes(x = reorder(OTU, -MEI), y = MEI, fill = Phylum)) +
  geom_bar(stat = "identity") + coord_flip() +
  scale_color_manual(aesthetics = "fill", values = colors)
```



Plot comp responder OTUs' MEI

```
ggplot(comp_OTUS, aes(x = reorder(OTU, -MEI), y = MEI, fill = Phylum)) +  
  geom_bar(stat = "identity") + coord_flip() +  
  scale_color_manual(aesthetics = "fill", values = colors)
```

Plot mix responder OTUs' MEI

```
ggplot(mix_OTUS, aes(x = reorder(OTU, -MEI), y = MEI, fill = Phylum)) +  
  geom_bar(stat = "identity") + coord_flip() +  
  scale_color_manual(aesthetics = "fill", values = colors)
```

