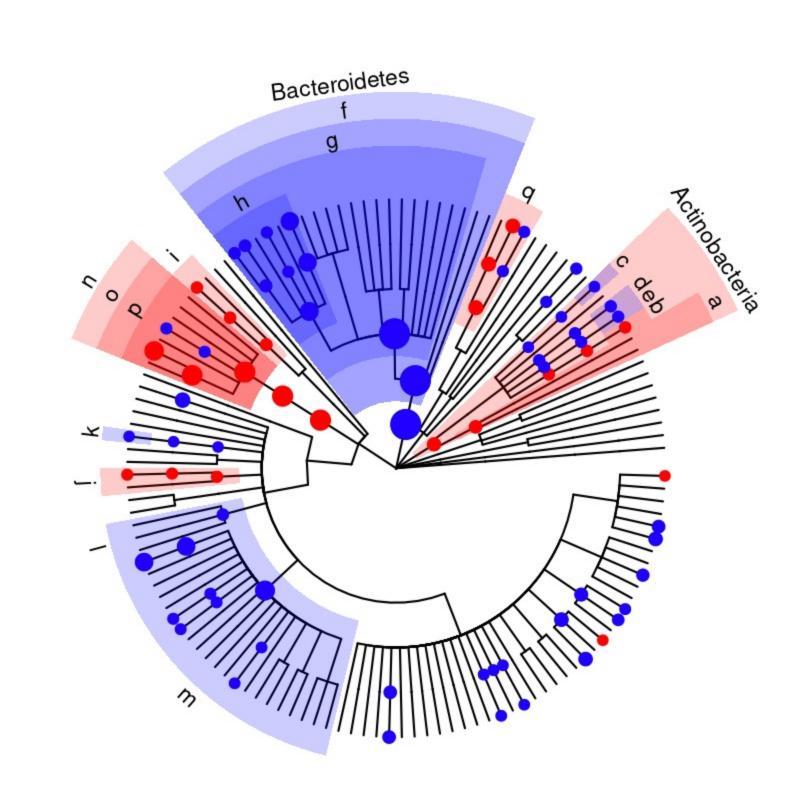
Metadata input MDS plot Data input Tree plot Parameters for pruning tree: **Prevalence cutoff** 0.1 **Abundance cutoff** 0 Is the test metadata continuous? False **FDR** cutoff 0.05 **Breaks for node size** 0,0.01,0.05,0.5,5 **Colors for plot** red,blue,orange,green Remove taxa from plot? Remove the parent branch if there is only one child branch within the parent branch? False Remove the child branch if there is only one child branch within the parent branch? False Run Download figure: ♣ Download



Data filter

Taxa barplot

Alpha diversity plot

abundance

< <0.01%

• 0.05-0.5%

0.5-5%

group

CTL

0.01-0.05%

- a Actinobacteria
  b Atopobiaceae
  c Coriobacteriales\_Incertae\_Sedis
  d Eggerthellaceae
  e uncultured
  f Bacteroidia
  g Bacteroidales
  h Prevotellaceae

Correlation plot

P vs P plot

Boxplot plot

Tree plot

Statistical test

- i Streptococcaceae
  j Clostridiaceae\_1
  k Eubacteriaceae
  I Family\_XIII
  m Lachnospiraceae
  n Erysipelotrichia
  o Erysipelotrichales
  p Erysipelotrichaceae
  q Burkholderiaceae