

Melanoma BCR repertoire analysis

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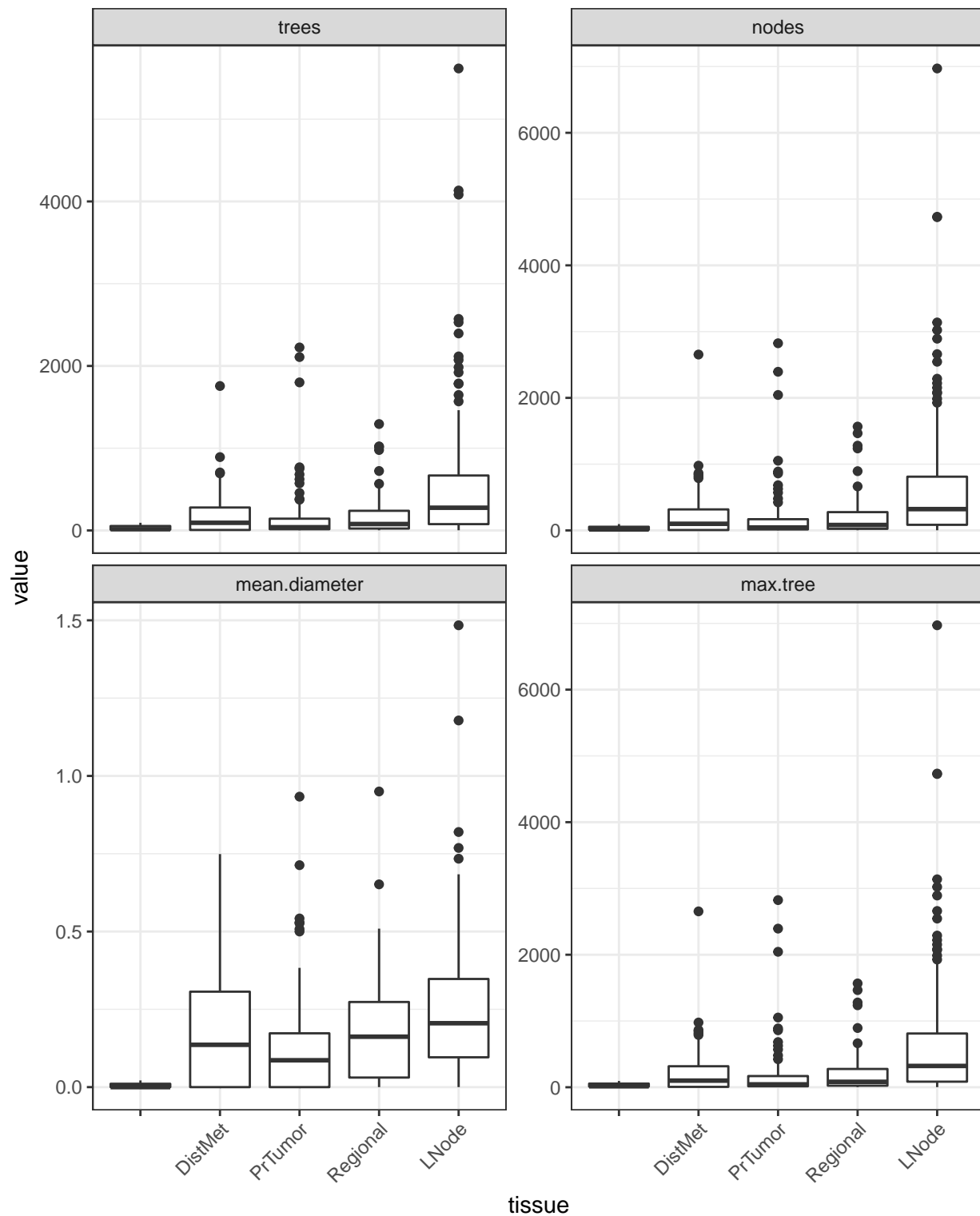
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```
library(dplyr)
library(ggplot2)
library(reshape2)
library(plyr)

load('clones.rda')
load('shm.rda')
codes <- read.table('SKCM-codes-samples-for-patients-tss.txt', header=F, sep="\t")
colnames(codes) <- c('patient_id', 'c1', 'c2', 'c3', 'tissue')
clones <- merge(clones, codes)
clones$tissue <- revalue(clones$tissue, c("Distant Metastasis" = "DistMet",
                                         "Primary Tumor" = "PrTumor",
                                         "Regional Cutaneous or Subcutaneous Tissue (includes satellite)" = "LNNode"))
clones$LN <- ifelse(clones$tissue == "LNNode", 'LNNode', 'Other')

c <- clones %>% group_by(patient_id, tissue) %>%
  dplyr::summarise(trees = n(), nodes = sum(nodes), mean.diameter = mean(diameter),
                  max.tree = max(nodes)) %>%
  dplyr::select(tissue, patient_id, trees, nodes, mean.diameter, max.tree) %>%
  melt(id.vars = c('tissue', 'patient_id'))

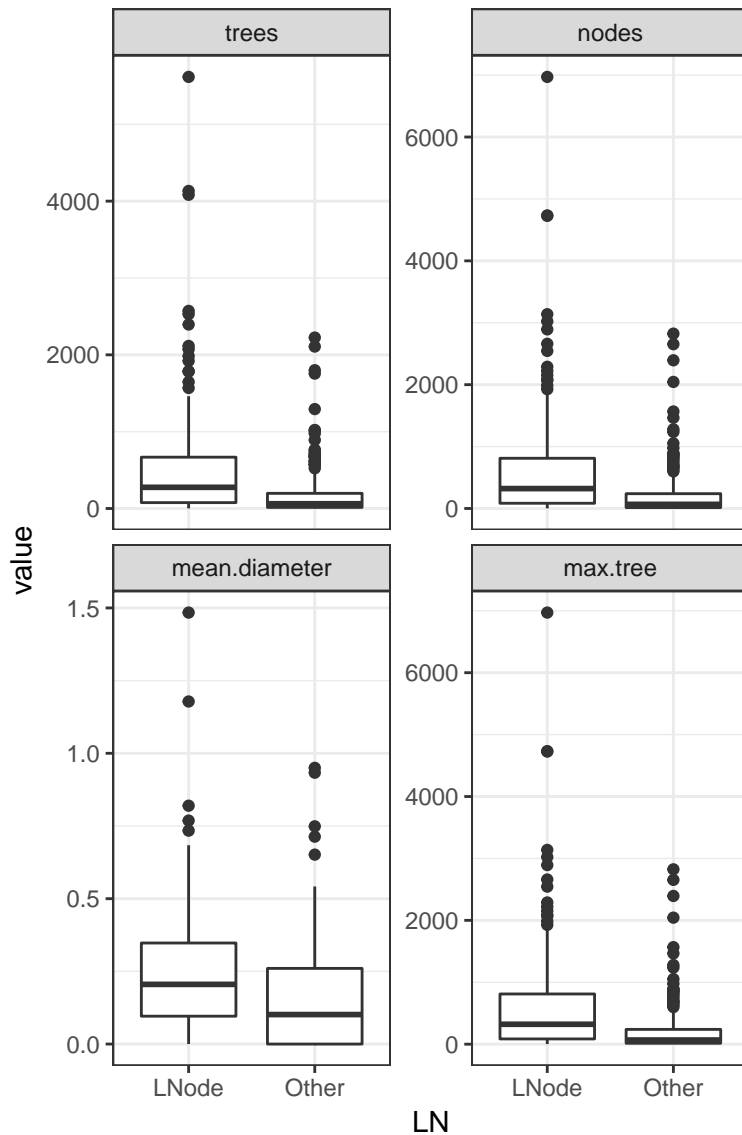
ggplot(c, aes(x = tissue, y = value)) +
  geom_boxplot() +
  facet_wrap(~variable, scales="free_y") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
c1 <- clones %>% group_by(patient_id, LN) %>%
  dplyr::summarise(trees = n(), nodes = sum(nodes), mean.diameter = mean(diameter),
                  max.tree = max(nodes)) %>%
  dplyr::select(LN, patient_id, trees, nodes, mean.diameter, max.tree)

ggplot(melt(c1, id.vars = c('LN', 'patient_id')), aes(x = LN, y = value)) +
```

```
geom_boxplot() +
facet_wrap(~variable, scales="free_y") +
theme_bw()
```



```
for (i in c('trees', 'nodes', 'mean.diameter', 'max.tree')){
  cat(i, 't-Test p-value\n', t.test(c1[[i]] ~ c1[['LN']])$p.value, '\n')
}
```

```
## trees t-Test p-value
## 2.927765e-09
## nodes t-Test p-value
## 6.669639e-09
## mean.diameter t-Test p-value
## 1.566748e-05
## max.tree t-Test p-value
## 6.669639e-09
```