

# ger\_summary\_plots.R

*rhickey*

*Wed Oct 28 22:30:13 2015*

```
## Perform exploratory ecological analysis on taxonomic data
## 2015-10-27
## Roxana Hickey <roxana.hickey@gmail.com>
```

```
setwd('~/Documents/gerlinger/')
library(ggplot2)
library(RColorBrewer)
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.3-1
```

```
library(labdsv)
```

```
## Loading required package: mgcv
## Loading required package: nlme
## This is mgcv 1.8-8. For overview type 'help("mgcv-package")'.
## Loading required package: MASS
##
## Attaching package: 'labdsv'
##
## The following object is masked from 'package:stats':
##
##     density
```

```
library(plyr)
library(phyloseq)
```

```
## Creating a generic function for 'nchar' from package 'base' in package 'S4Vectors'
```

```
library(gplots)
```

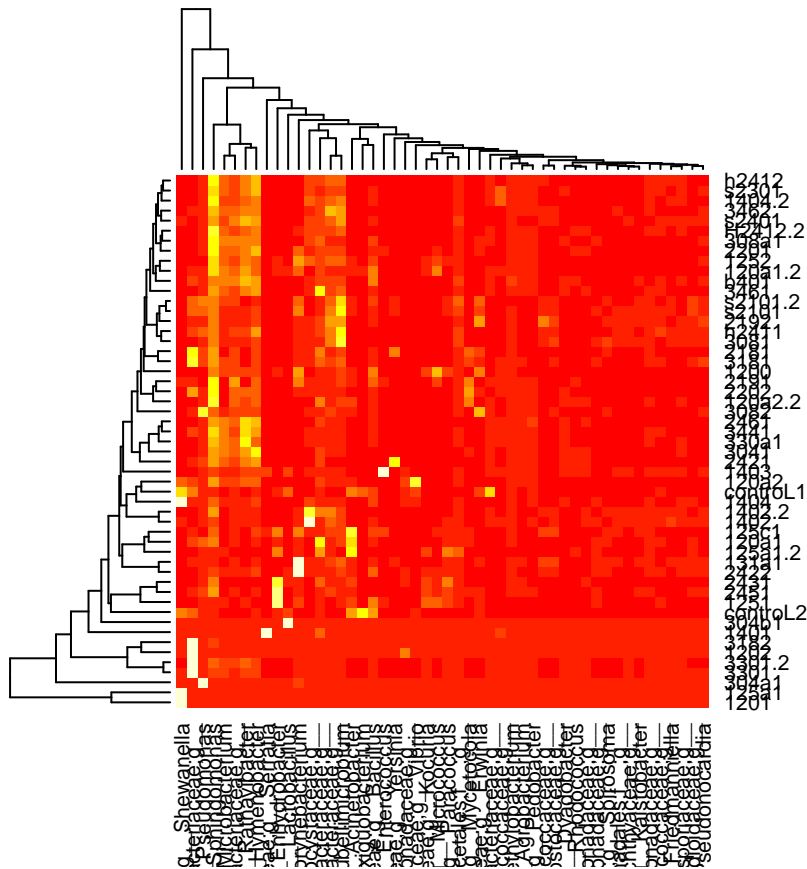
```
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:stats':
##
##     lowess
```

```
## load custom functions
# source('code/custom_ggplot_settings.R')
# source('code/custom_heatmap.3.R')
```

```
## load OTU table and map file from setup
load('results/otu_setup/ger_otu_setup.RData')

## heatmap
## write dataframe with shorter taxa names
df.taxa <- data.frame(full = colnames(otu.g.prop),
                      short = '')

## subset to top 50 taxa
pick <- order(colSums(otu.g.prop), decreasing=TRUE)[1:50]
heatmap(otu.g.prop[, pick], trace = NULL)
```



```
#####
## compute Bray-Curtis and Canberra distances on rarefied data
bc.g <- vegdist(otu.g.rare)
can.g <- vegdist(otu.g.rare, 'canberra')

#####
## PCoA
pcoa.bc.g <- cmdscale(t(bc.g), eig = TRUE)
pcoa.can.g <- cmdscale(t(can.g), eig = TRUE)

#####
## plot Bray-Curtis pcoa with ggplot
df.pcoa.bc.g <- as.data.frame(pcoa.bc.g$points)
```

```

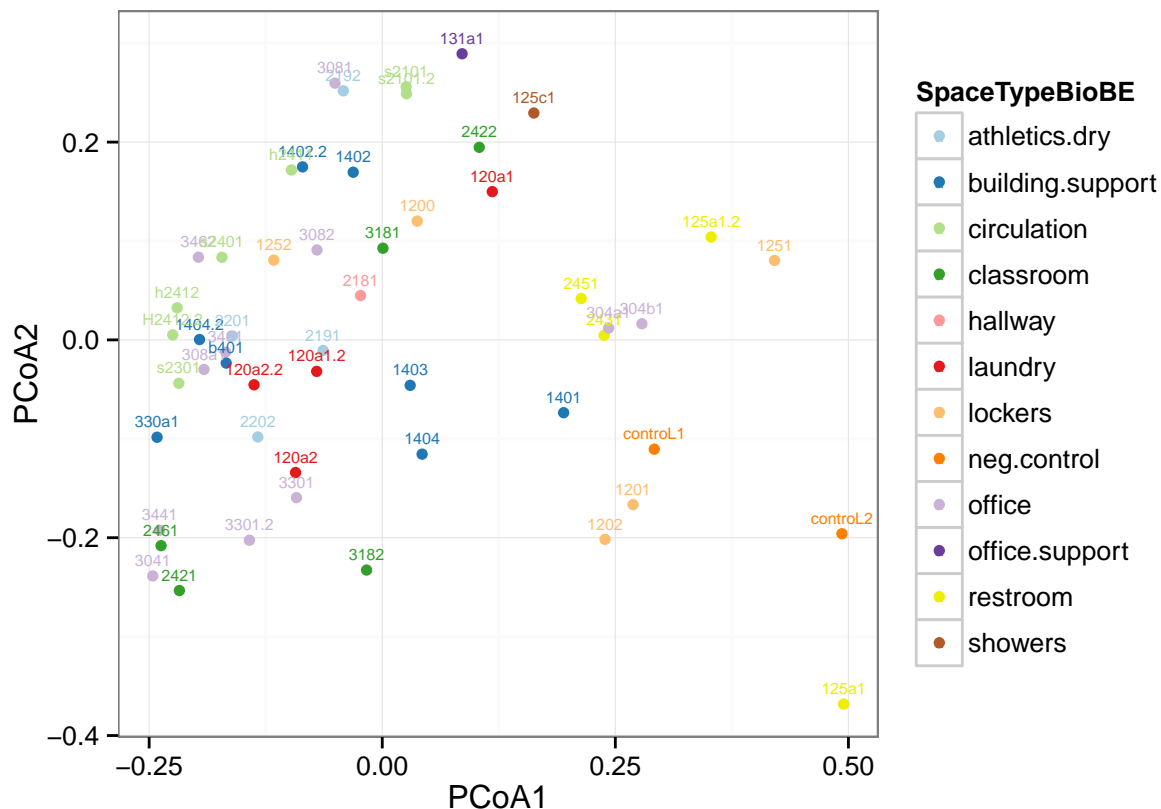
colnames(df.pcoa.bc.g) <- c('PCoA1', 'PCoA2')
df.pcoa.bc.g$Description <- rownames(df.pcoa.bc.g)
df.pcoa.bc.g.all <- merge(df.pcoa.bc.g, ger.map)

## specify 12 colors for space types
mycol.12 <- c('#A6CEE3', '#1F78B4', '#B2DF8A', '#33A02C', '#FB9A99', '#E31A1C',
              '#FDBF6F', '#FF7F00', '#CAB2D6', '#6A3D9A', '#EEEE00', '#B15928')

## set theme_bw
theme_set(theme_bw())

## all samples by space type
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE))
gg.pcoa.bc.g + geom_point(size = 2) +
  geom_text(aes(y = PCoA2 + 0.01, label = Description), size = 2, vjust = 0) +
  scale_color_manual(values = mycol.12)

```



```

ggsave('figures/pcoa_bc_g_sampletype.png')

```

```

## Saving 6.5 x 4.5 in image

```

```

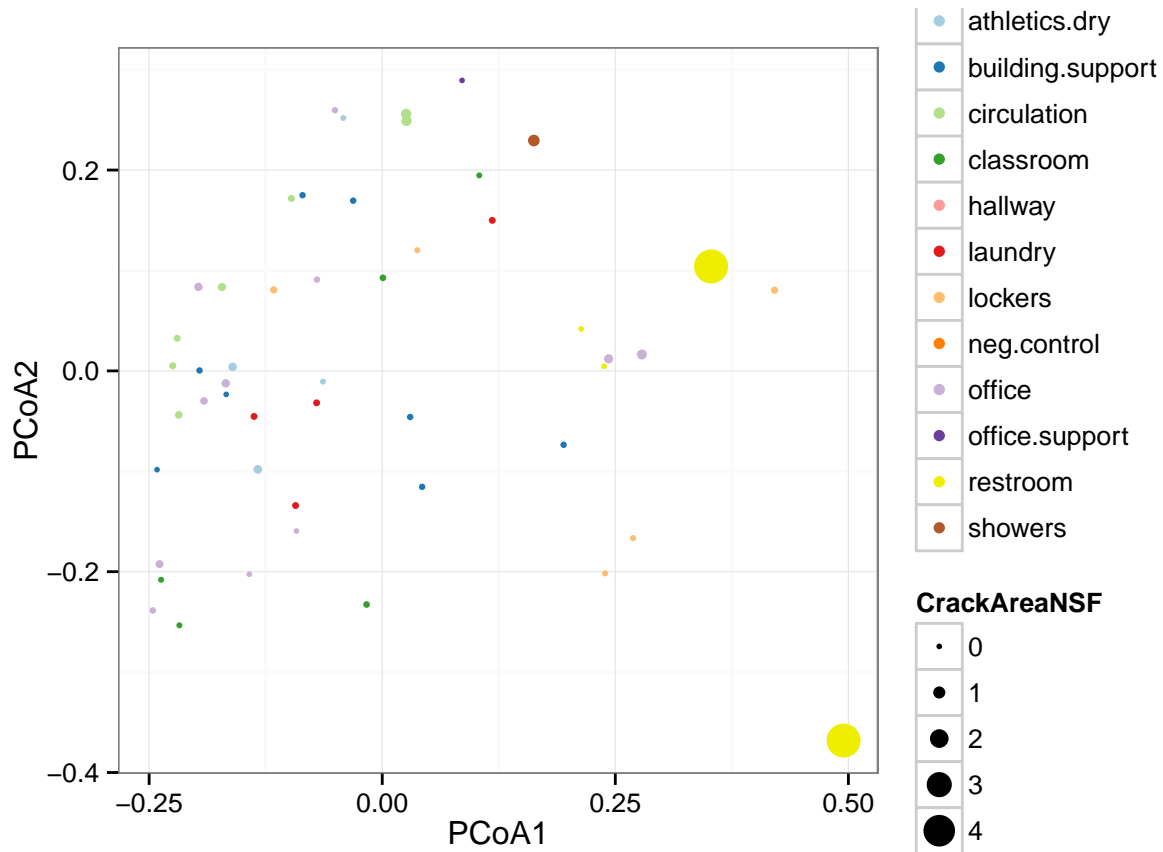
## crack area NSF
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = CrackArea))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)

```

```

## Warning: Removed 3 rows containing missing values (geom_point).

```



```
ggsave('figures/pcoa_bc_g_crackarea.png')
```

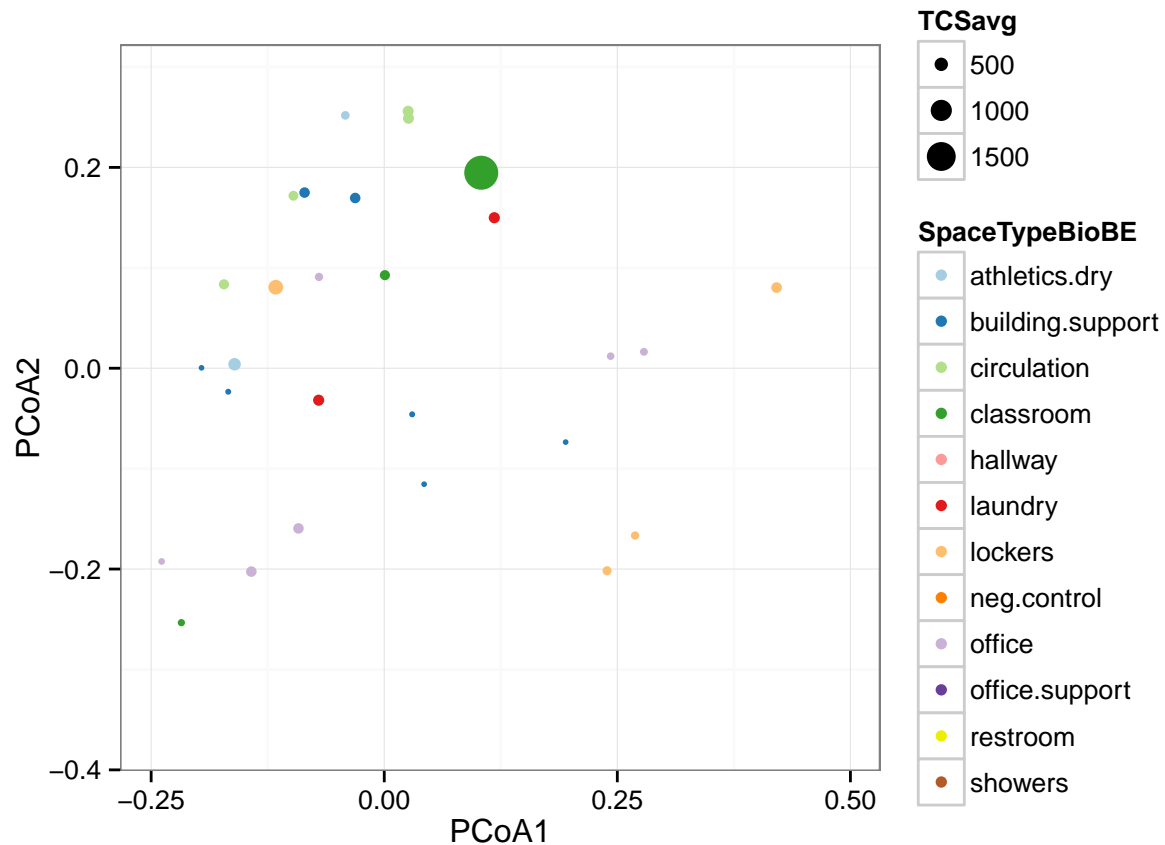
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## chem = TCSavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = TCSavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_bc_g_TCSavg.png')
```

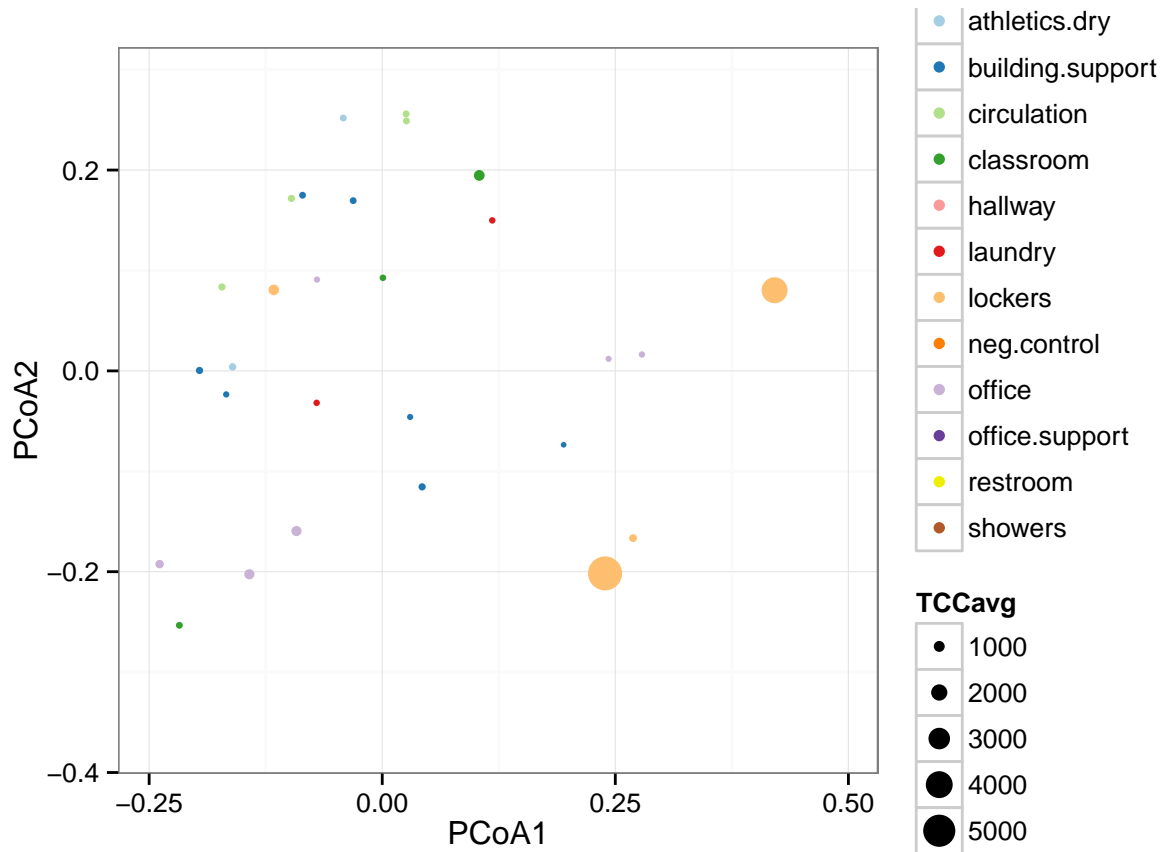
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = TCCavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = TCCavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_bc_g_TCCavg.png')
```

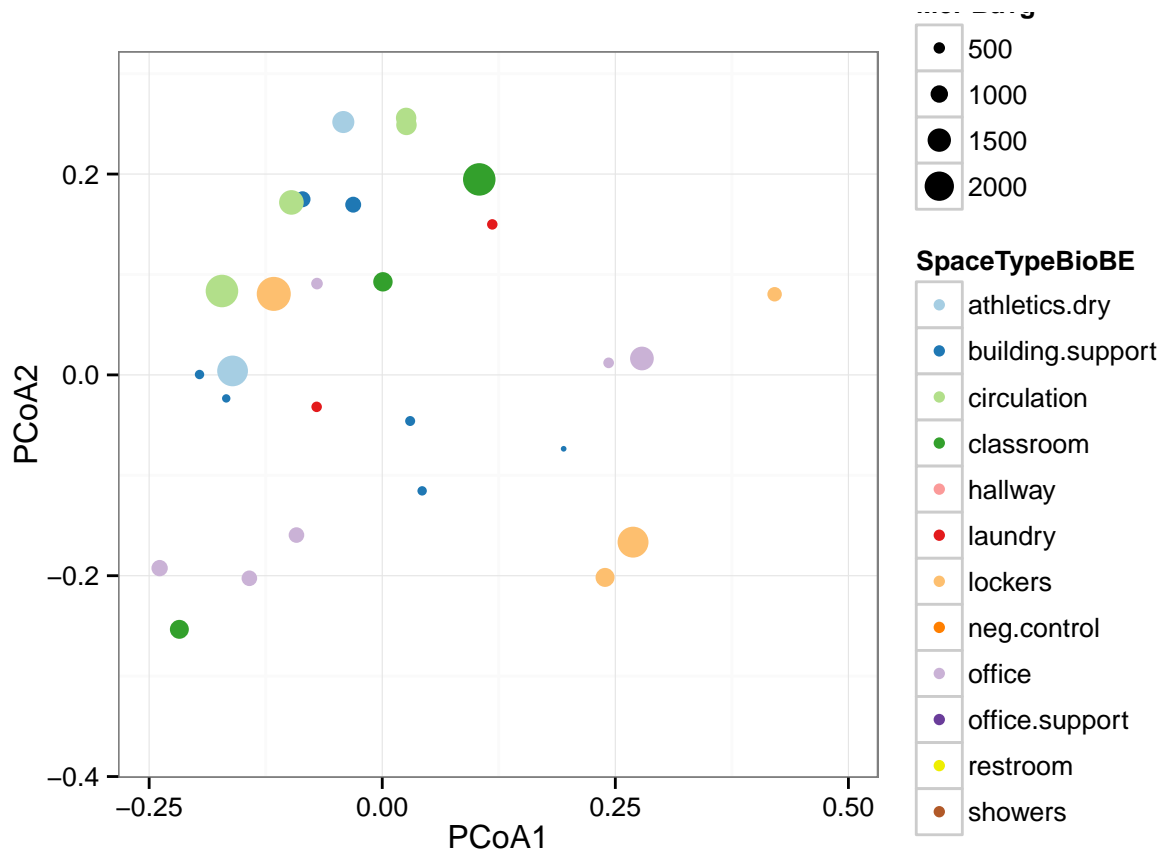
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = MePBavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = MePBavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_bc_g_MePBavg.png')
```

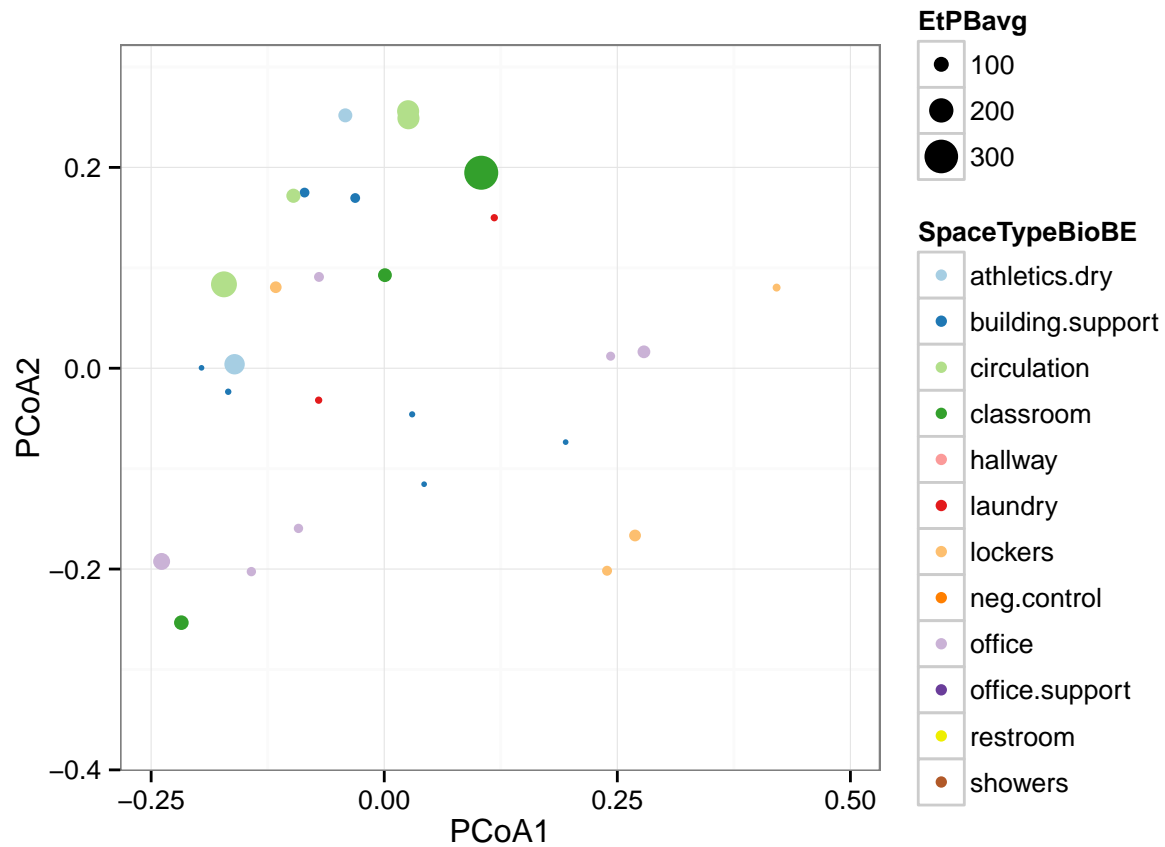
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = EtPBavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = EtPBavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_bc_g_EtPBavg.png')
```

```
## Saving 6.5 x 4.5 in image
```

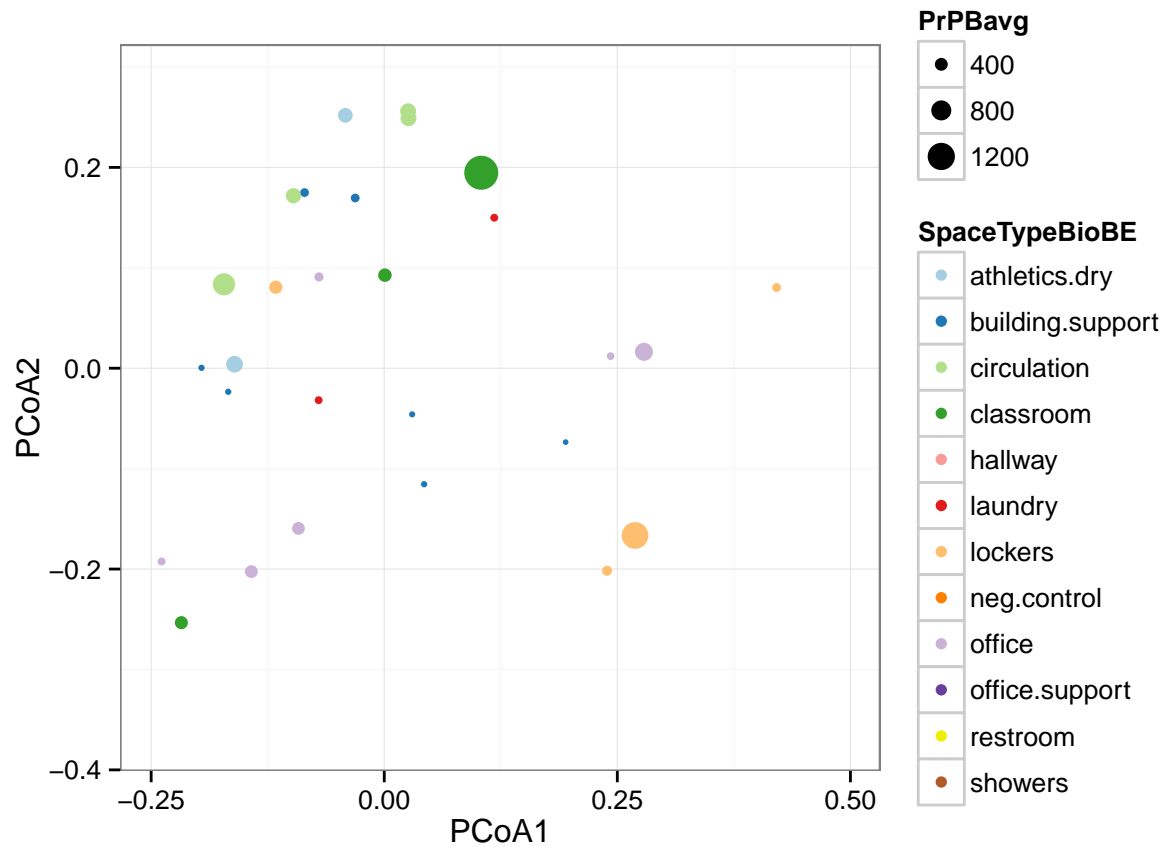
```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = PrPBavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = PrPBavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```





```
ggsave('figures/pcoa_bc_g_PrPBavg.png')
```

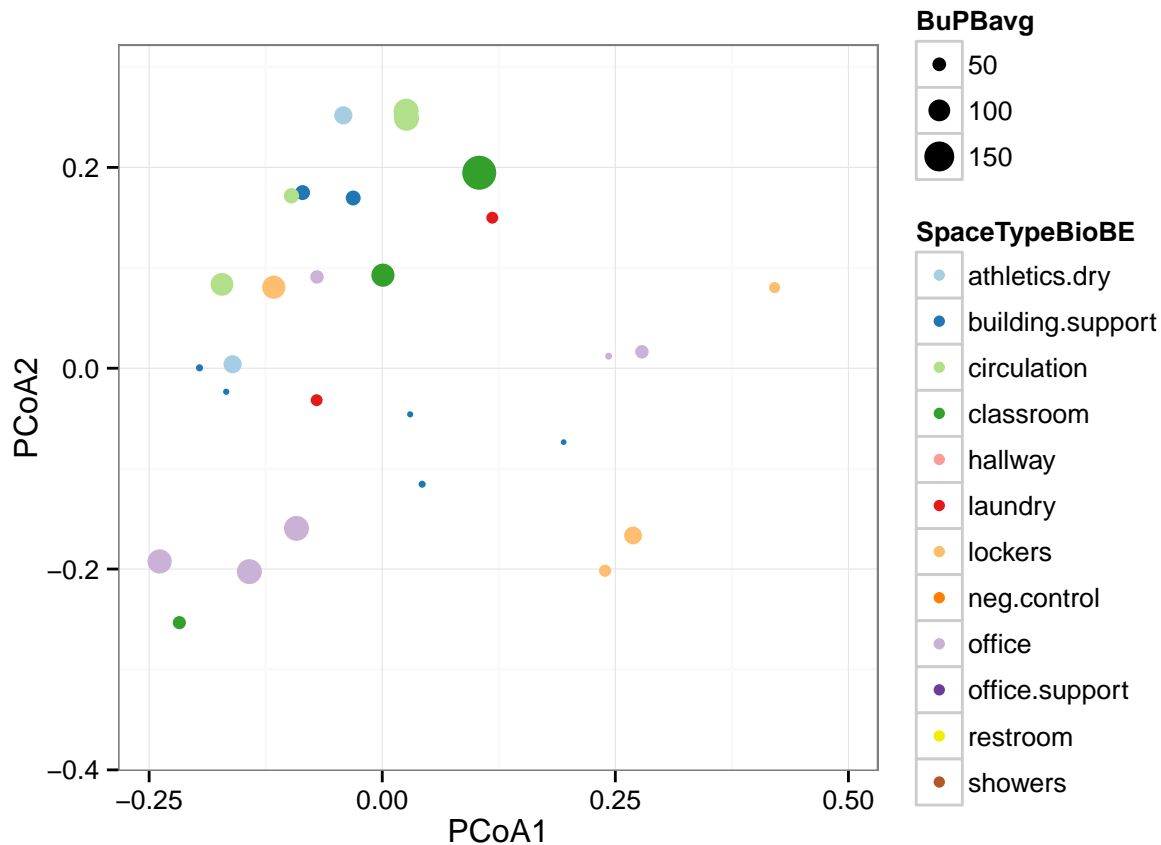
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = BuBPavg
```

```
gg.pcoa.bc.g <- ggplot(df.pcoa.bc.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = BuPBavg))
gg.pcoa.bc.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



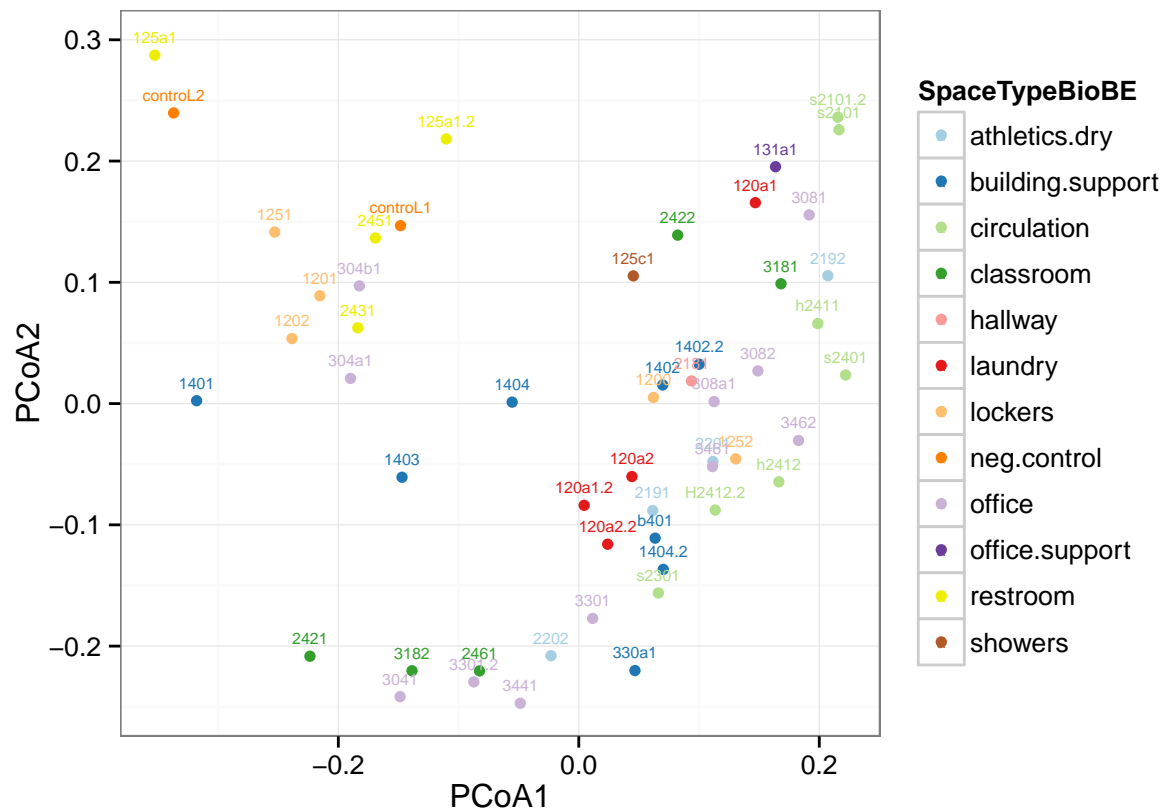
```
ggsave('figures/pcoa_bc_g_BuPBavg.png')
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
#####
## plot Canberra pcoa with ggplot
df.pcoa.can.g <- as.data.frame(pcoa.can.g$points)
colnames(df.pcoa.can.g) <- c('PCoA1', 'PCoA2')
df.pcoa.can.g$Description <- rownames(df.pcoa.can.g)
df.pcoa.can.g.all <- merge(df.pcoa.can.g, ger.map)

## all samples by space type
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE))
gg.pcoa.can.g + geom_point(size = 2) +
  geom_text(aes(y = PCoA2 + 0.01, label = Description), size = 2, vjust = 0) +
  scale_color_manual(values = mycol.12)
```



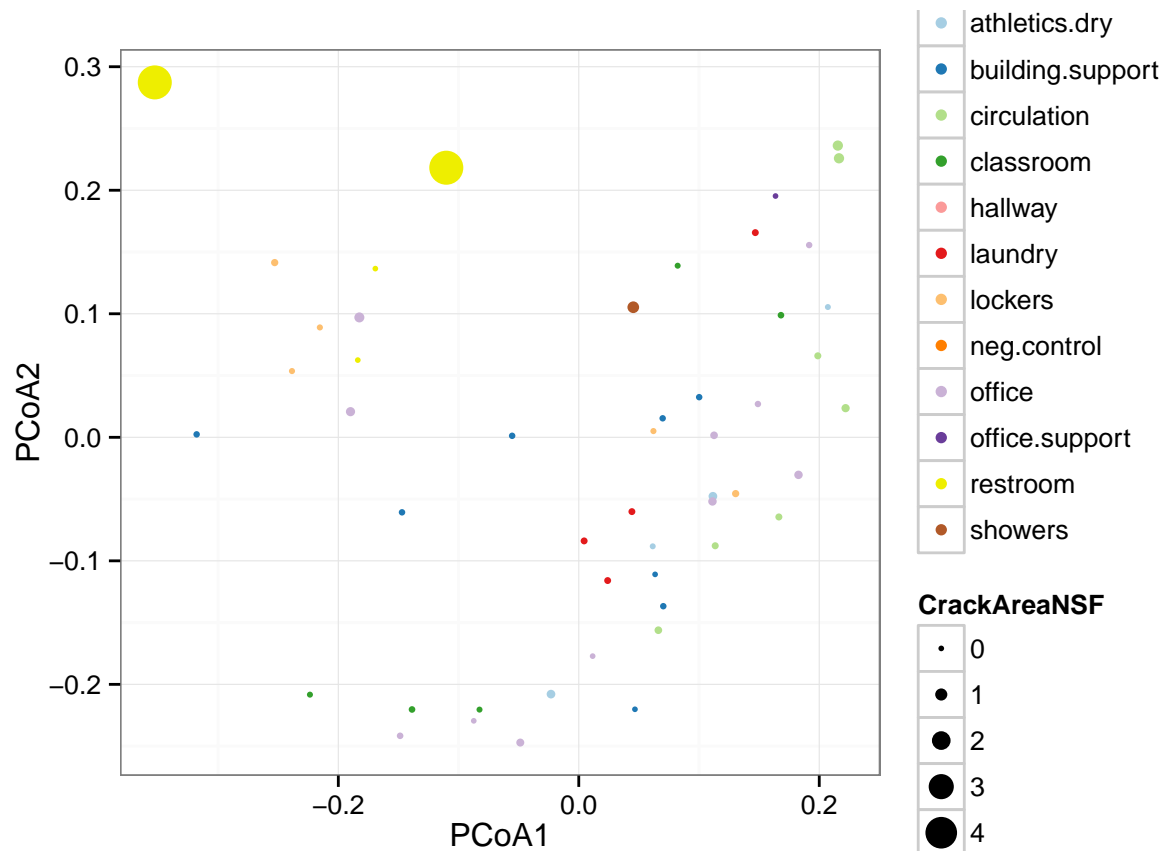
```
ggsave('figures/pcoa_can_g_sampletype.png')
```

```
## Saving 6.5 x 4.5 in image
```

```
## crack area NSF
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = Cra
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_crackarea.png')
```

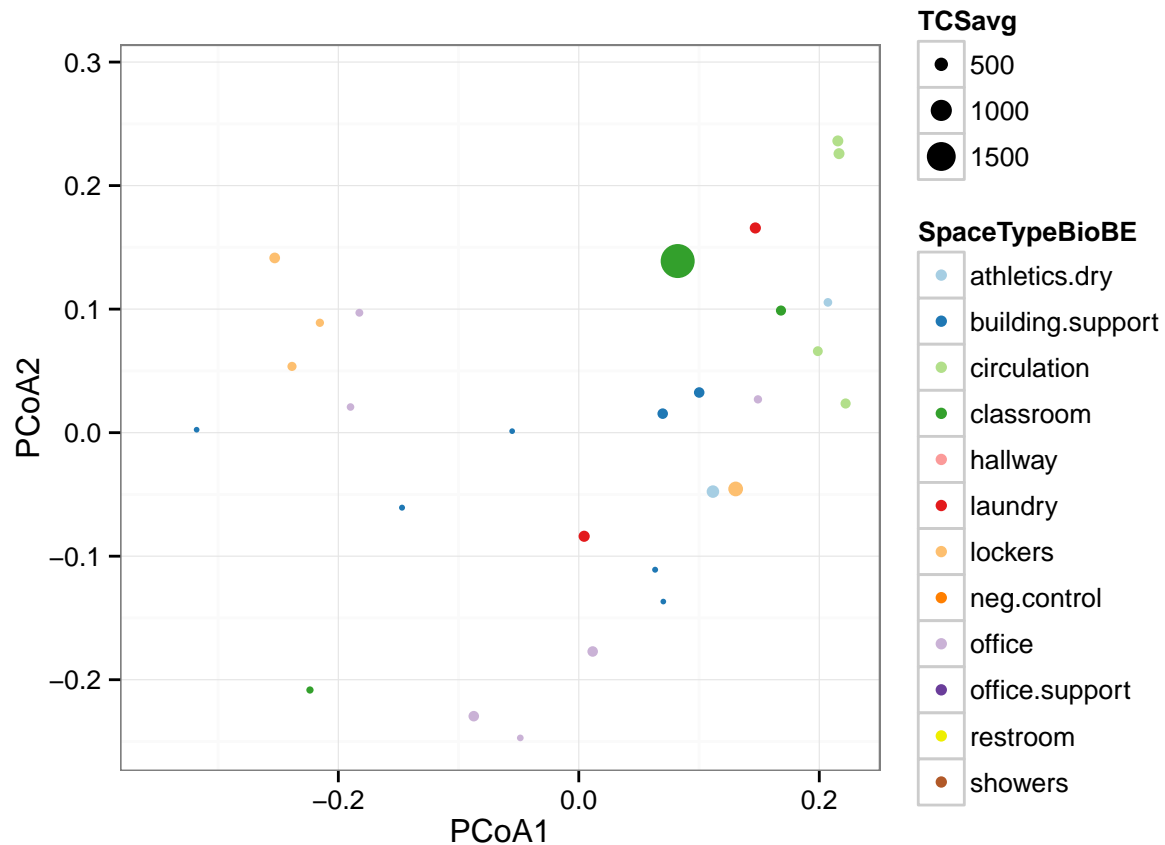
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## chem = TCSavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = TCSavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_TCSavg.png')
```

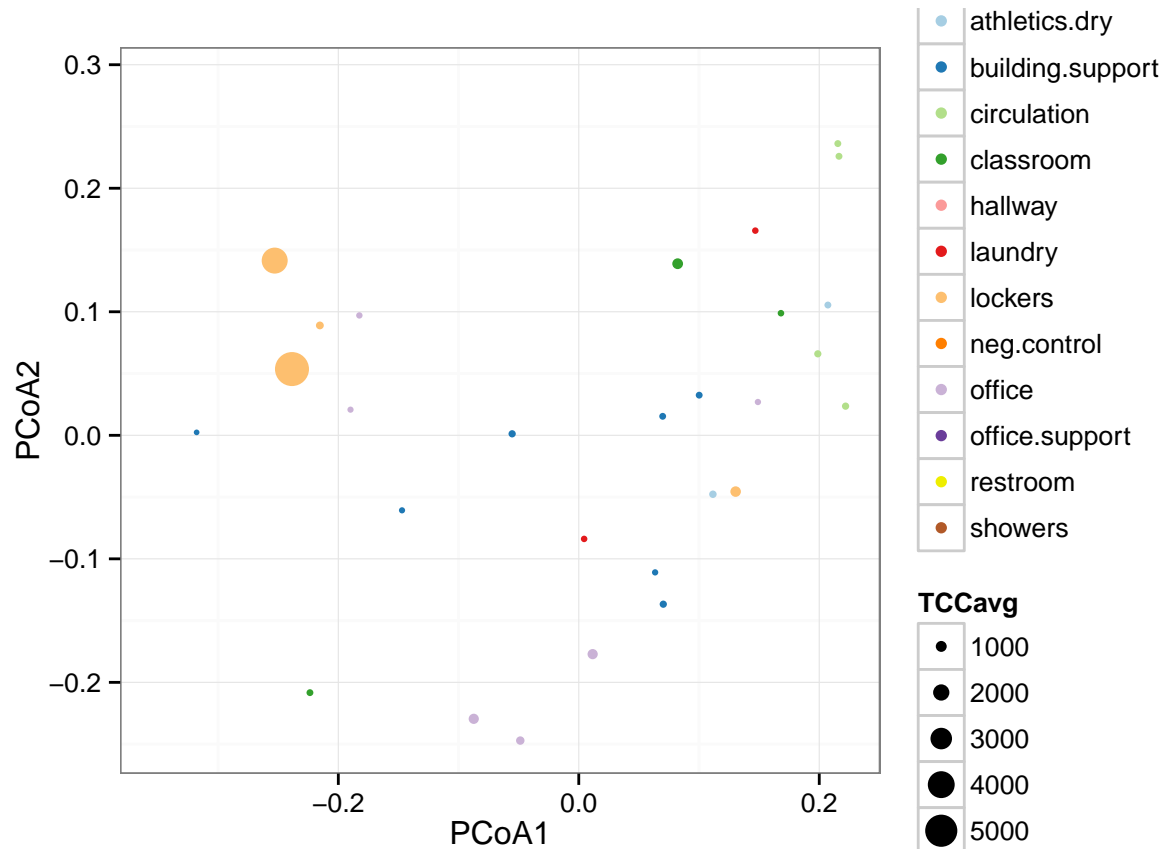
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = TCCavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = TCCavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_TCCavg.png')
```

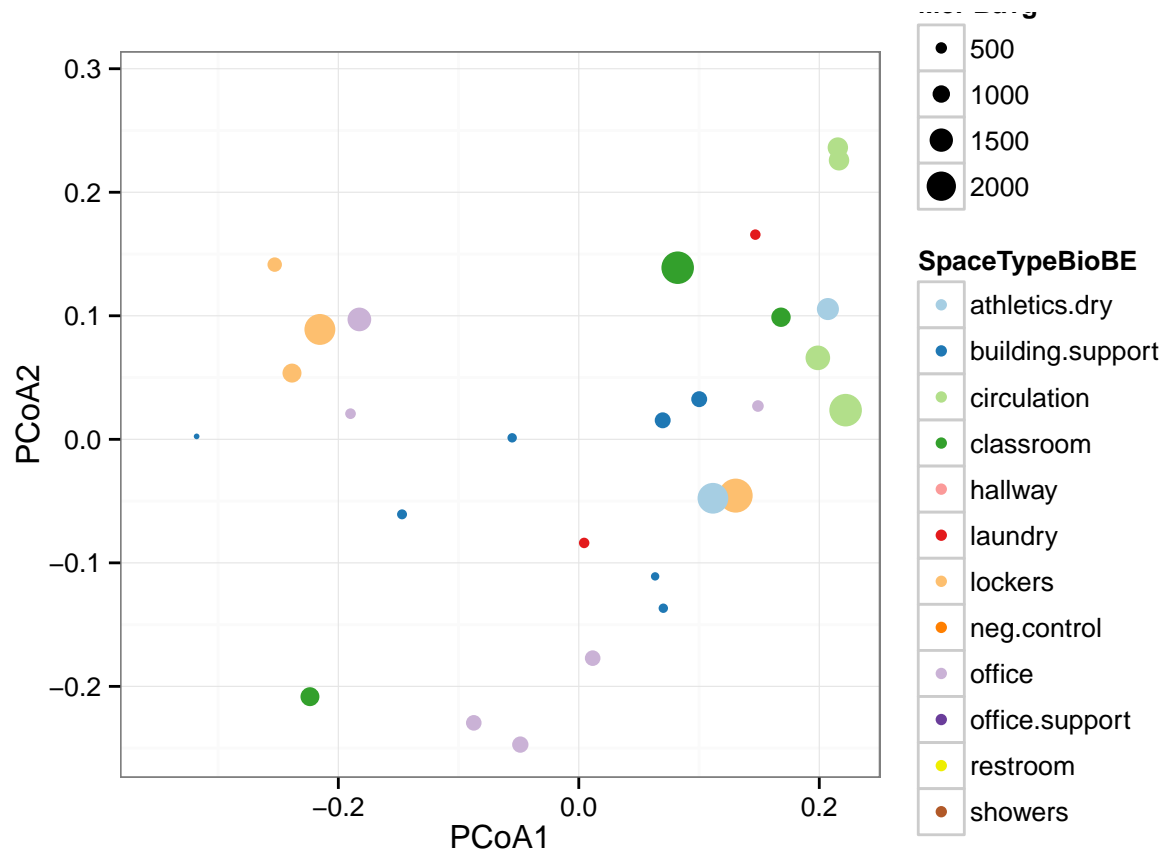
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = MePBavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = MePBavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_MePBavg.png')
```

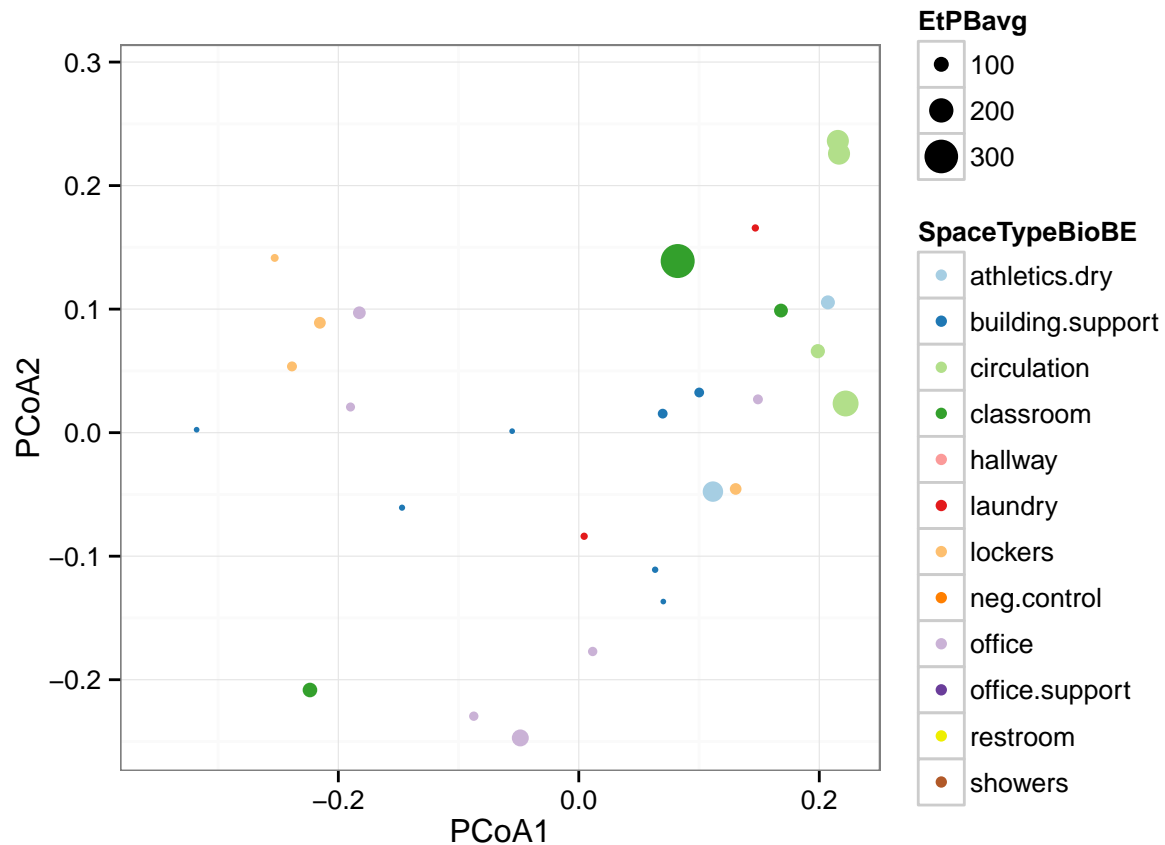
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = EtPBavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = EtPBavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_EtPBavg.png')
```

```
## Saving 6.5 x 4.5 in image
```

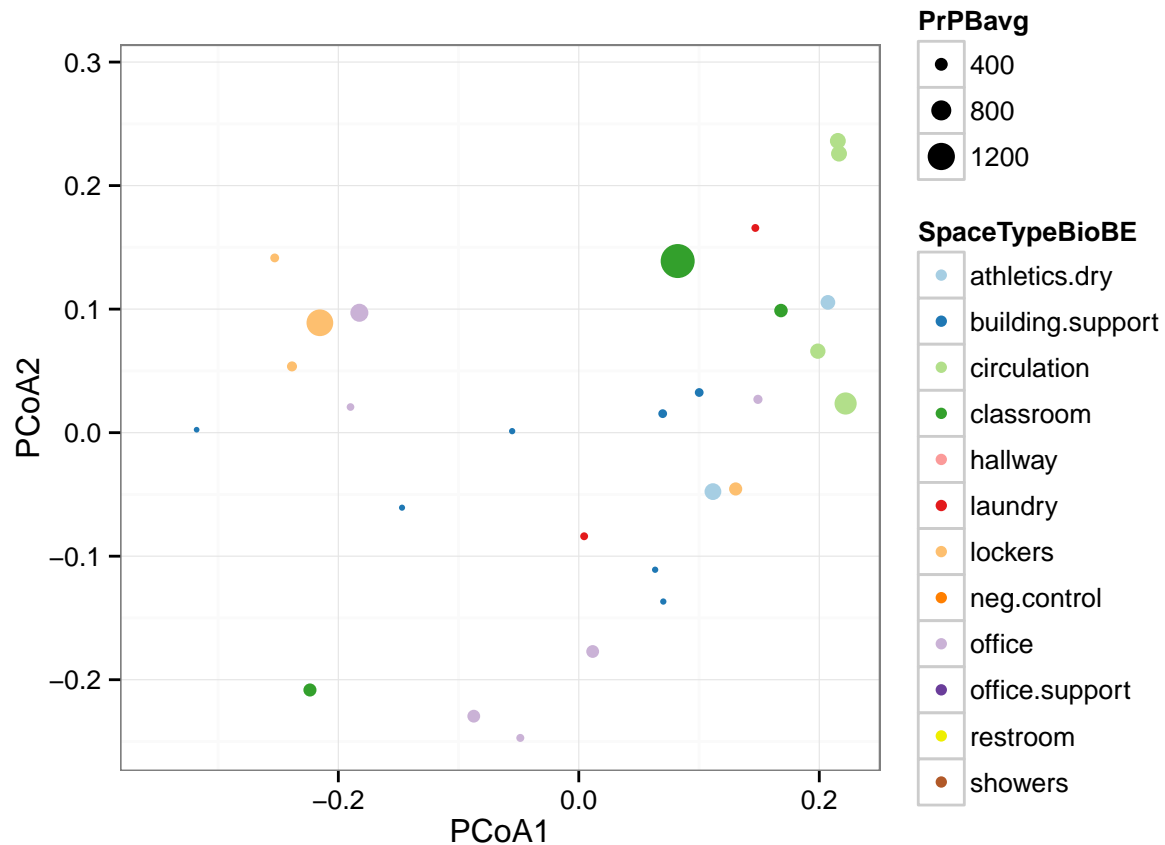
```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = PrPBavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = PrPBavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```





```
ggsave('figures/pcoa_can_g_PrPBavg.png')
```

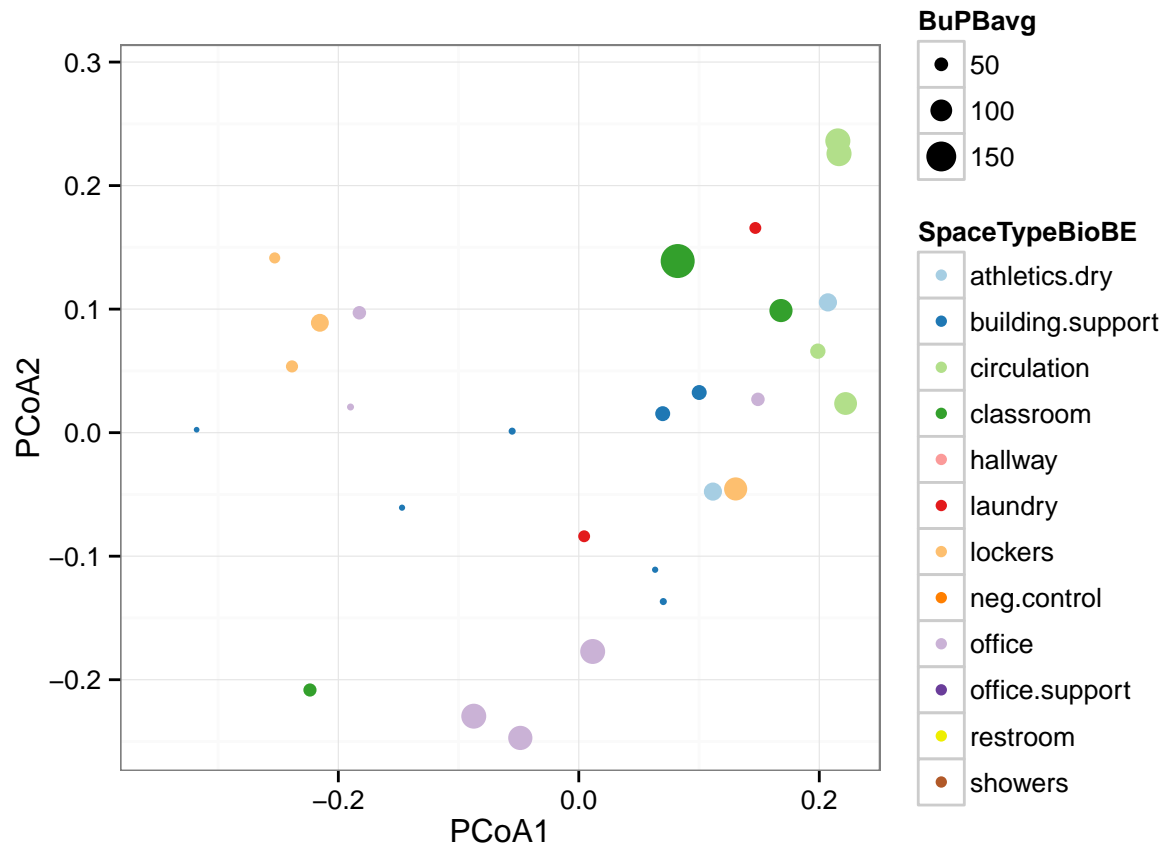
```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```

```
## chem = BuBPavg
```

```
gg.pcoa.can.g <- ggplot(df.pcoa.can.g.all, aes(x = PCoA1, y = PCoA2, color = SpaceTypeBioBE, size = BuPBavg))
gg.pcoa.can.g + geom_point() + scale_color_manual(values = mycol.12)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```
ggsave('figures/pcoa_can_g_BuPBavg.png')
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```