

This file contains all the commands you find in the Chapter

```
# load the library  
library(ggplot2)
```

```
# read the data  
dd <- read.csv("../data/Aakala2015_data.csv", sep = "\t")  
# check dimensions  
dim(dd)
```

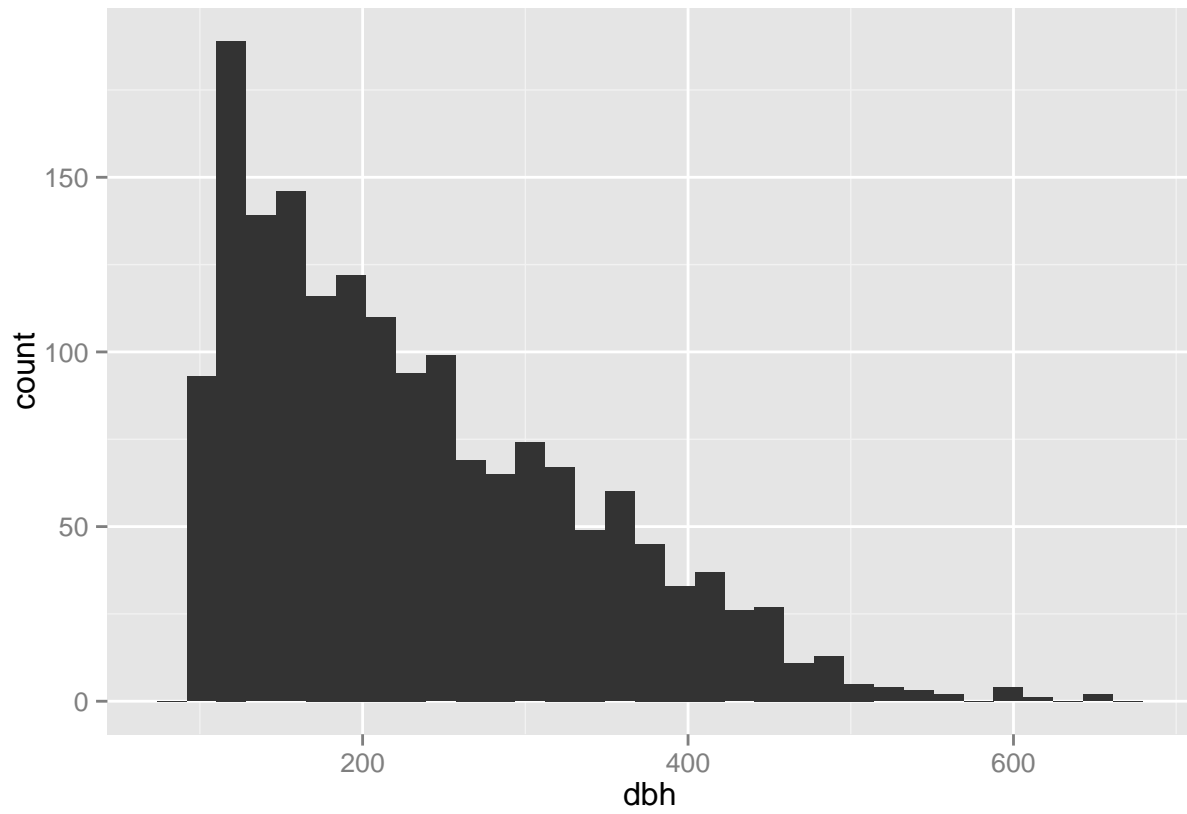
```
## [1] 1705    8
```

```
# show first few lines  
head(dd)
```

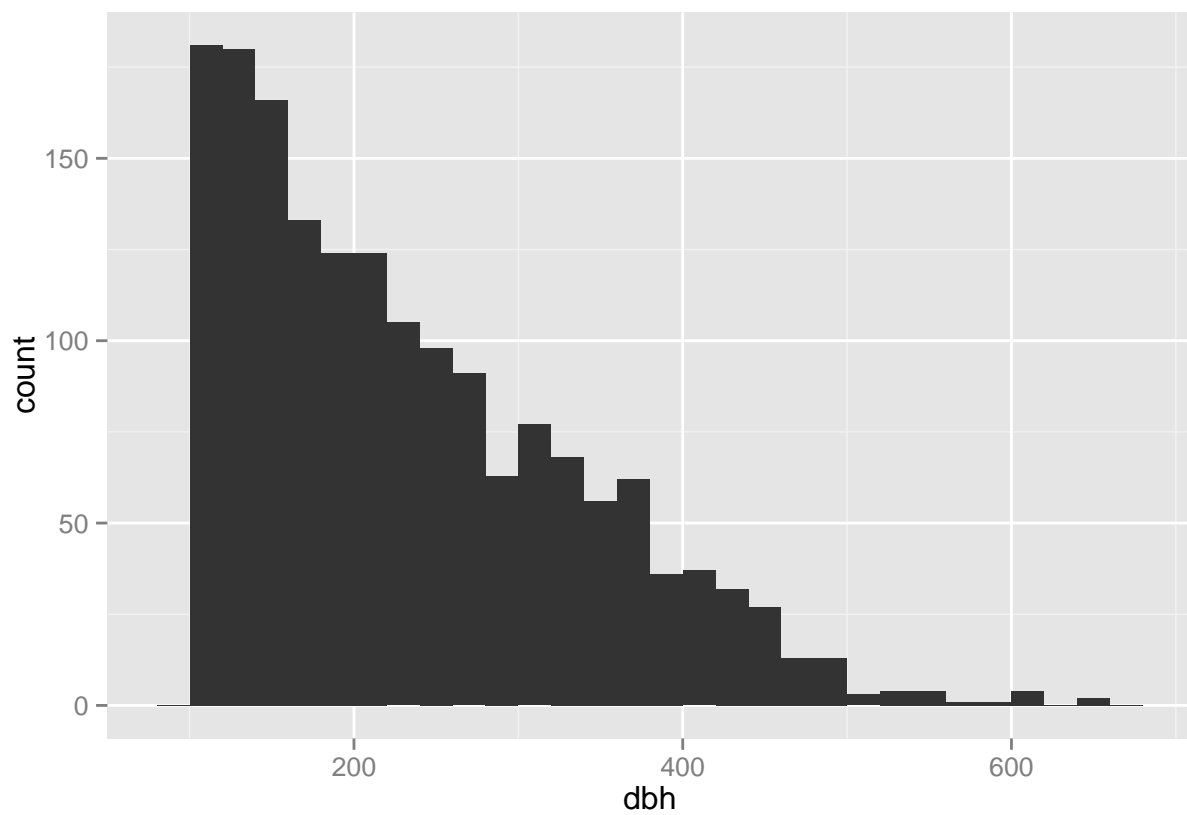
```
##   site id      x      y dbh height      species crown_area  
## 1    1  1  0.869  5.269 281 17.155 Pinus_sylvestris    8.687012  
## 2    1  2  5.397 17.467 503 17.303 Pinus_sylvestris   24.536951  
## 3    1  3  4.731  8.783 153 14.440 Pinus_sylvestris    0.801185  
## 4    1  4  5.833 10.330 186 15.416 Pinus_sylvestris    6.090272  
## 5    1  5  7.308  9.066 250 17.864 Pinus_sylvestris    4.692933  
## 6    1  6 11.768 15.171 119  8.285    Picea_abies    2.386878
```

```
# simple histograms of diameter at breast height  
ggplot(data = dd, aes(x = dbh)) + geom_histogram()
```

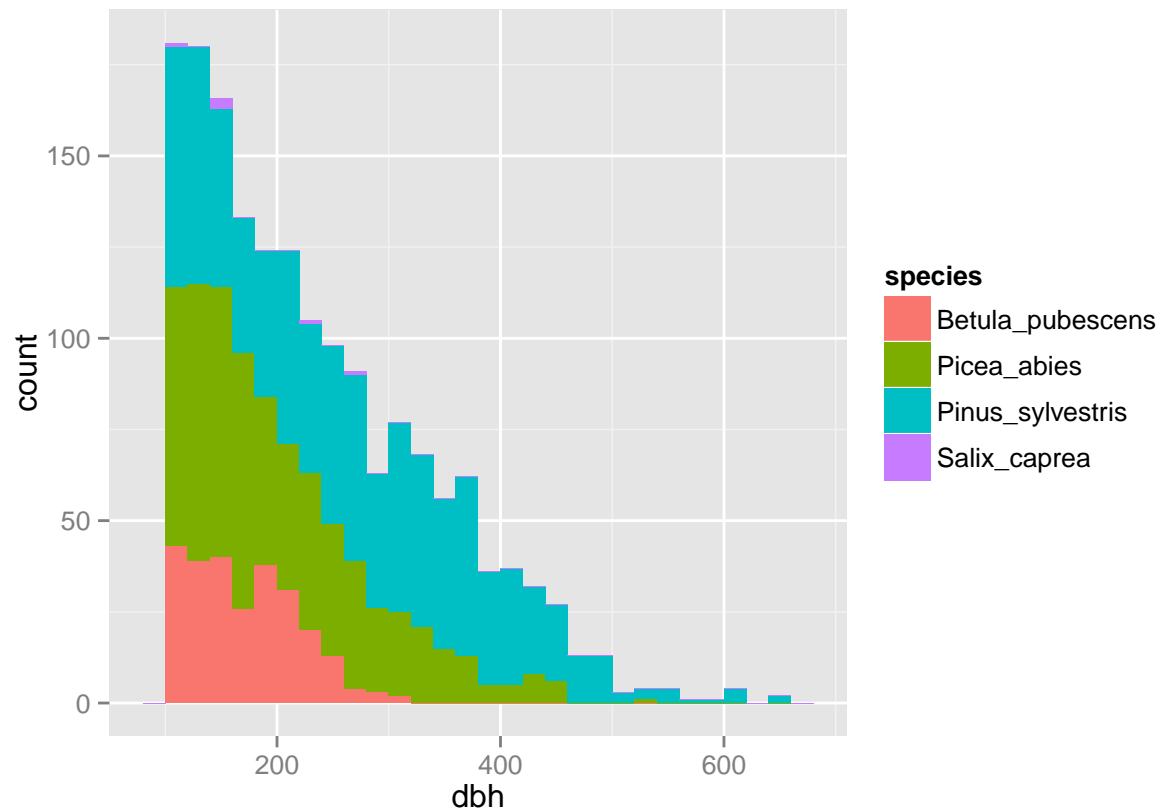
```
## stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to adjust this.
```



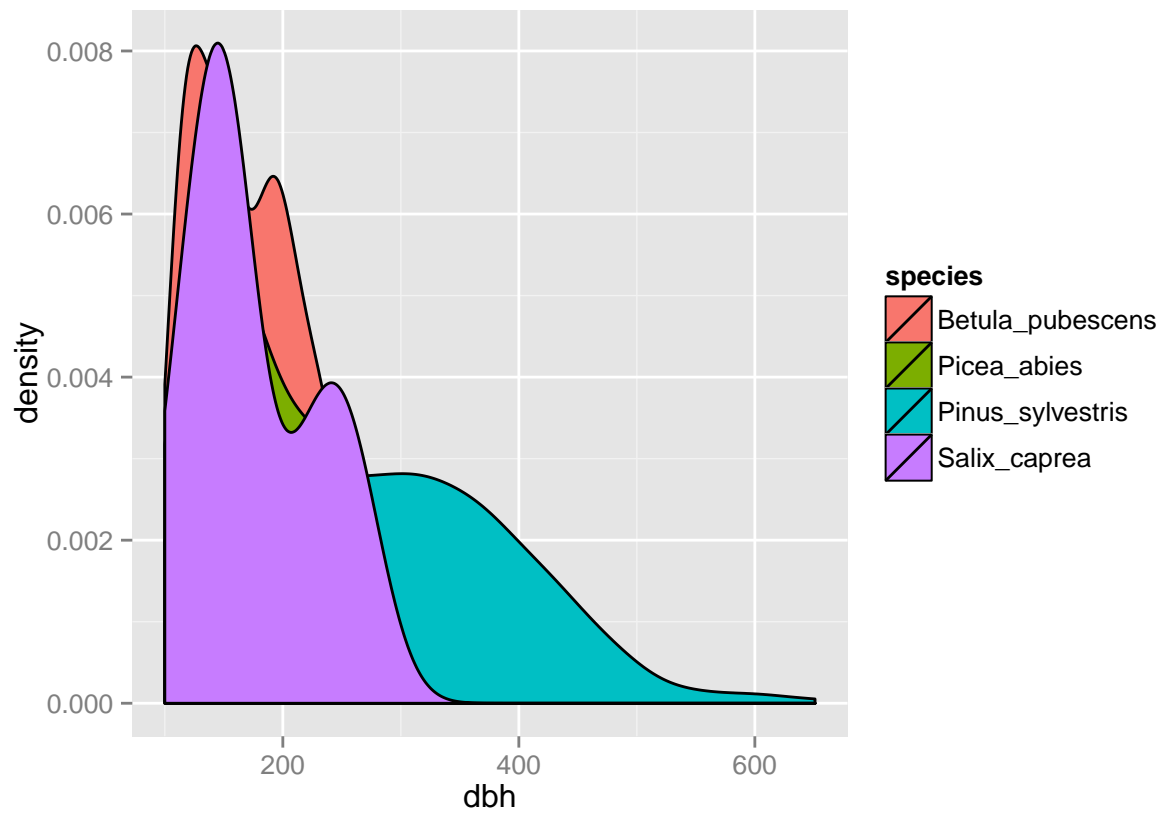
```
ggplot(data = dd, aes(x = dbh)) + geom_histogram(binwidth = 20)
```



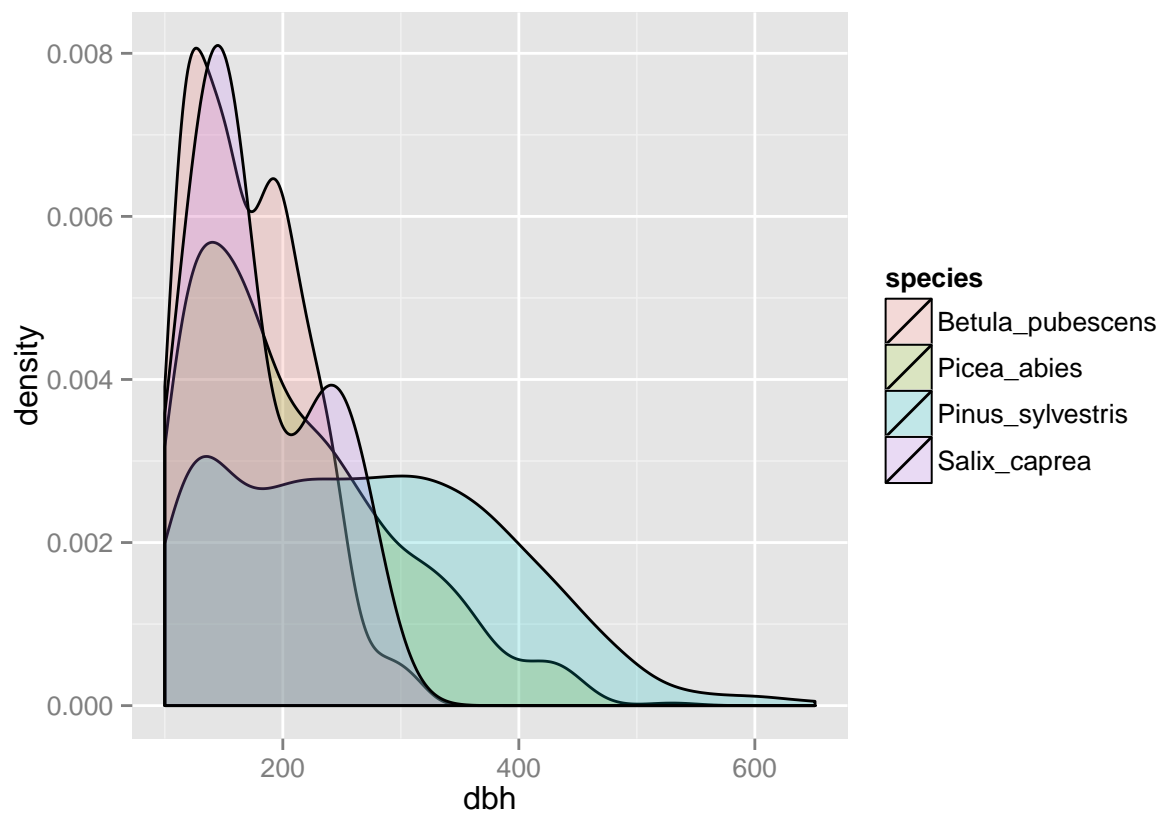
```
ggplot(data = dd, aes(x = dbh, fill = species)) + geom_histogram(binwidth = 20)
```



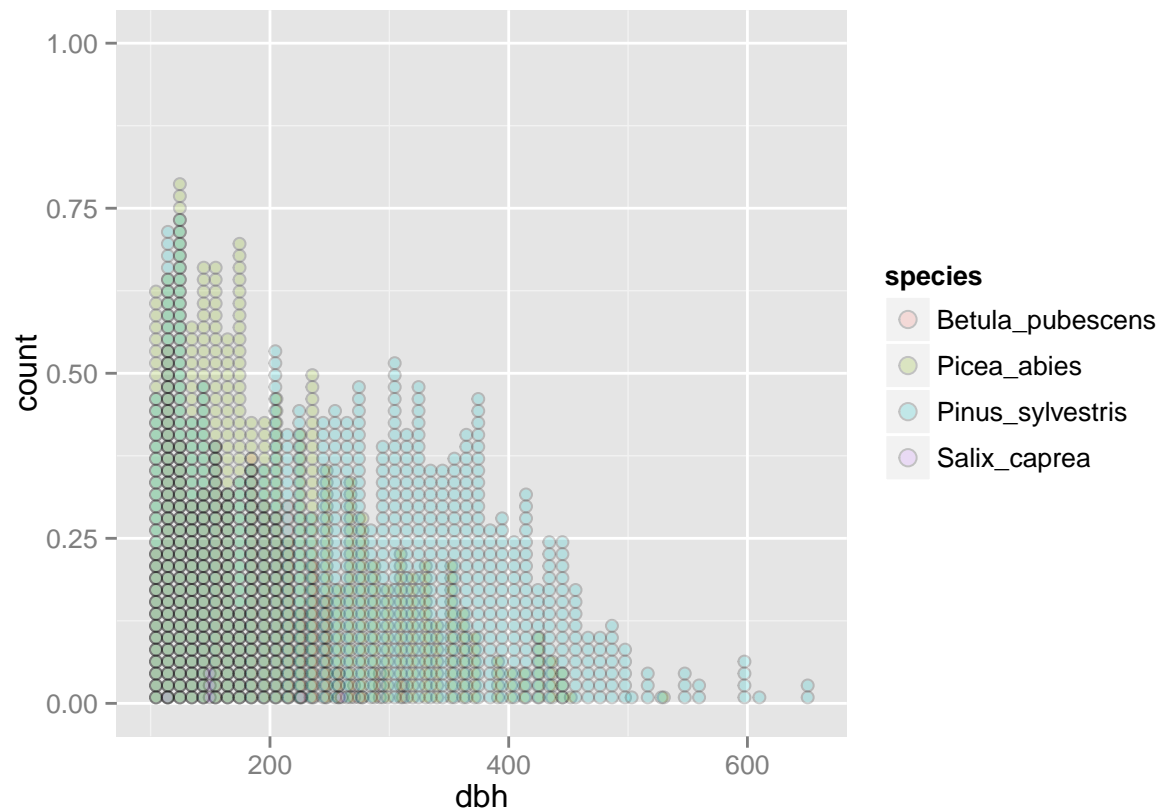
```
# density plots  
ggplot(data = dd, aes(x = dbh, fill = species)) + geom_density()
```



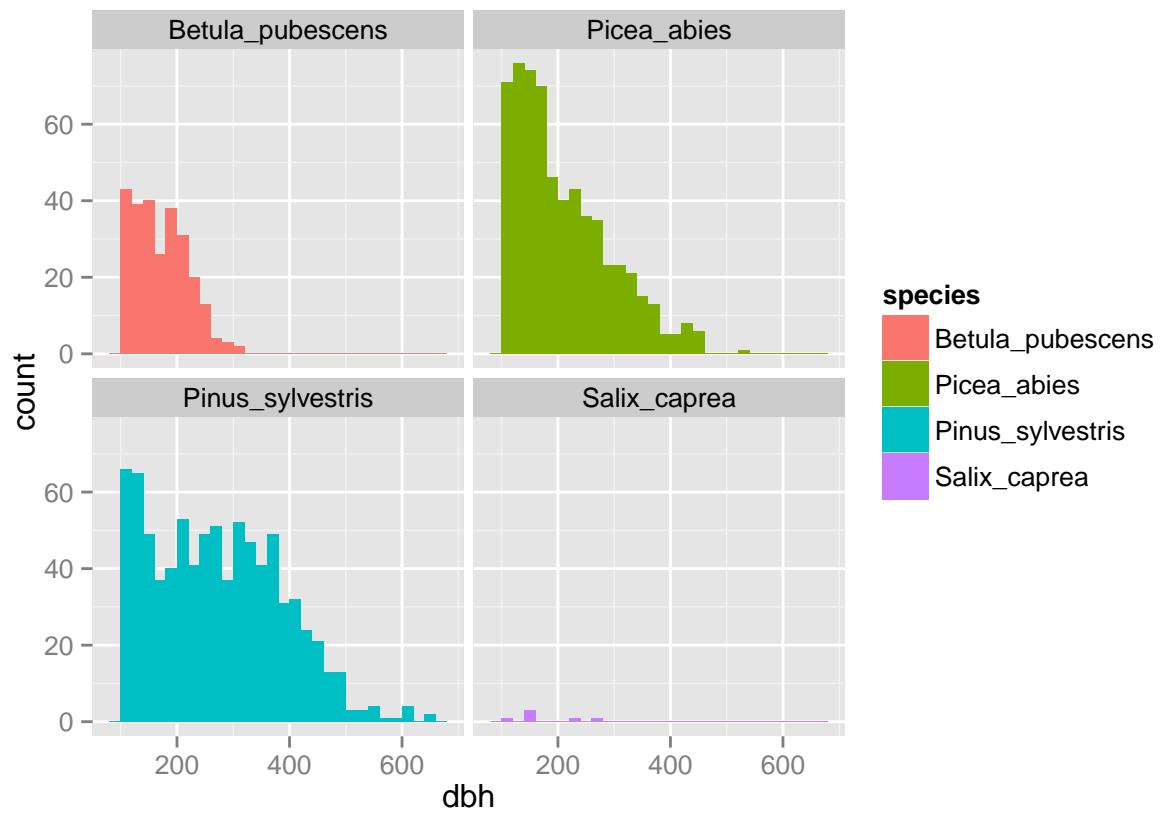
```
ggplot(data = dd, aes(x = dbh, fill = species)) + geom_density(alpha = 0.2)
```



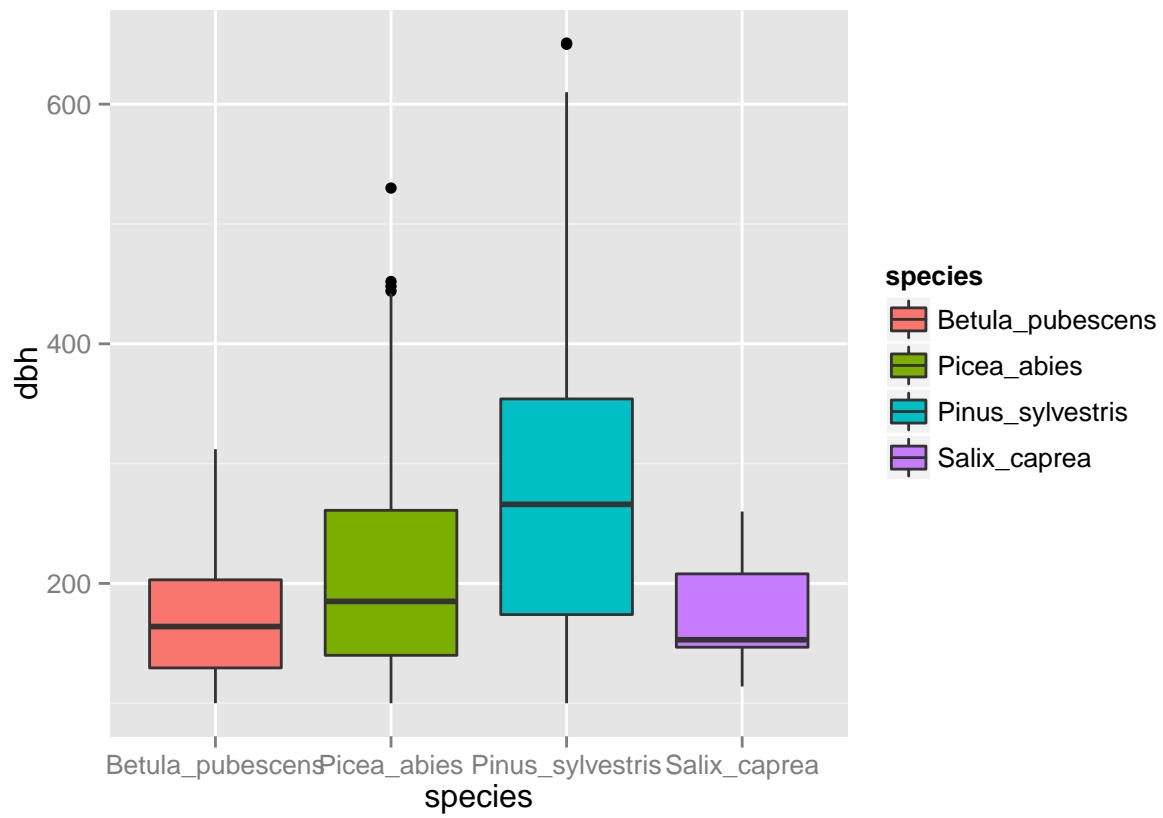
```
# dot plot
ggplot(data = dd, aes(x = dbh, fill = species)) + geom_dotplot(alpha = 0.2, binwidth = 10)
```



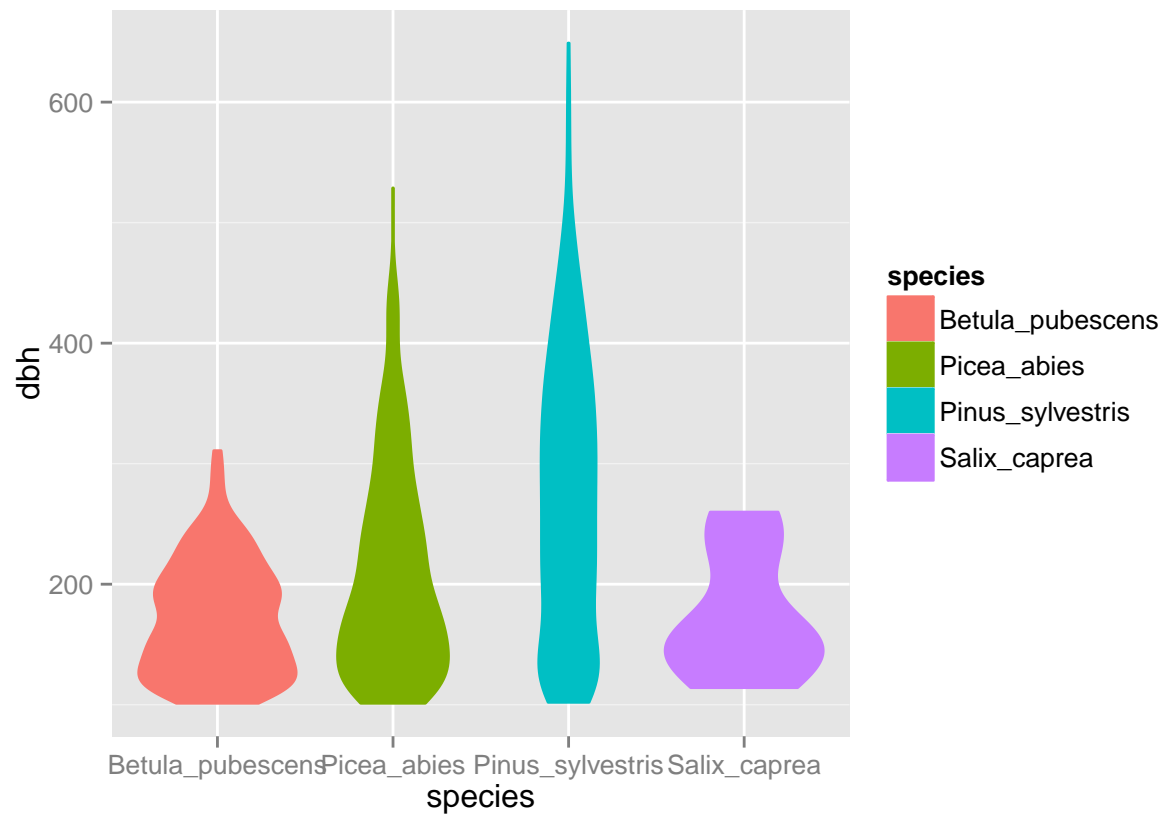
```
# example of faceting
ggplot(data = dd, aes(x = dbh, fill = species)) + geom_histogram(binwidth = 20) + facet_wrap(~species)
```



```
# boxplot
ggplot(data = dd, aes(x = species, y = dbh, fill = species)) + geom_boxplot()
```

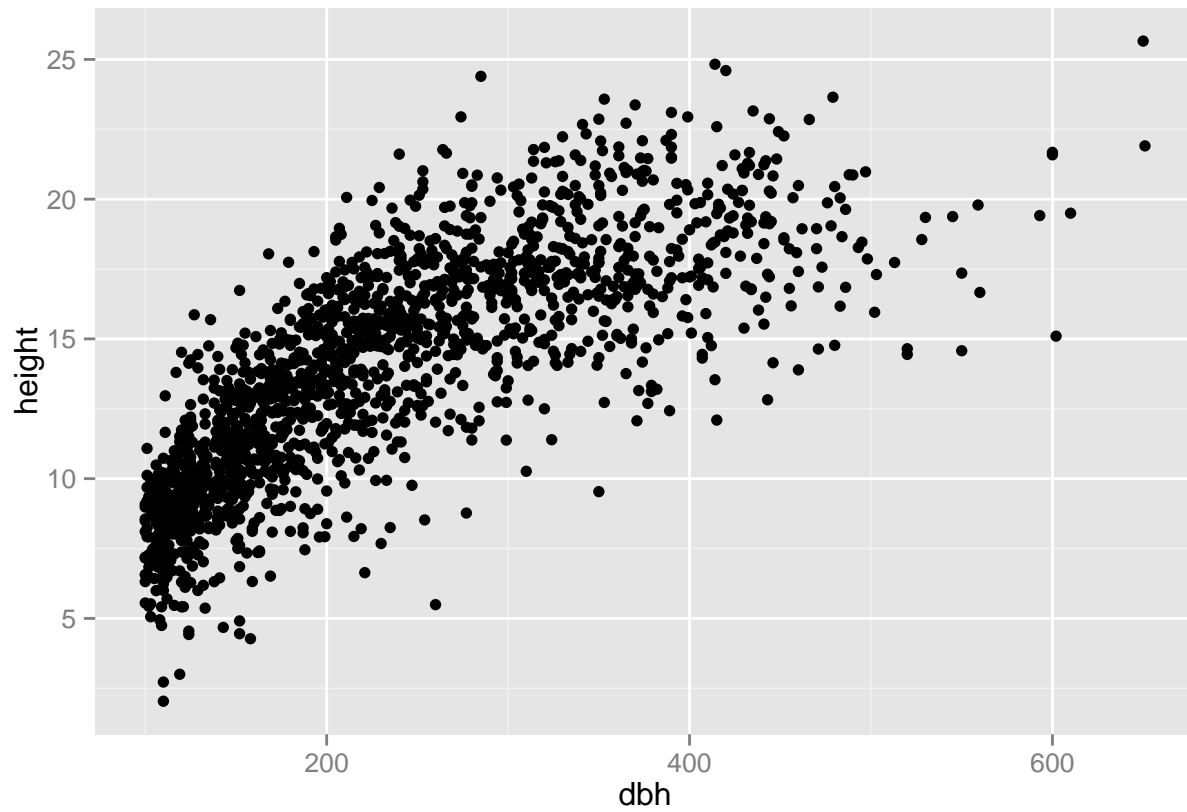


```
# violin plot  
ggplot(data = dd, aes(x = species, y = dbh, fill = species, colour = species)) + geom_violin()
```



```
# scatter plot  
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point()
```

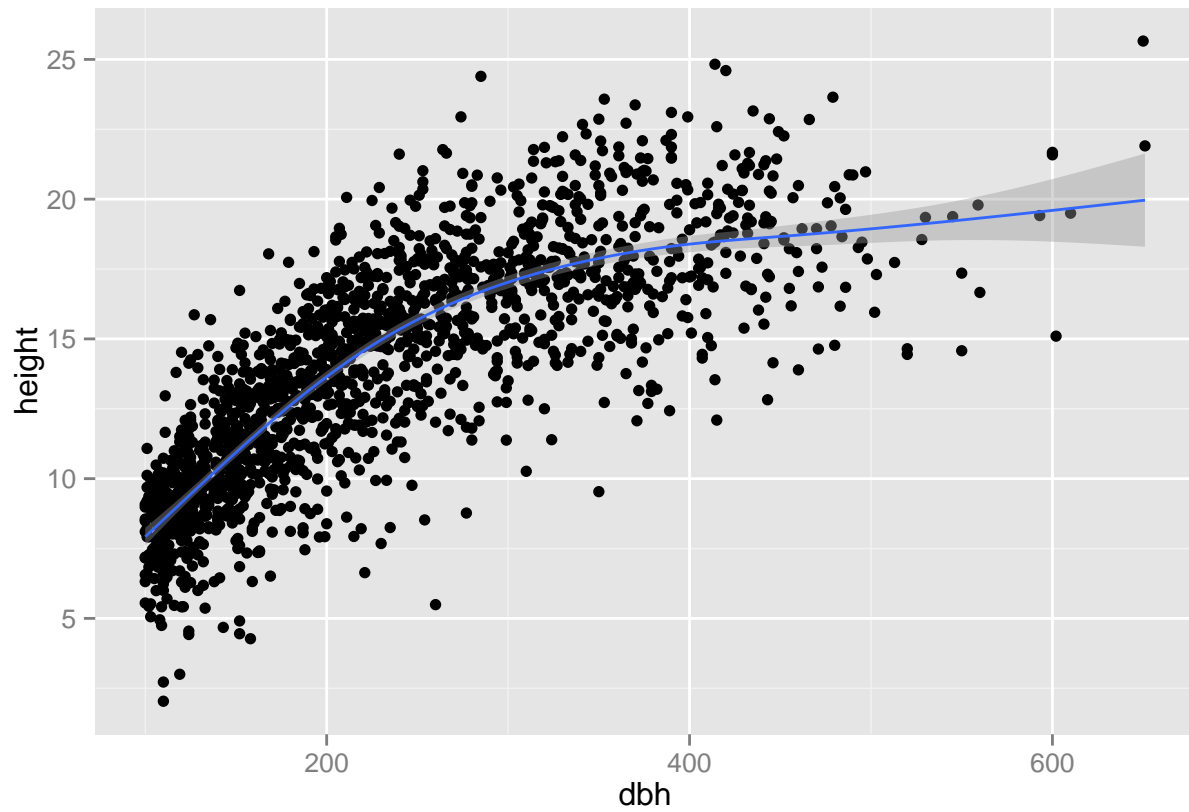




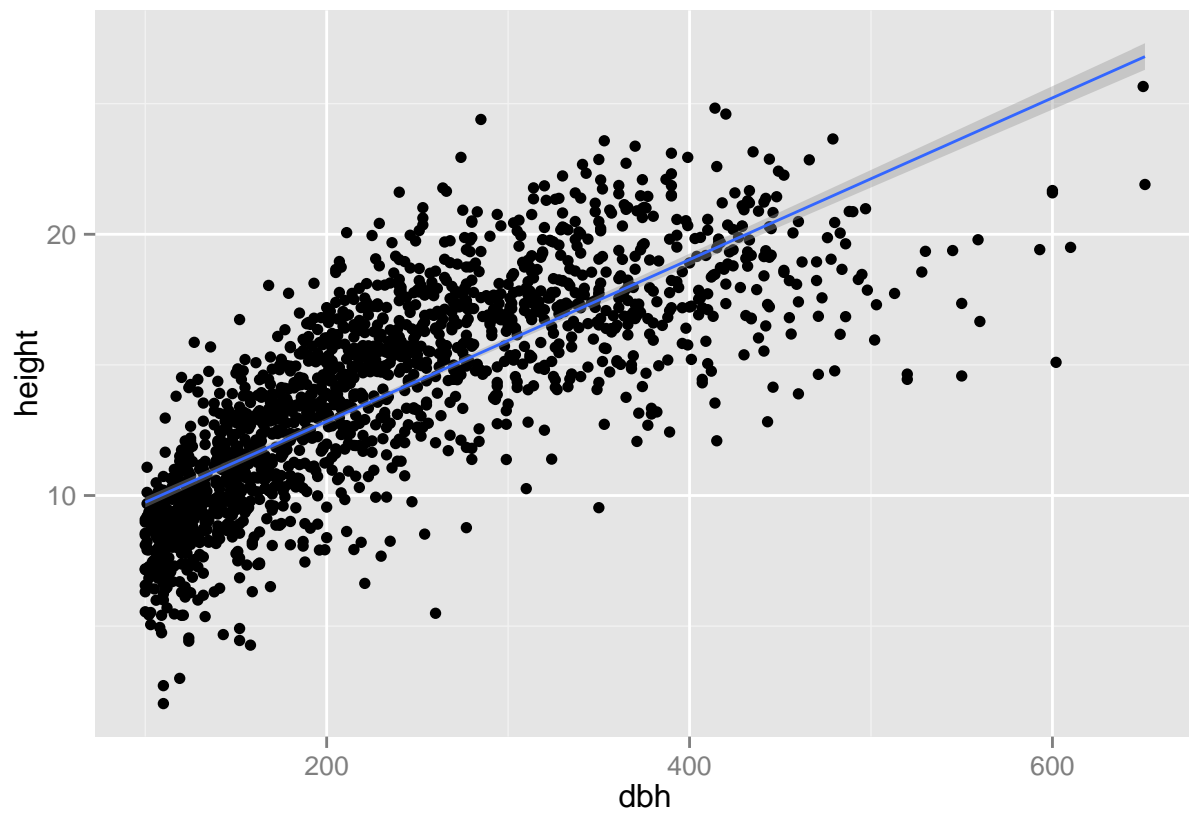
```
# smoothers and regressions
```

```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point() + geom_smooth()
```

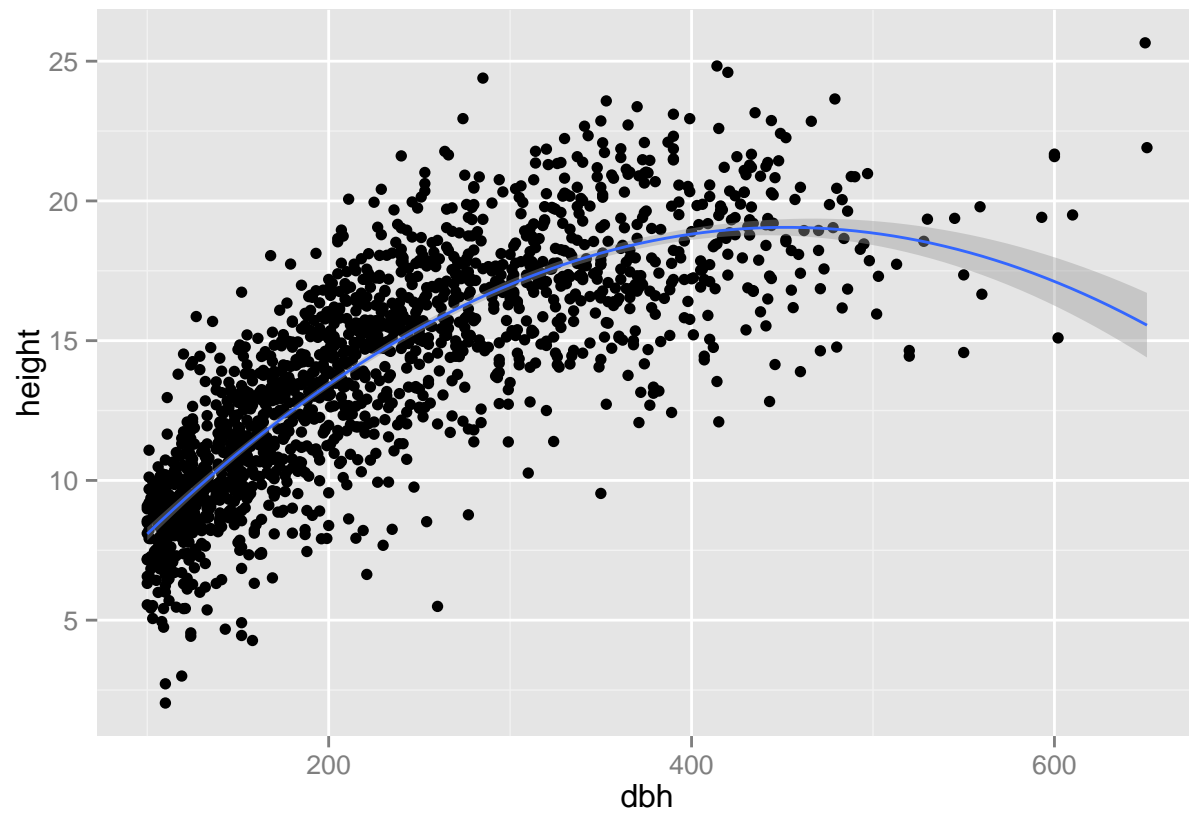
```
## geom_smooth: method="auto" and size of largest group is >=1000, so using gam with formula: y ~ s(x, l
```



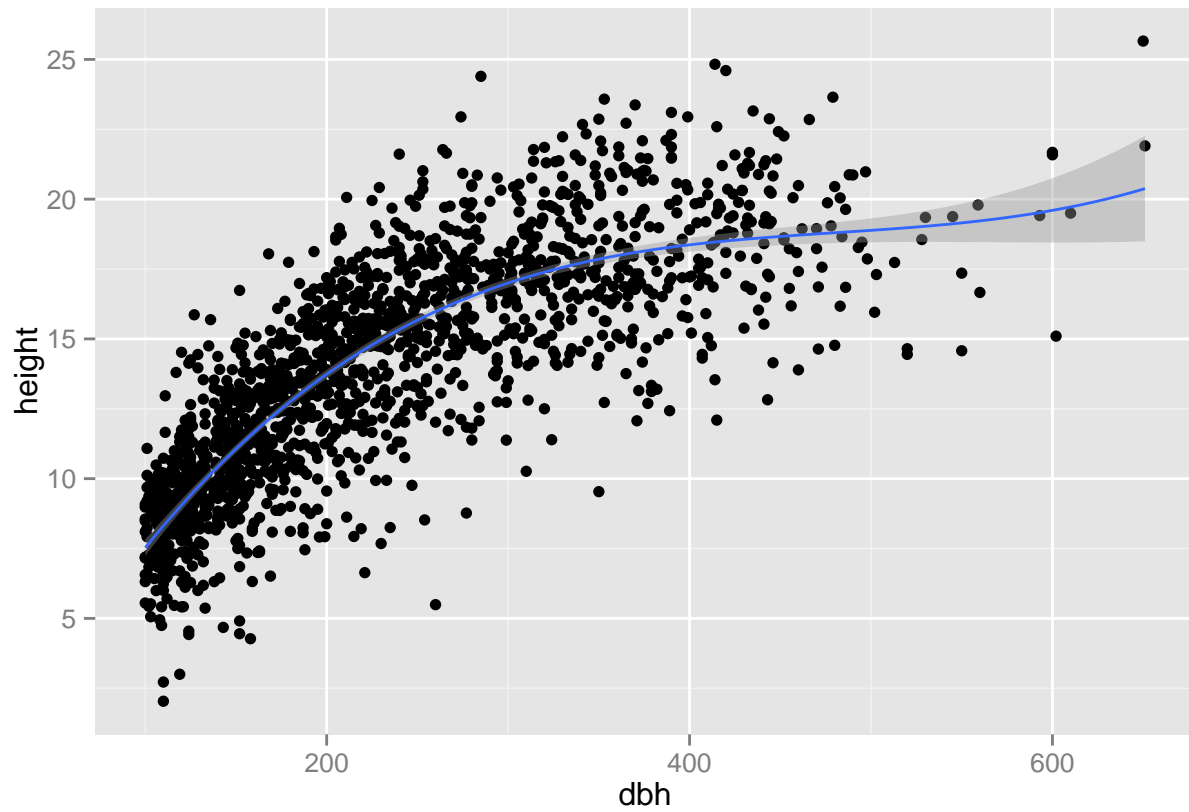
```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point() + geom_smooth(method = "lm")
```



```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point() + geom_smooth(method = "glm", formula = "y ~
```

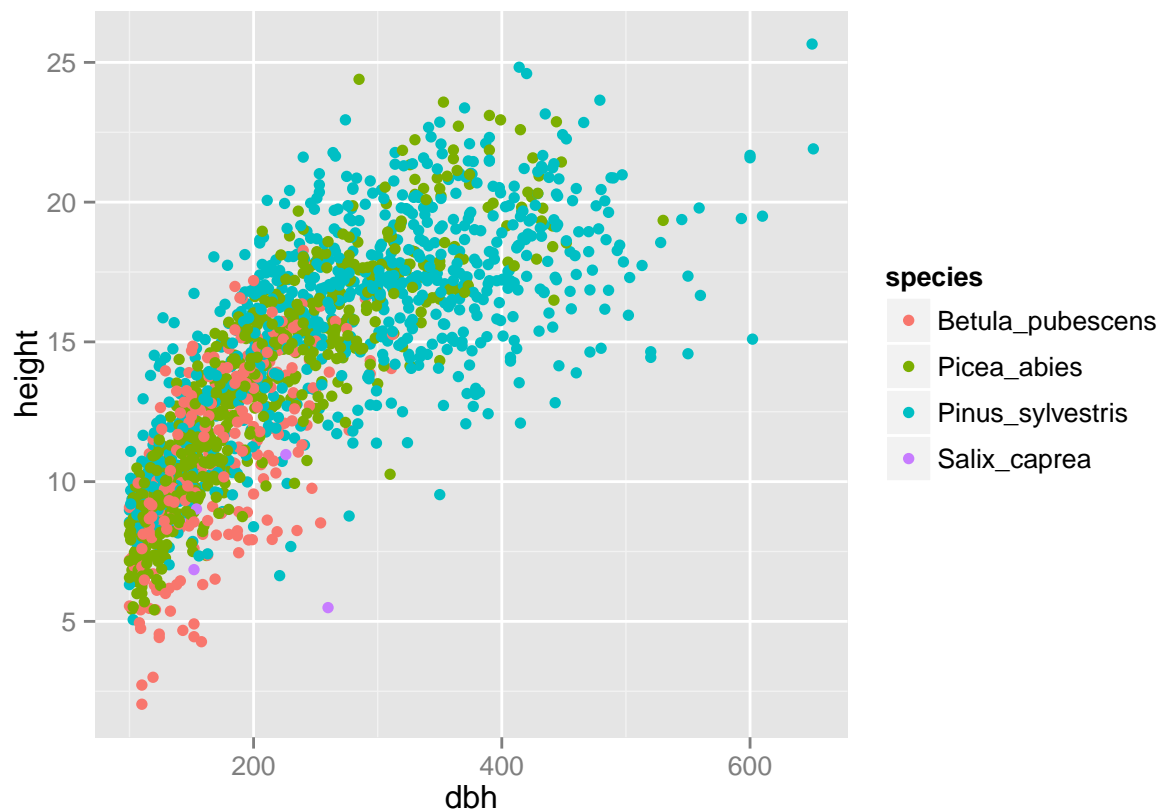


```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point() + geom_smooth(method = "glm", formula = "y ~
```

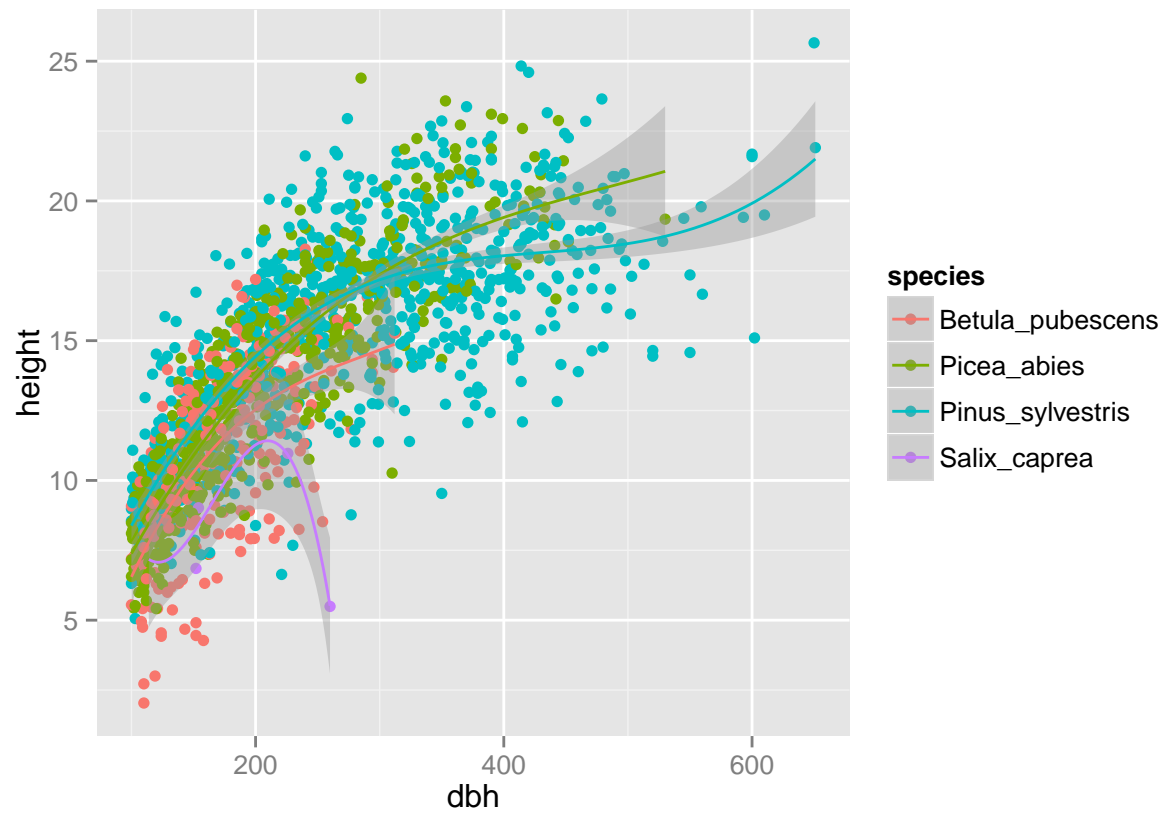


*# one smoother per species*

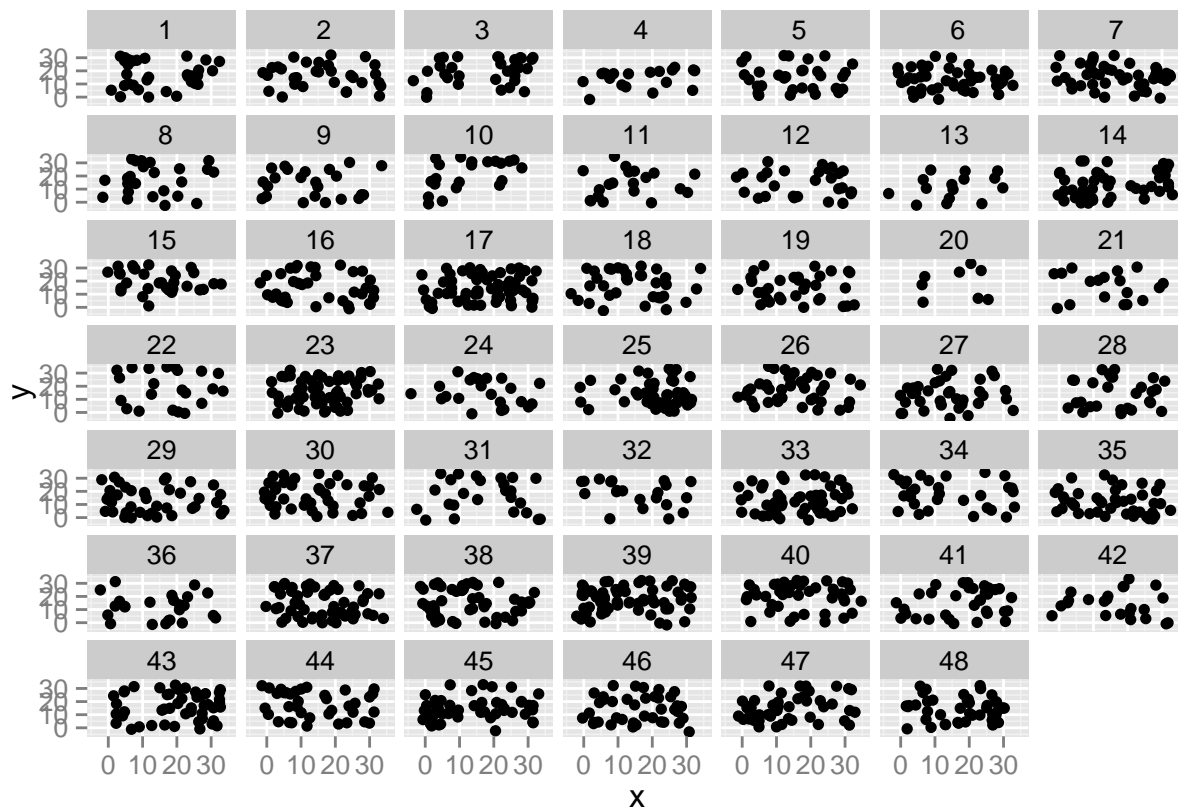
```
ggplot(data = dd, aes(x = dbh, y = height, colour = species)) + geom_point()
```



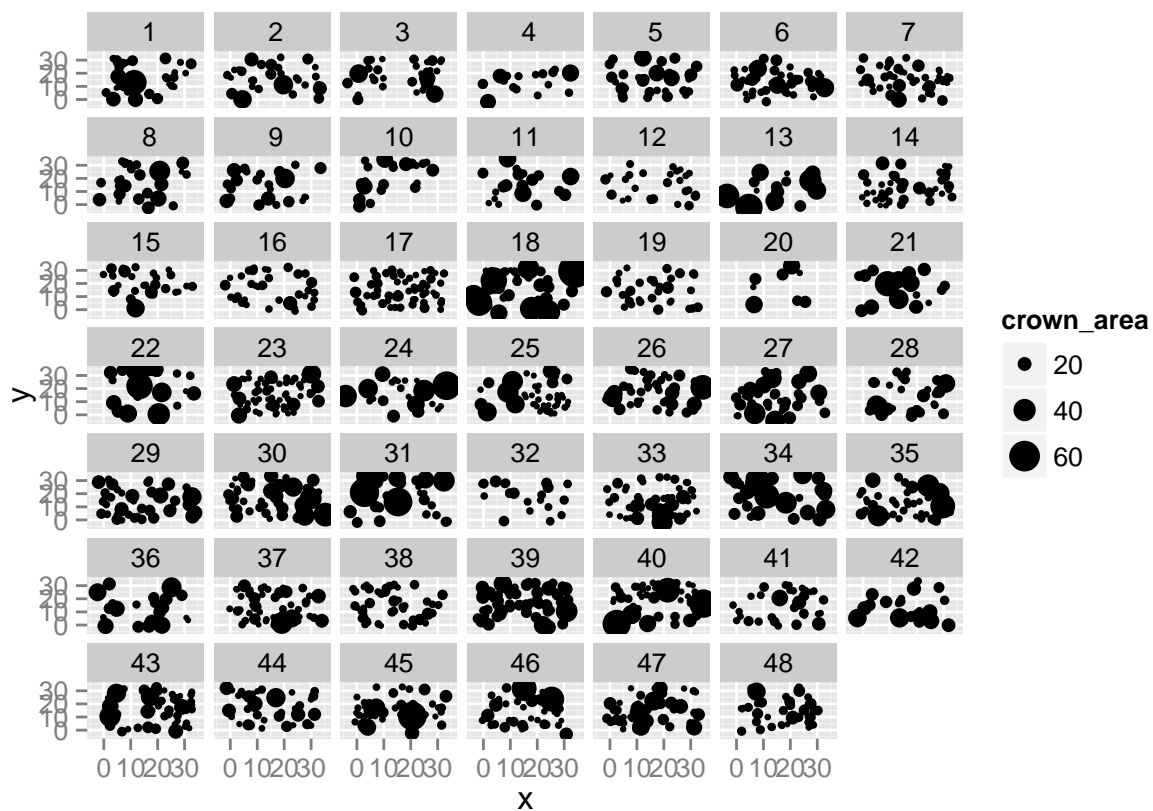
```
ggplot(data = dd, aes(x = dbh, y = height, colour = species)) + geom_point() + geom_smooth(method = "glm"
```



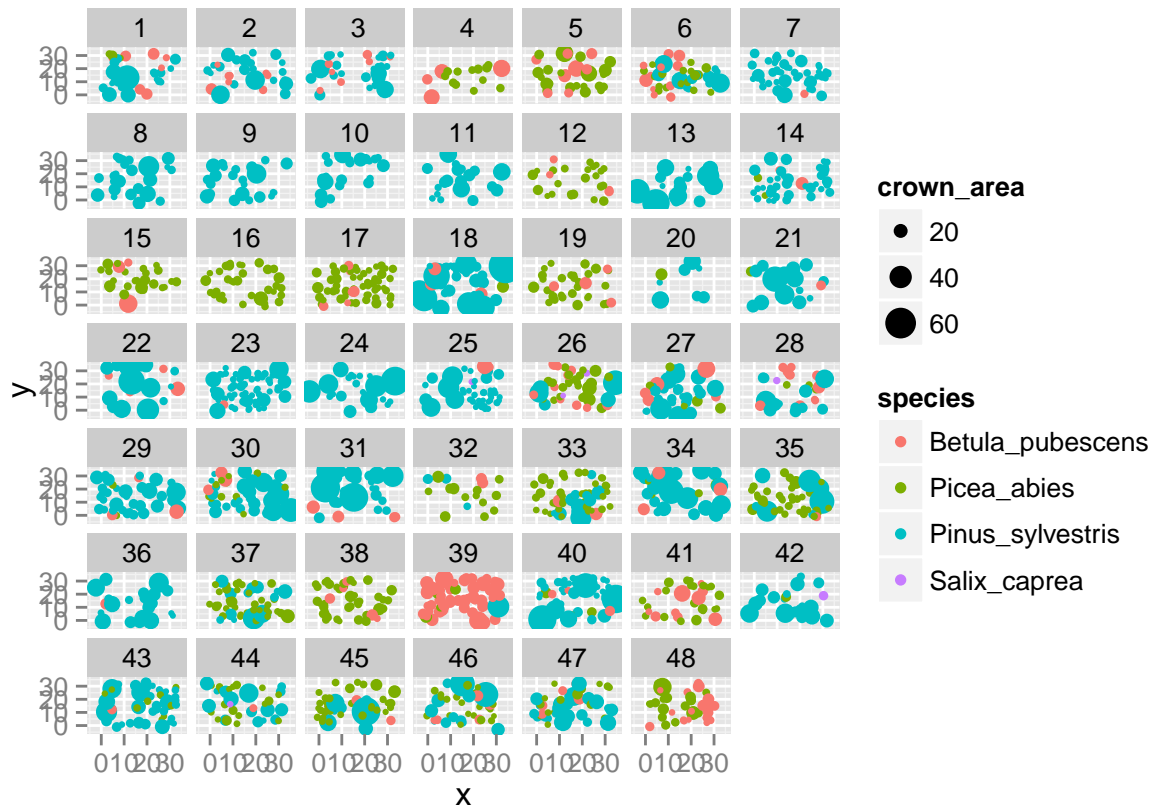
```
# location of trees in sites  
ggplot(data = dd, aes(x = x, y = y)) + geom_point() + facet_wrap(~site)
```



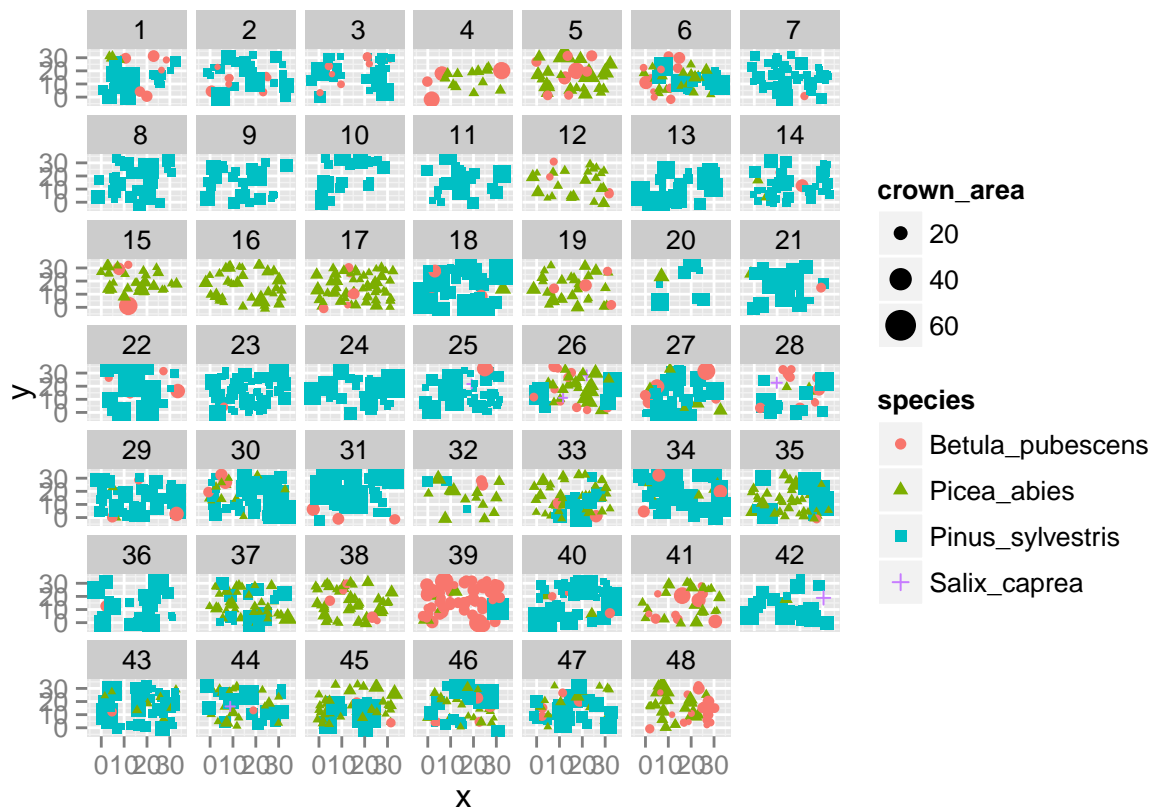
```
ggplot(data = dd, aes(x = x, y = y, size = crown_area)) + geom_point() + facet_wrap(~site)
```



```
ggplot(data = dd, aes(x = x, y = y, size = crown_area, colour = species)) + geom_point() + facet_wrap(~
```

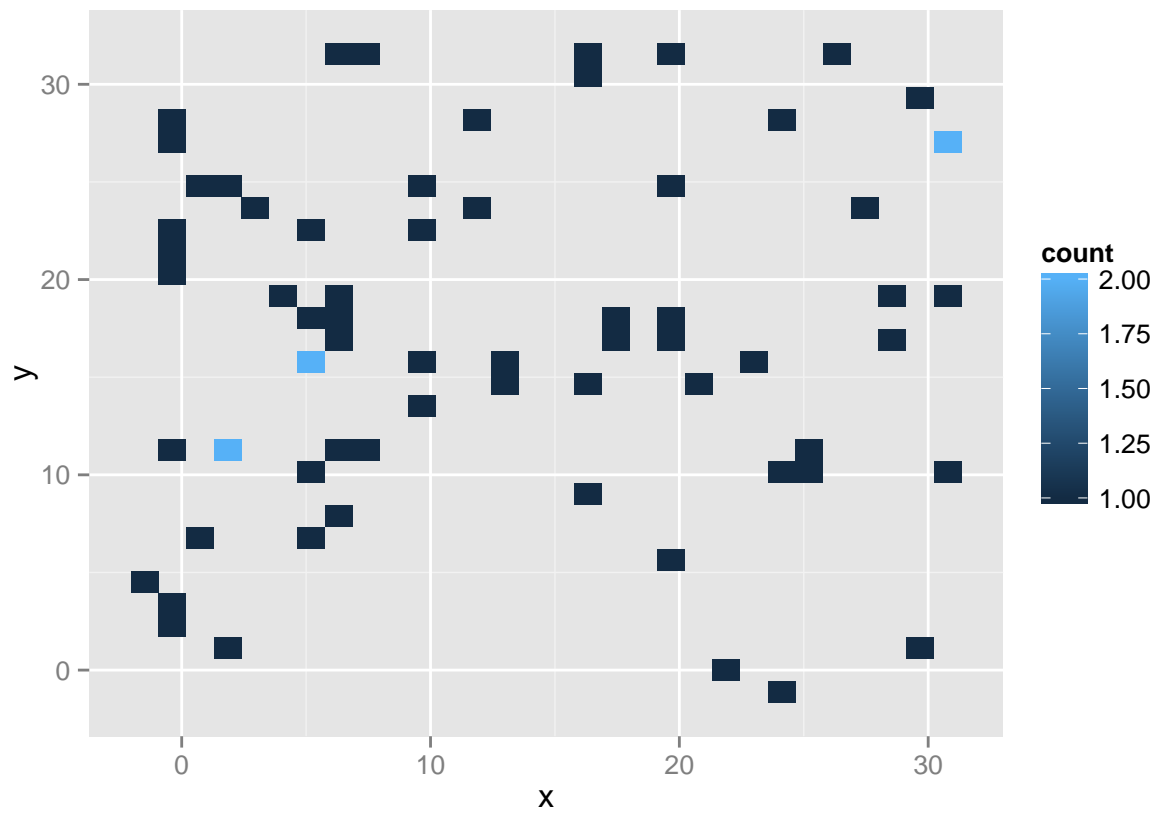


```
ggplot(data = dd, aes(x = x, y = y, size = crown_area, colour = species, shape = species)) + geom_point
```

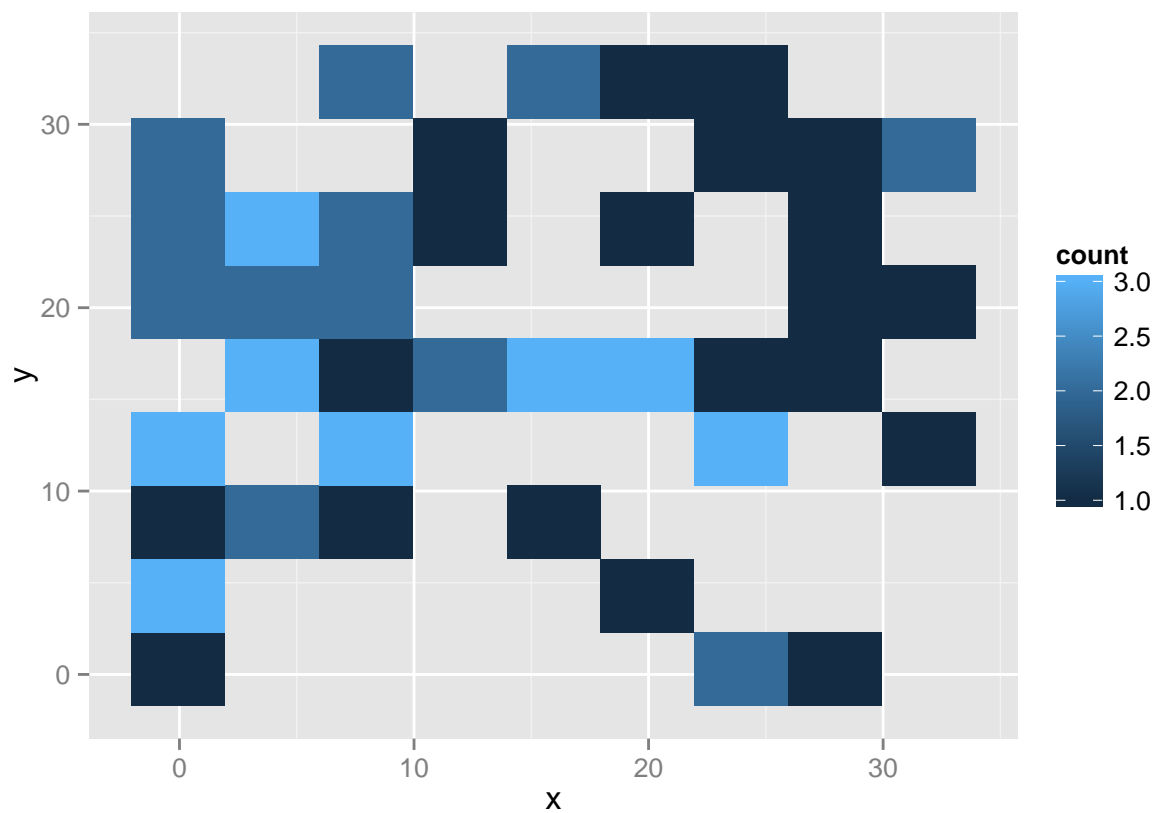


```
# 2D density plots
dd2 <- dd[dd$site == 39,]
ggplot(data = dd2, aes(x = x, y = y, z = 1)) + geom_bin2d()
```

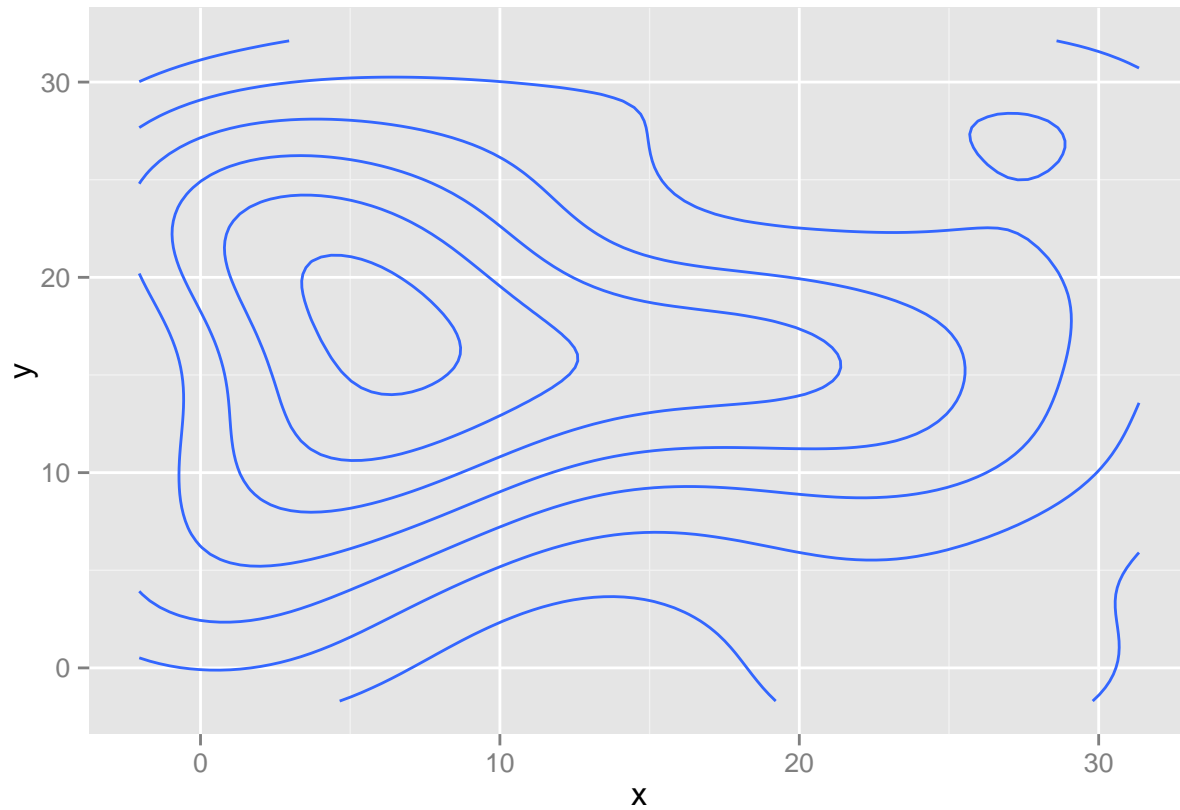




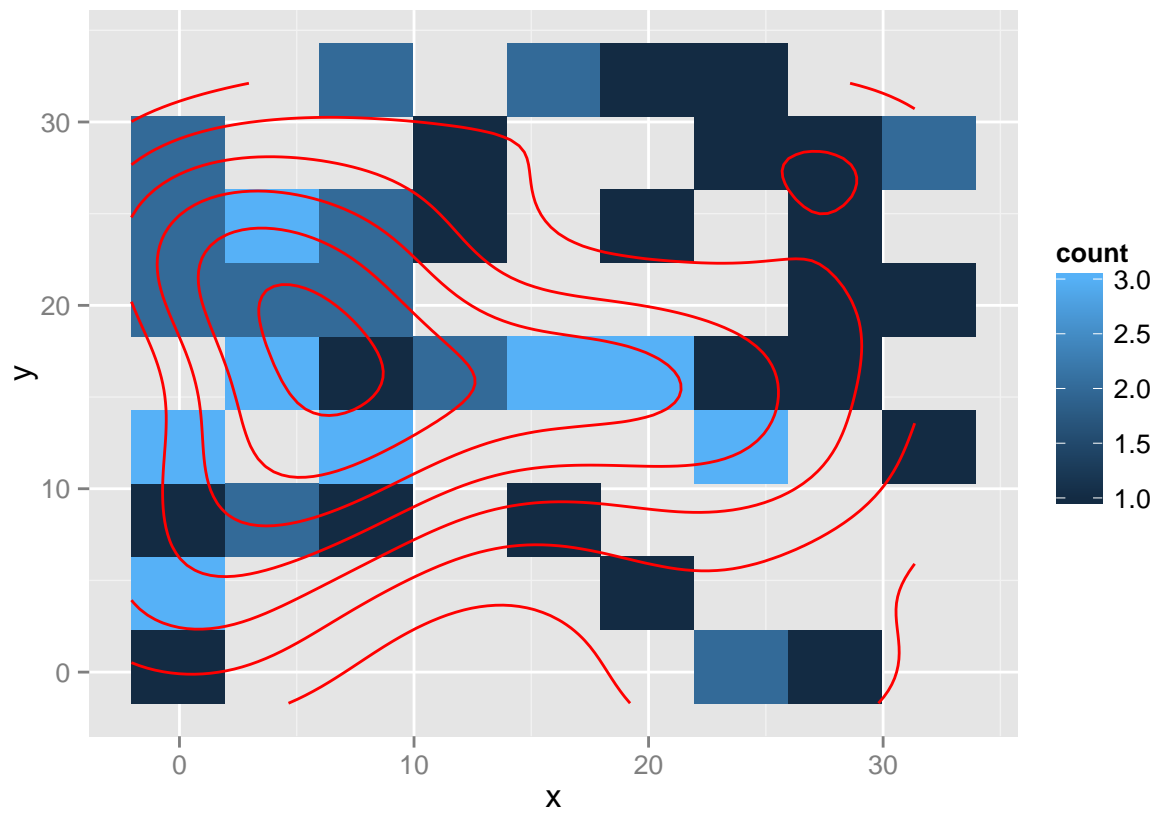
```
ggplot(data = dd2, aes(x = x, y = y, z = 1)) + geom_bin2d(binwidth = c(4, 4))
```



```
ggplot(data = dd2, aes(x = x, y = y, z = 1)) + geom_density2d()
```



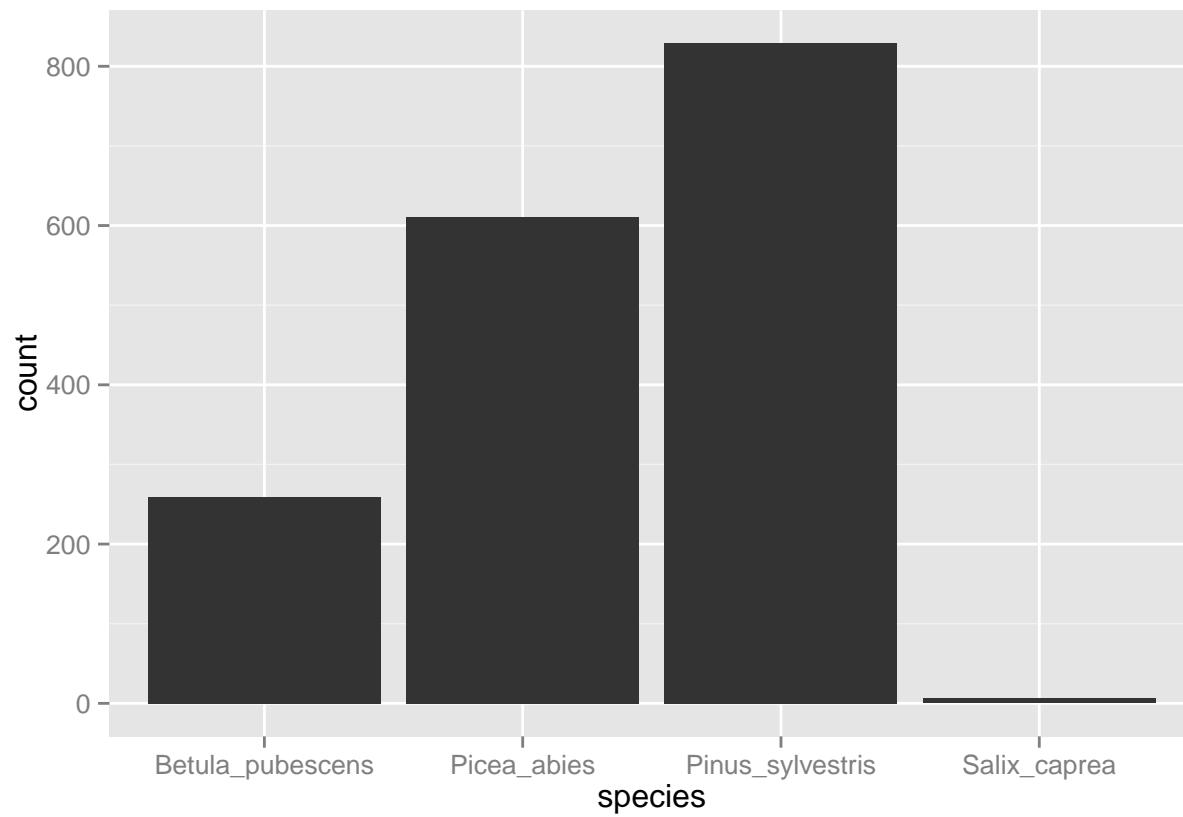
```
ggplot(data = dd2, aes(x = x, y = y, z = 1)) + geom_bin2d(binwidth = c(4, 4)) + geom_density2d(colour =
```



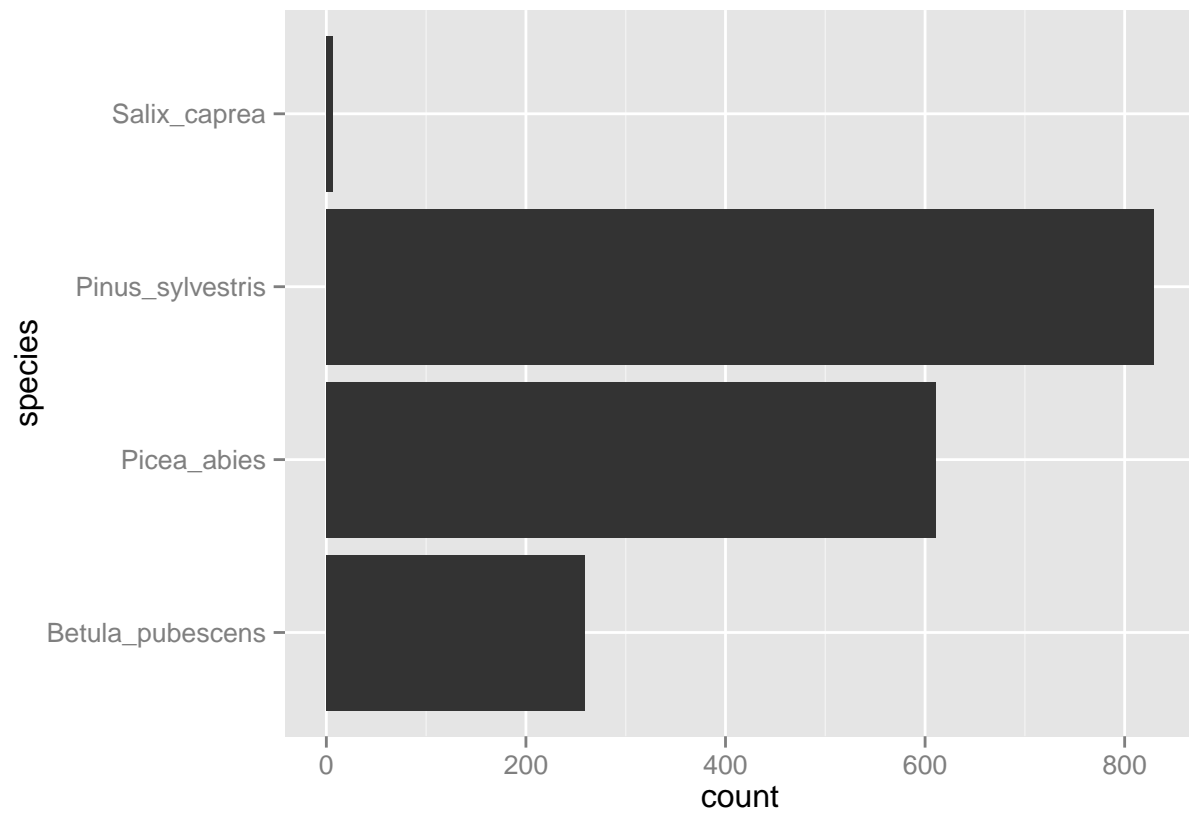
```
ggplot(data = dd2, aes(x = x, y = y, z = 1)) + geom_hex(binwidth = c(4,4)) # requires installing some
```



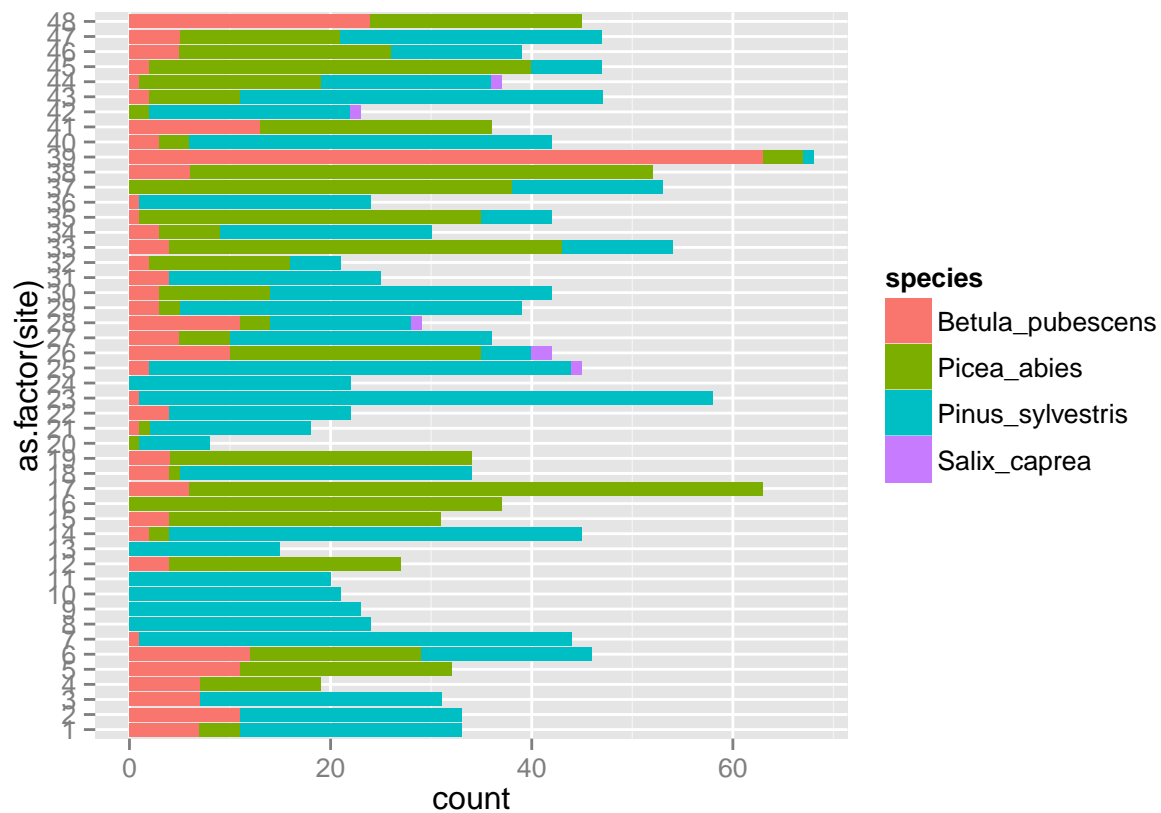
```
# barplots  
ggplot(data = dd, aes(x = species)) + geom_bar()
```



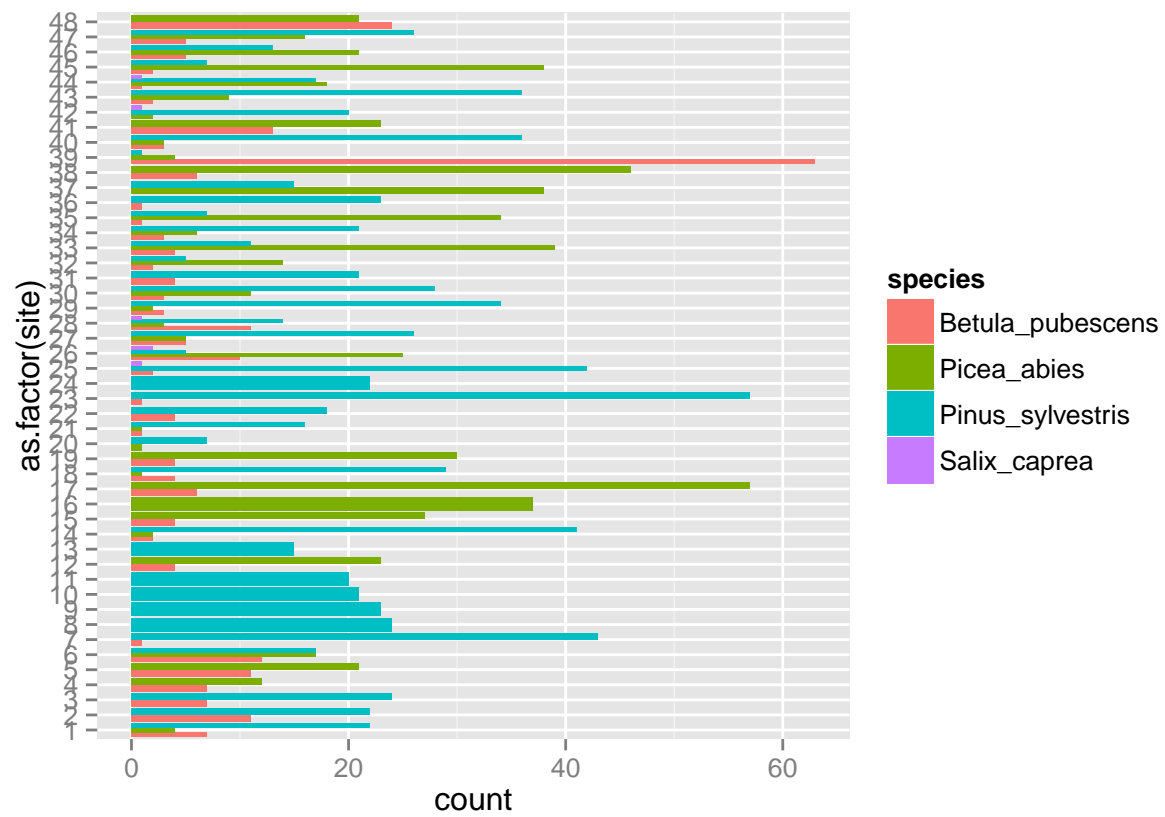
```
ggplot(data = dd, aes(x = species)) + geom_bar() + coord_flip()
```



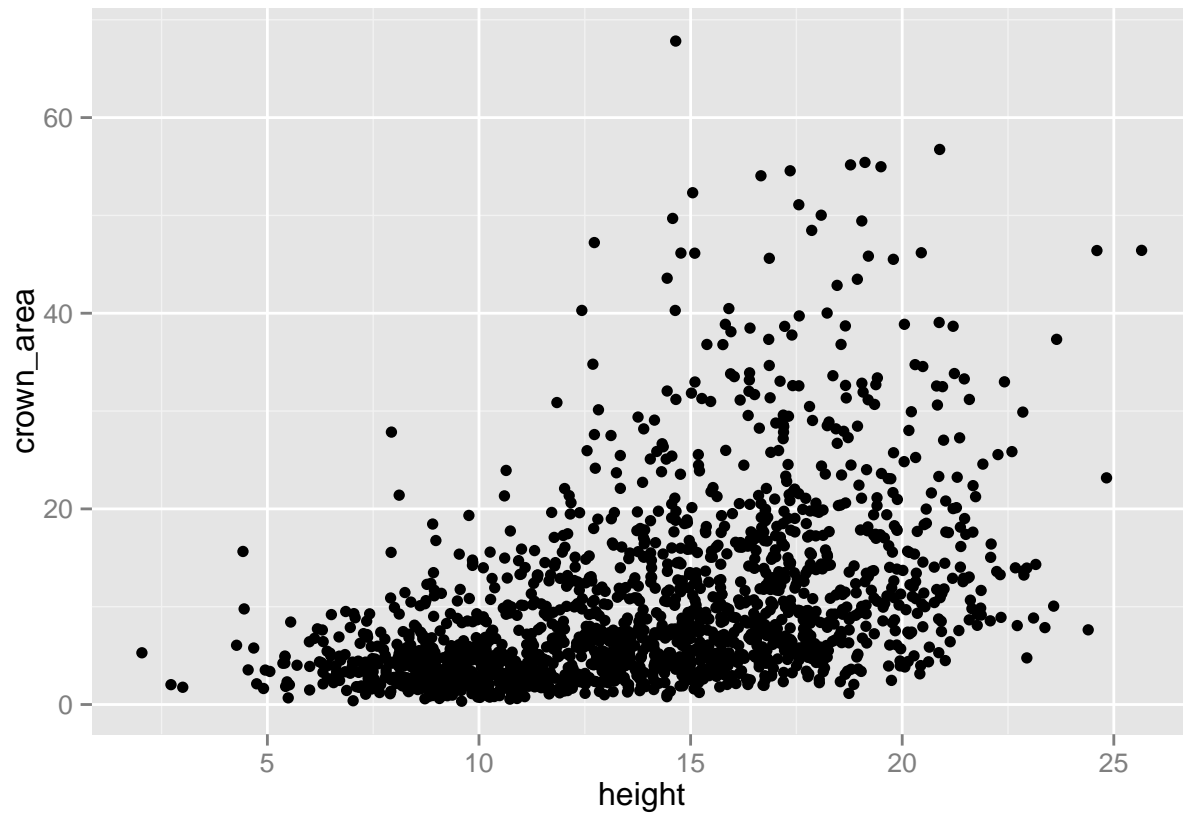
```
ggplot(data = dd, aes(x = as.factor(site), fill = species)) + geom_bar() + coord_flip()
```



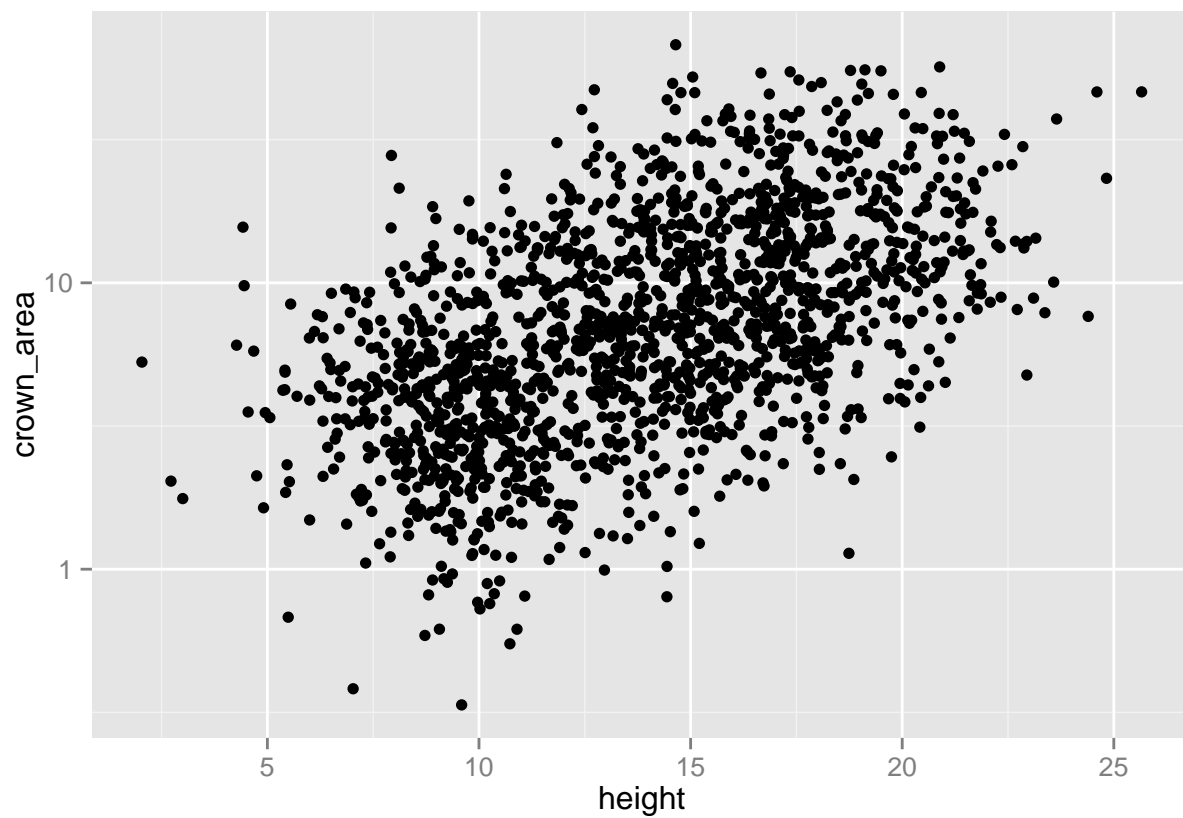
```
ggplot(data = dd, aes(x = as.factor(site), fill = species)) + geom_bar(position = "dodge") + coord_flip
```



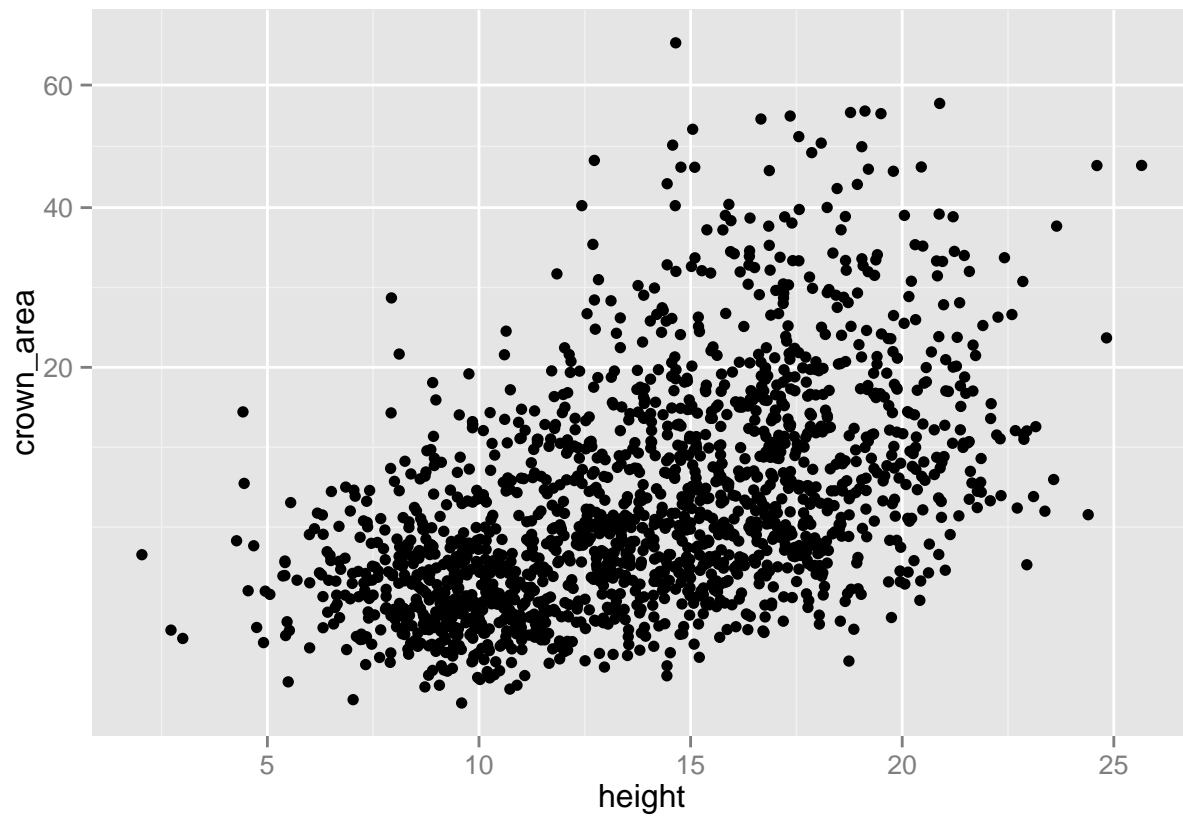
```
# scale_y
ggplot(data = dd, aes(x = height, y = crown_area)) + geom_point()
```



```
ggplot(data = dd, aes(x = height, y = crown_area)) + geom_point() + scale_y_log10()
```

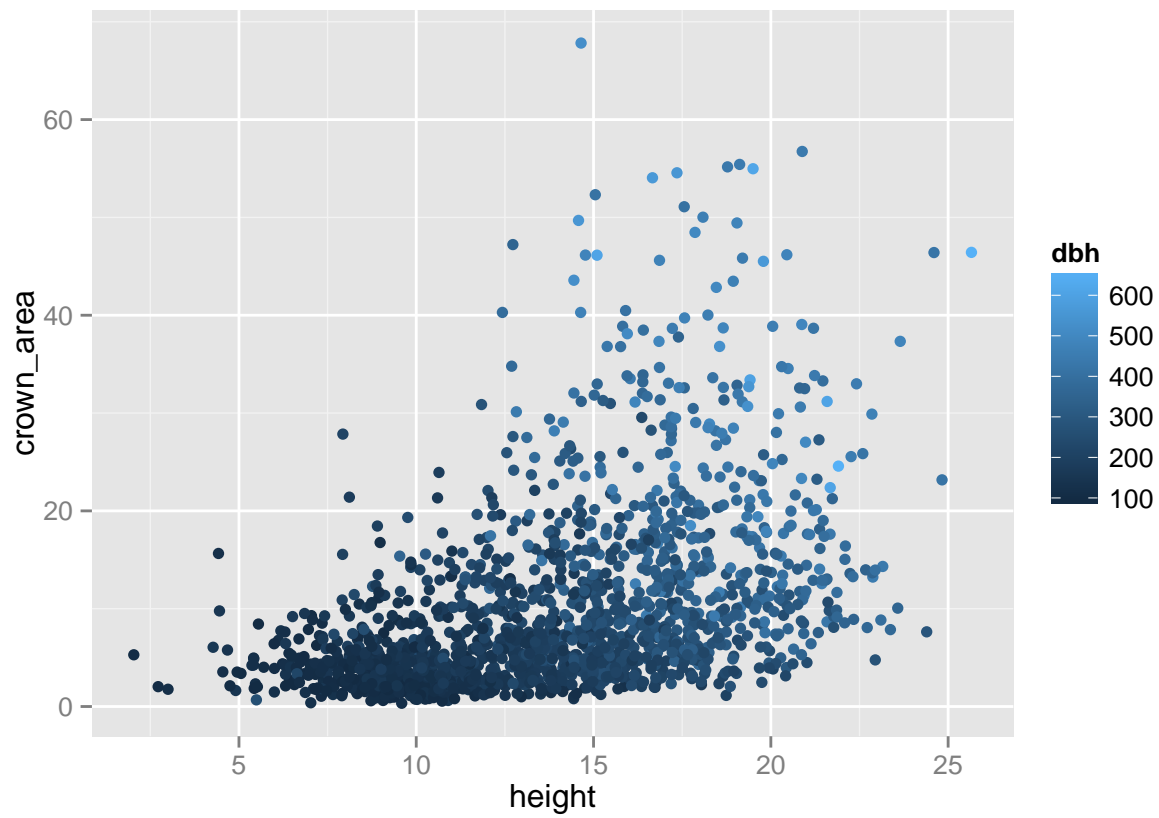


```
ggplot(data = dd, aes(x = height, y = crown_area)) + geom_point() + scale_y_sqrt()
```

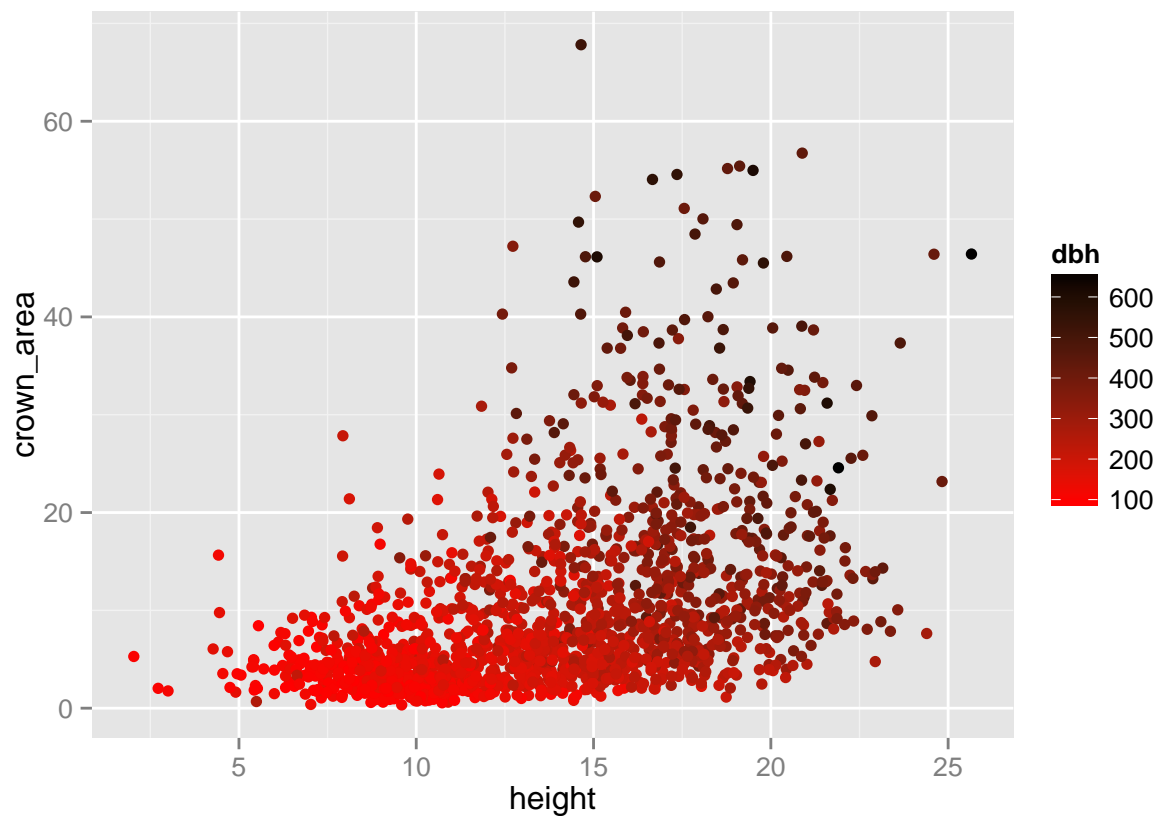


```
# scale_color  
ggplot(data = dd, aes(x = height, y = crown_area, colour = dbh)) + geom_point()
```

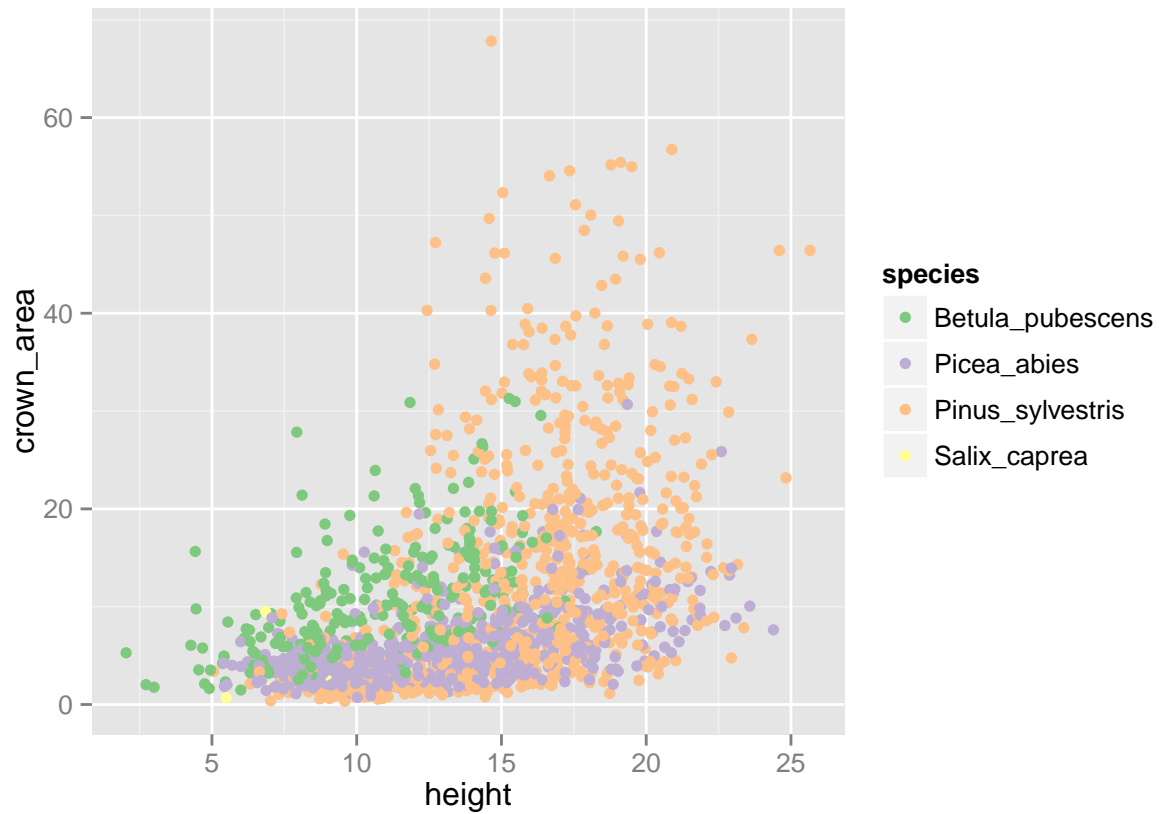




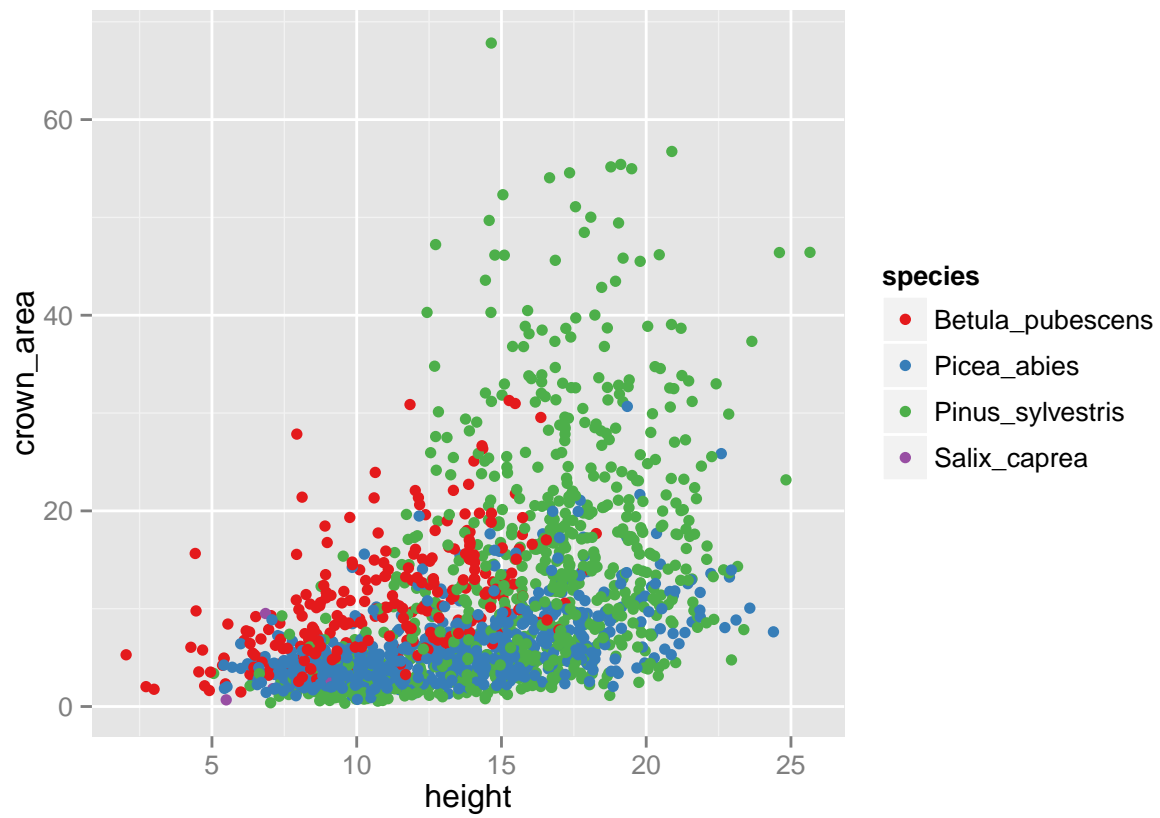
```
ggplot(data = dd, aes(x = height, y = crown_area, colour = dbh)) + geom_point() + scale_color_gradient()
```



```
# playing with colors
pl <- ggplot(data = dd, aes(x = height, y = crown_area, colour = species)) + geom_point()
pl + scale_color_brewer(palette = "Accent")
```

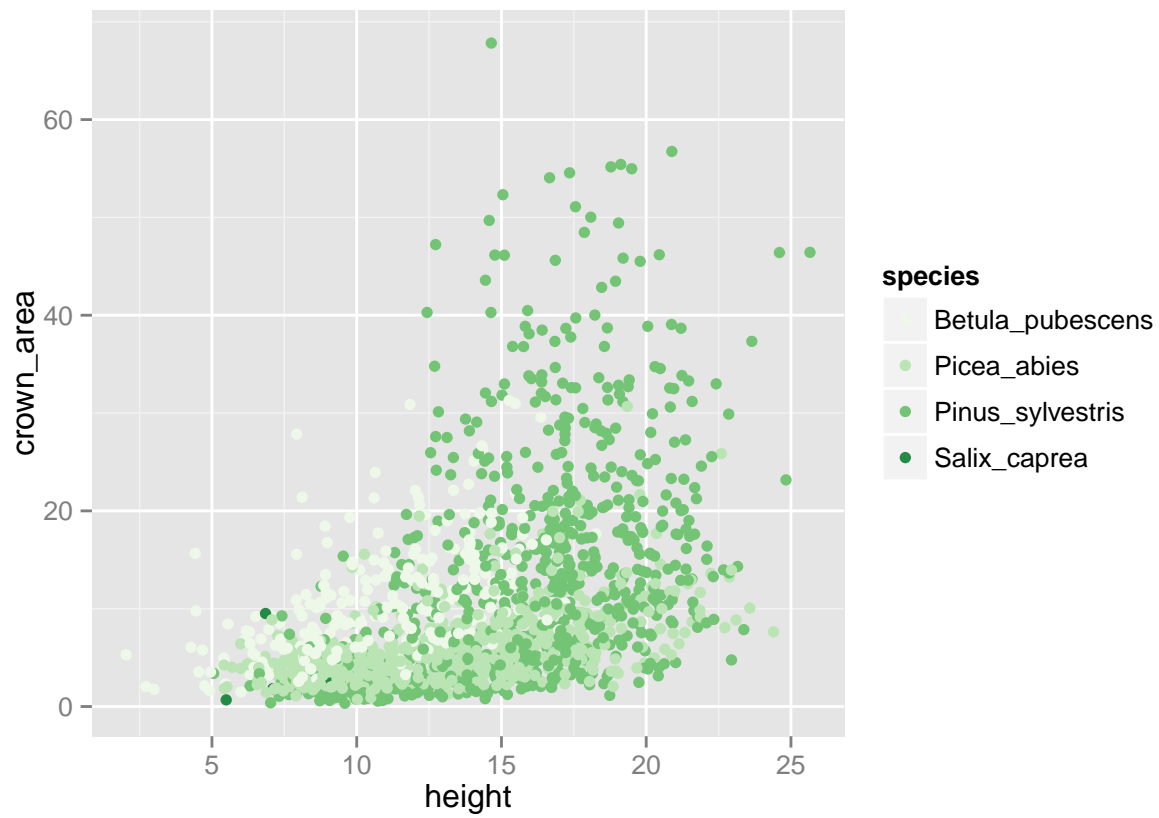


```
pl + scale_color_brewer(palette = "Set1")
```

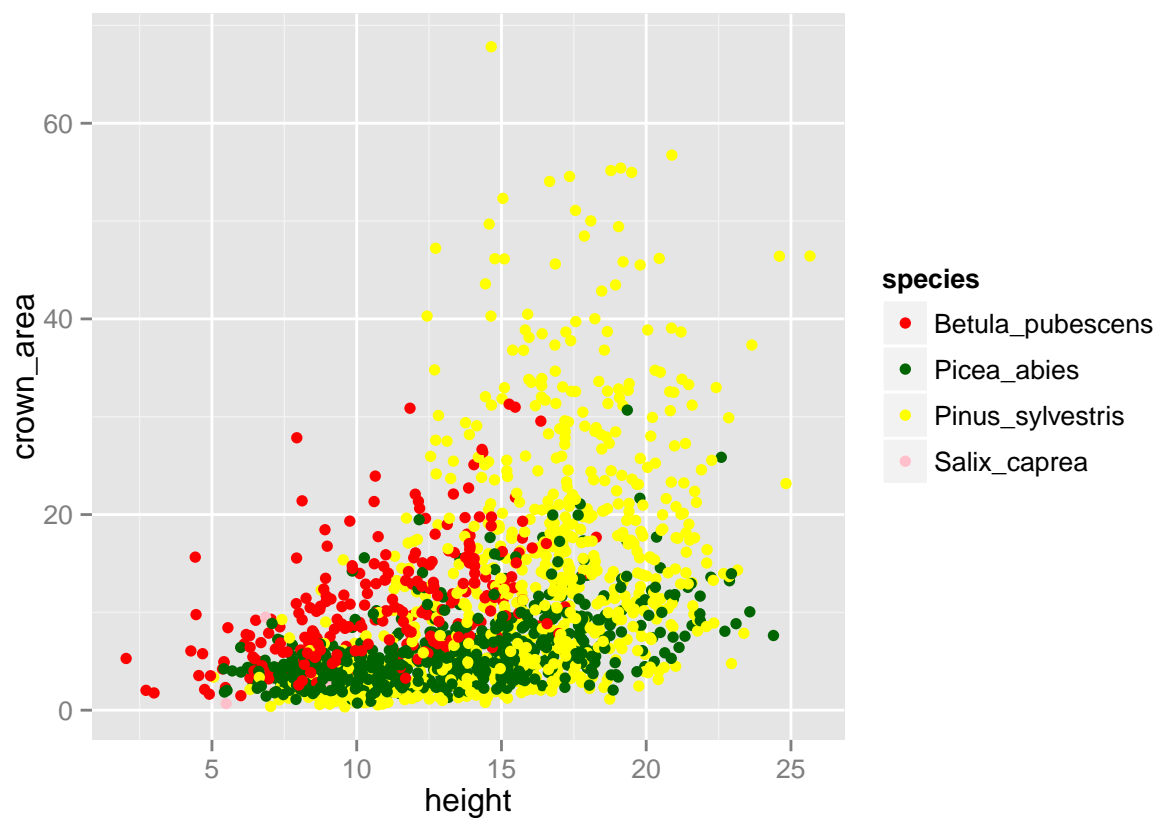


```
pl + scale_color_brewer(palette = "Pastel")
```

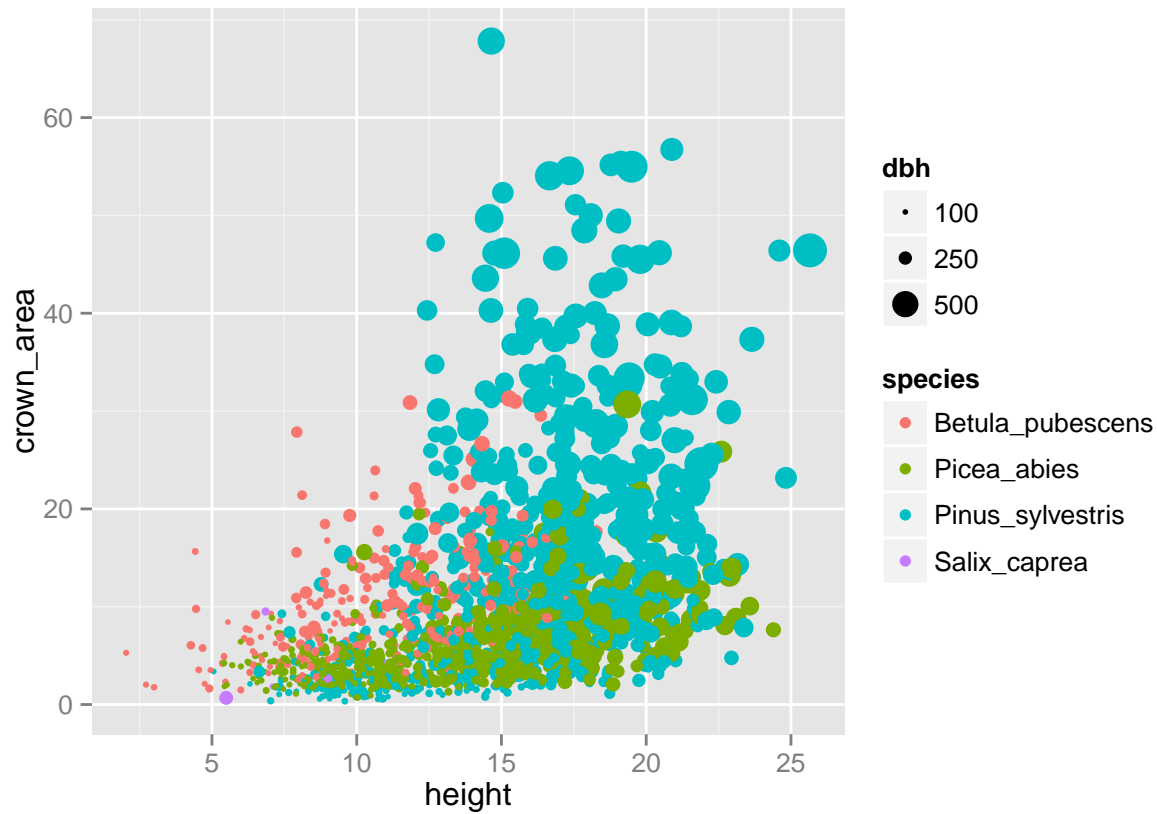
```
## Warning in pal_name(palette, type): Unknown palette Pastel
```



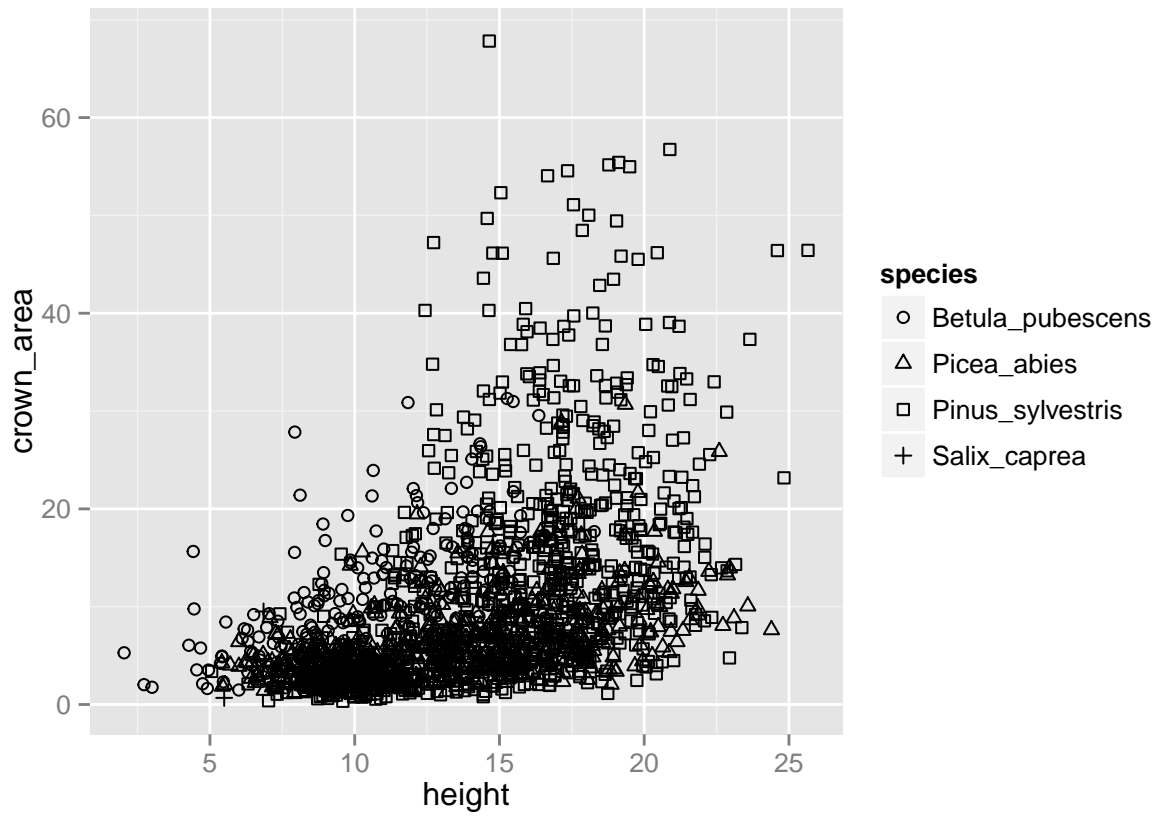
```
pl + scale_color_manual(values = c("red", "darkgreen", "yellow", "pink"))
```



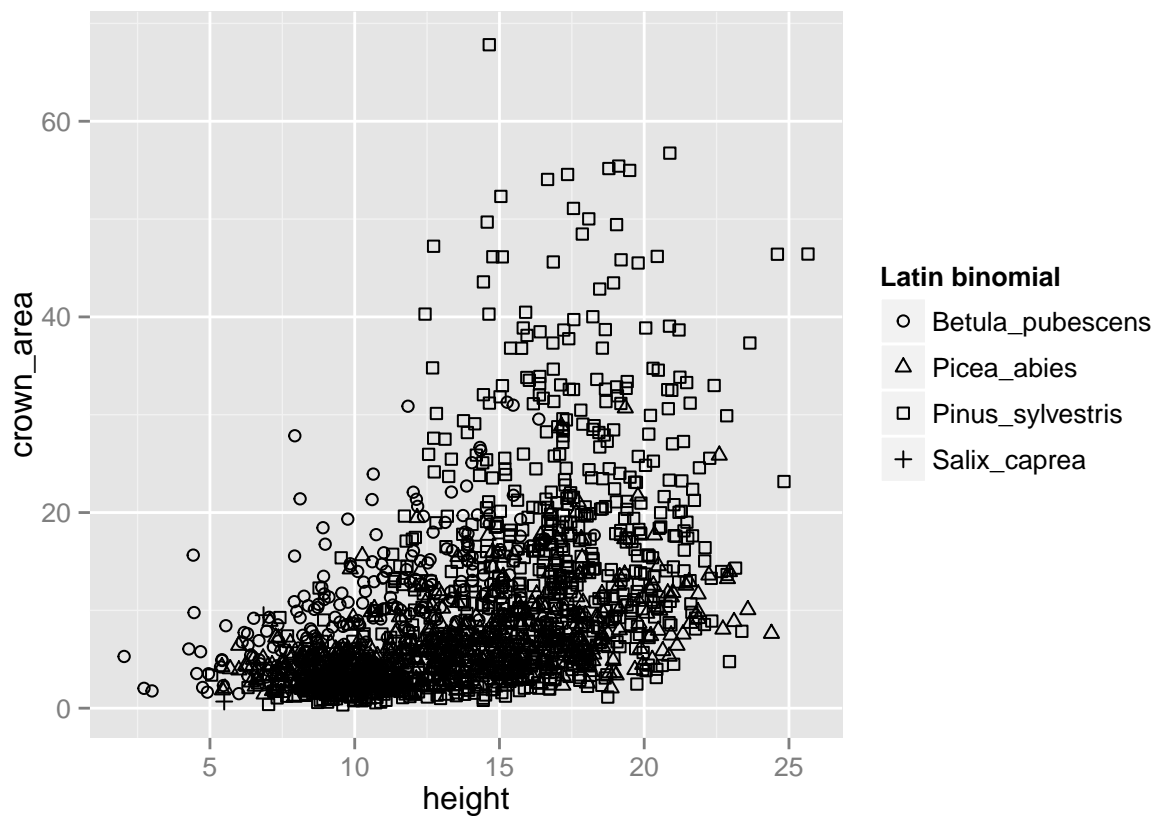
```
# scale_size
pl <- ggplot(data = dd, aes(x = height, y = crown_area, colour = species, size = dbh)) + geom_point()
pl + scale_size(breaks = c(1,10,100,250,500))
```



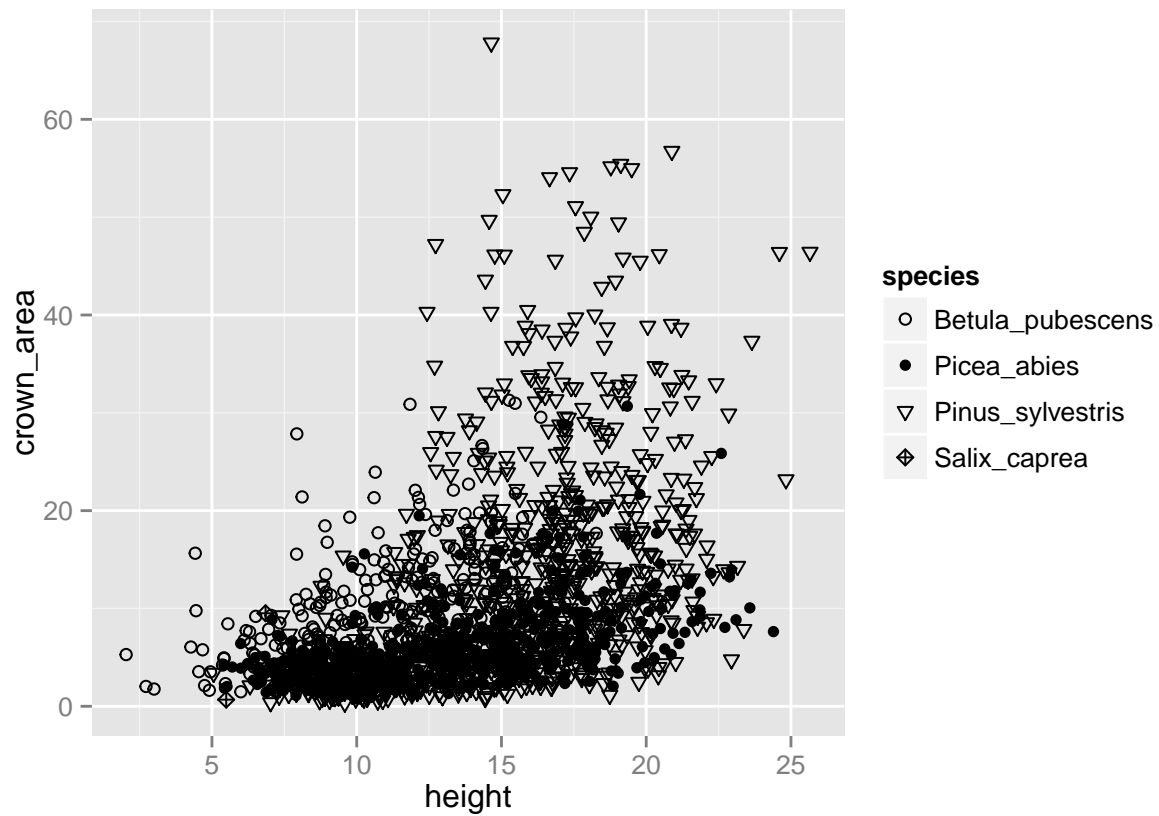
```
# scale_shape
pl <- ggplot(data = dd, aes(x = height, y = crown_area, shape = species)) + geom_point()
pl + scale_shape(solid = FALSE)
```



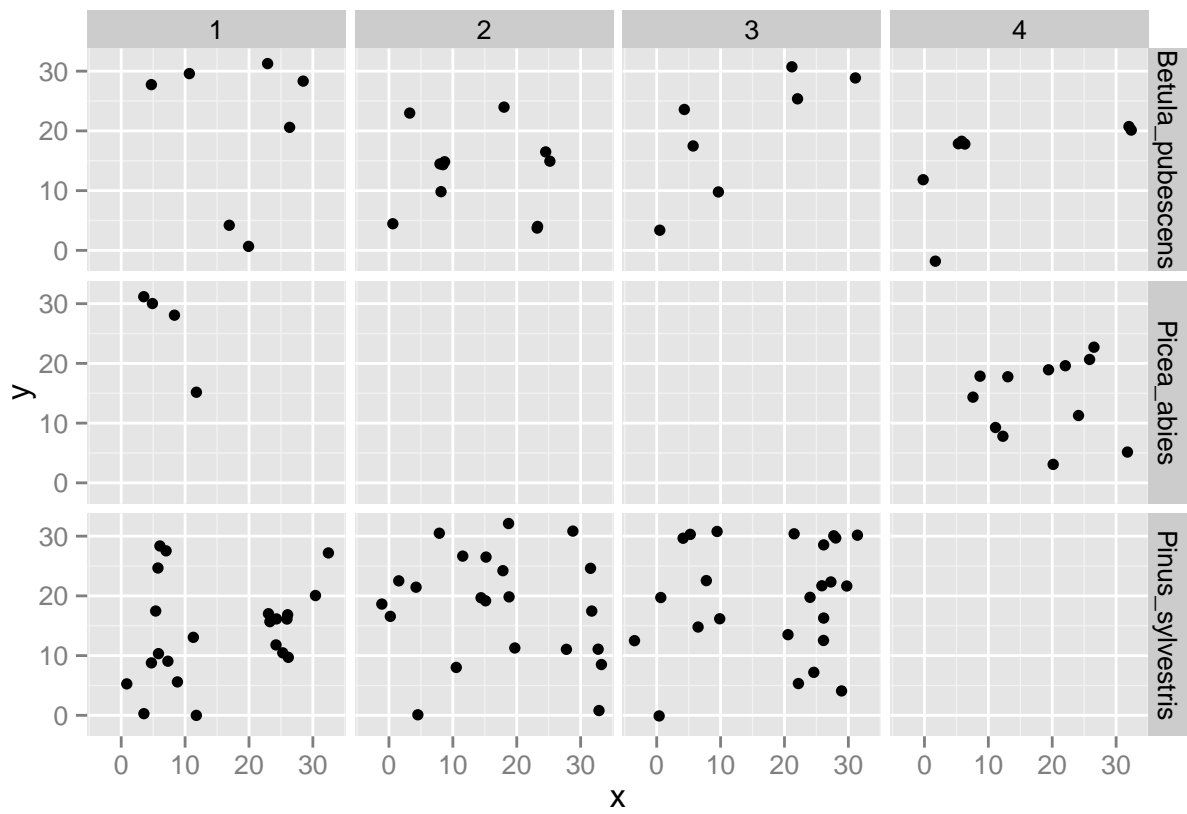
```
pl + scale_shape(solid = FALSE, name = "Latin binomial")
```



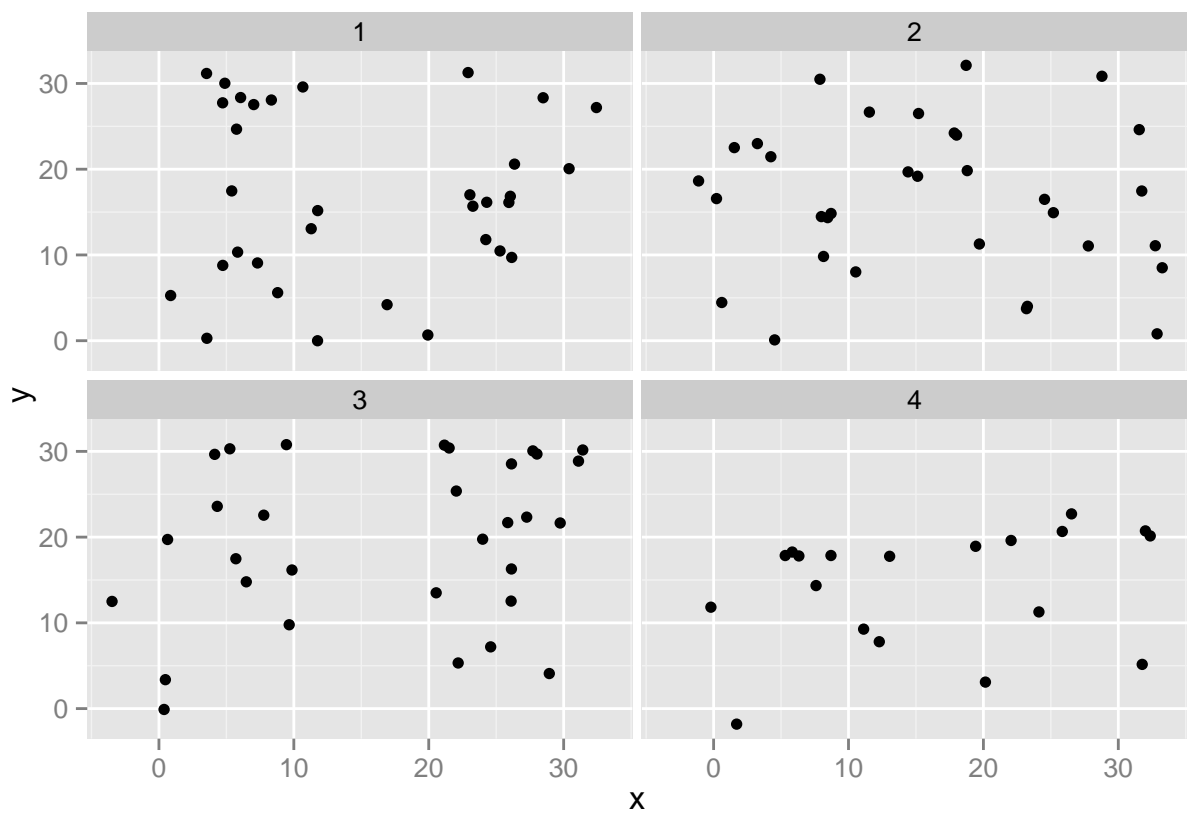
```
pl + scale_shape_manual(values = c(1,16,6,9))
```



```
# faceting  
dd3 <- dd[dd$site < 5,]  
pl <- ggplot(data = dd3, aes(x = x, y = y)) + geom_point()  
pl + facet_grid(species~site)
```

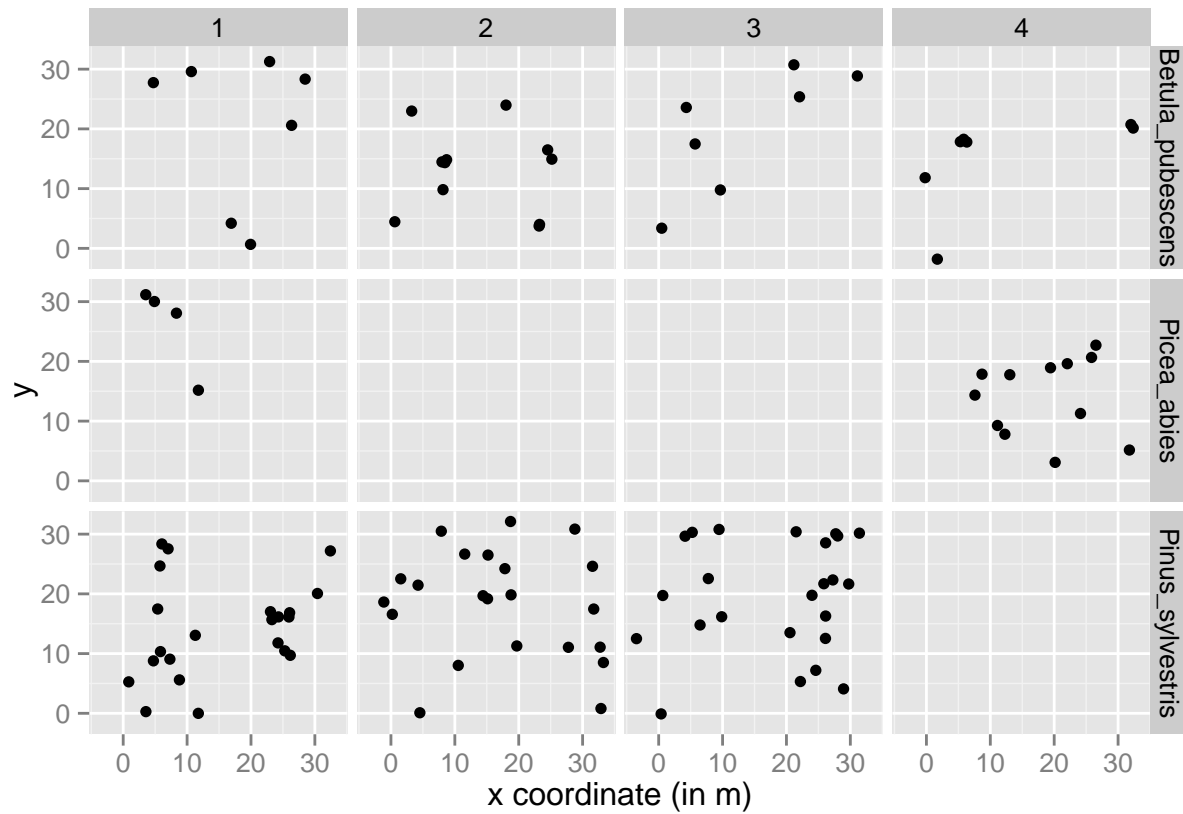


```
pl + facet_wrap(~site)
```





```
# labels
pl <- ggplot(data = dd3, aes(x = x, y = y)) + geom_point() + facet_grid(species~site)
pl + xlab("x coordinate (in m)")
```

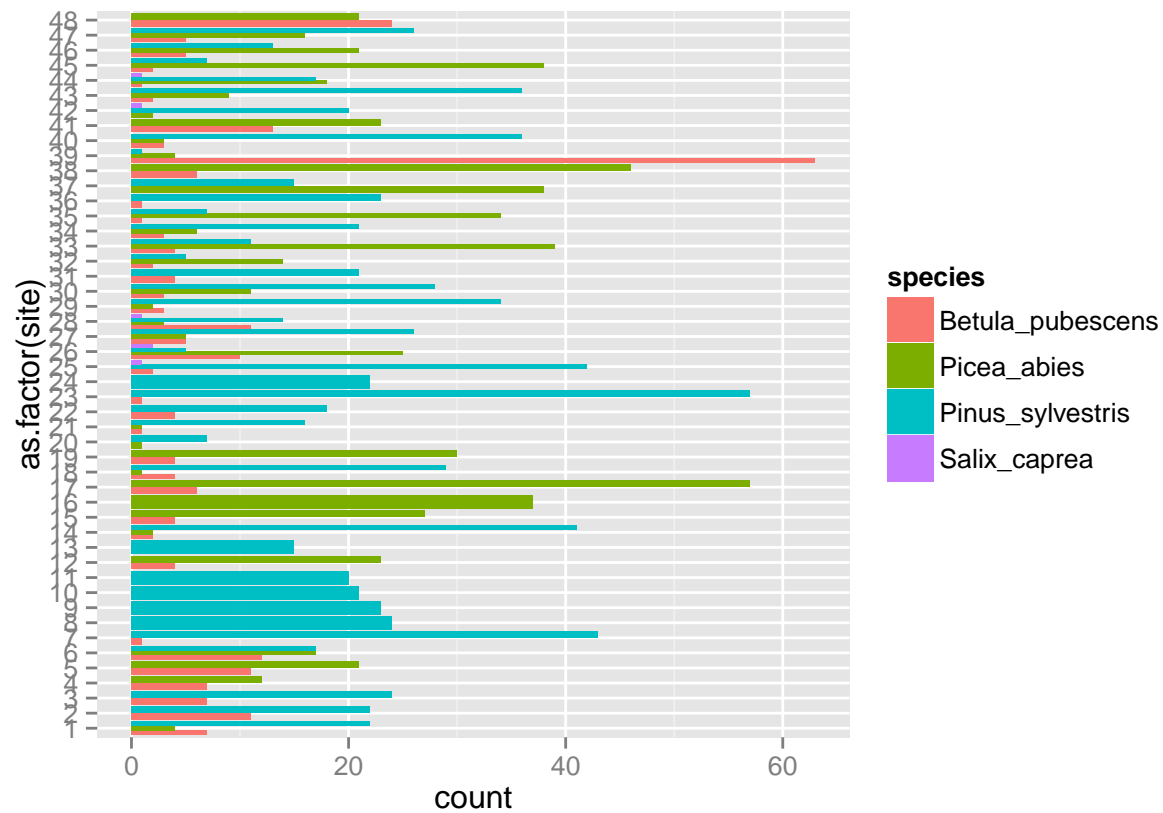


```
pl + ylab("y coordinate (in m)")
```

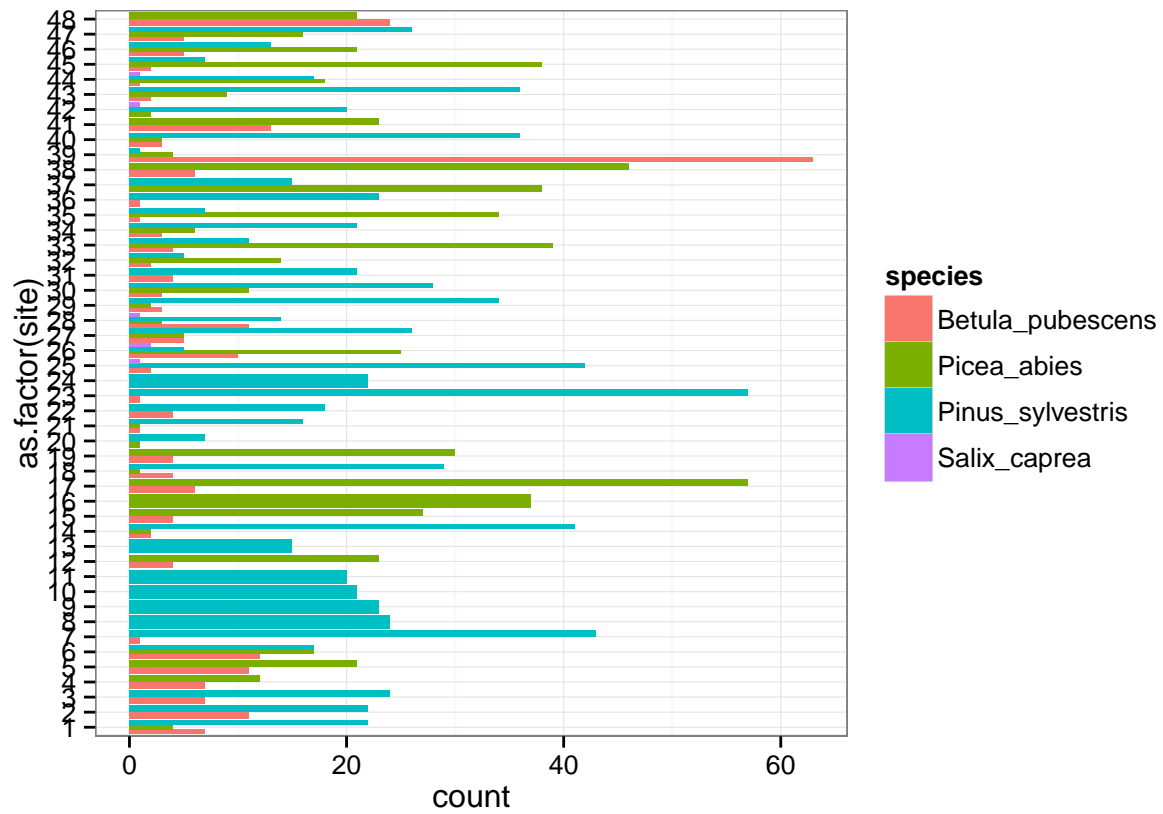


```
# themes
```

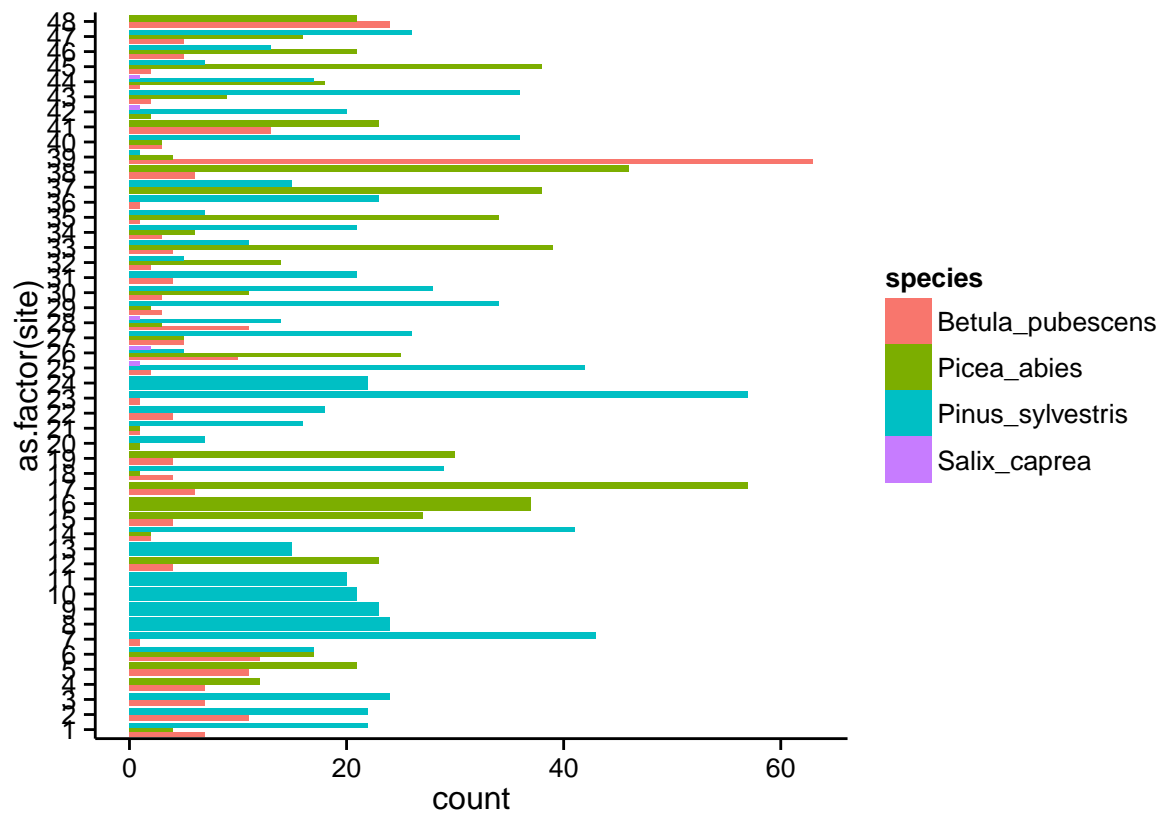
```
p1 <- ggplot(data = dd, aes(x = as.factor(site), fill = species)) + geom_bar(position = "dodge") + coord_flip()
p1 + theme_grey() # default theme with grey background and white gridlines
```



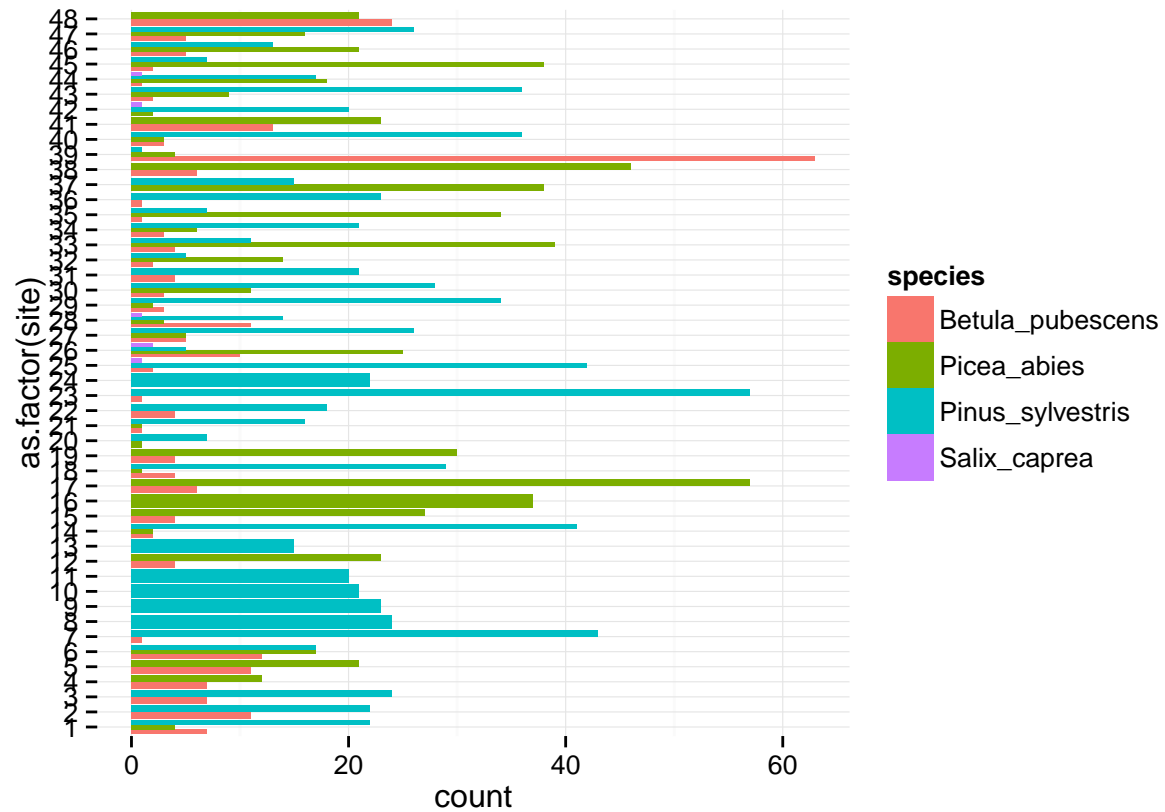
```
p1 + theme_bw() # white background and black gridlines
```



```
pl + theme_classic() # no gridlines
```

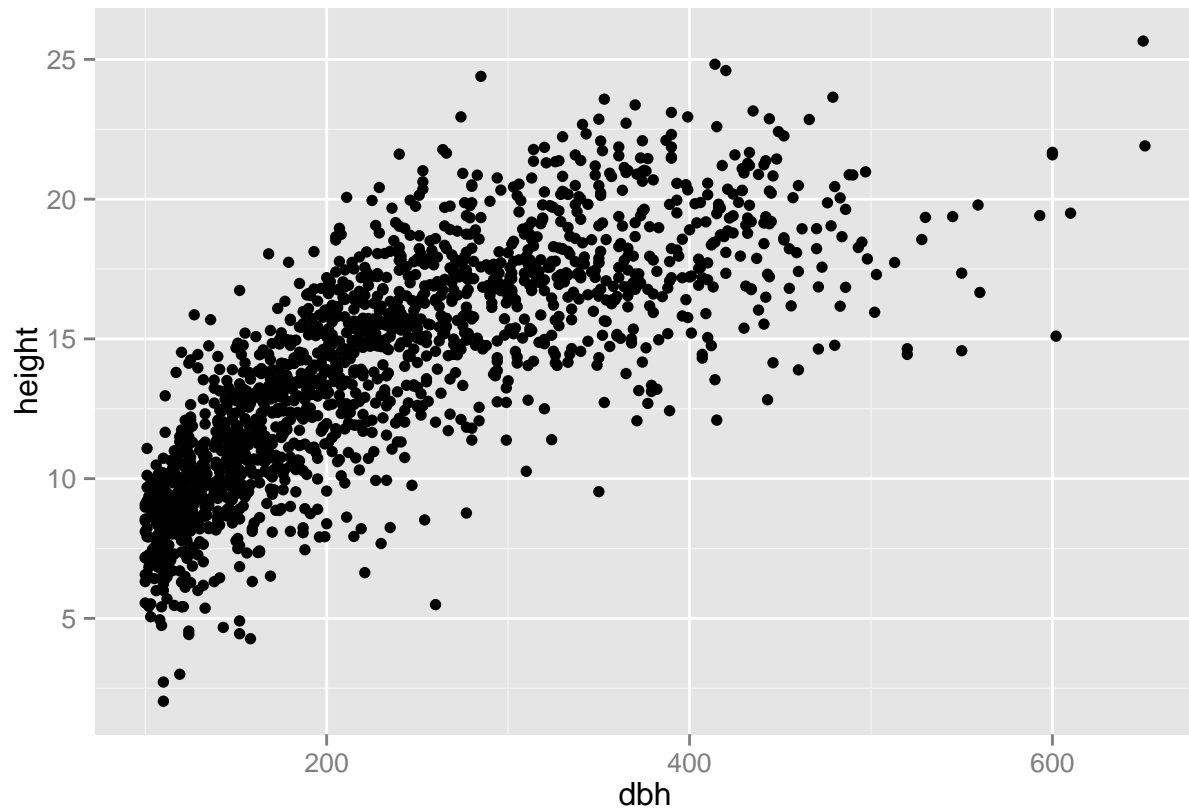


```
pl + theme_minimal() # clean theme
```

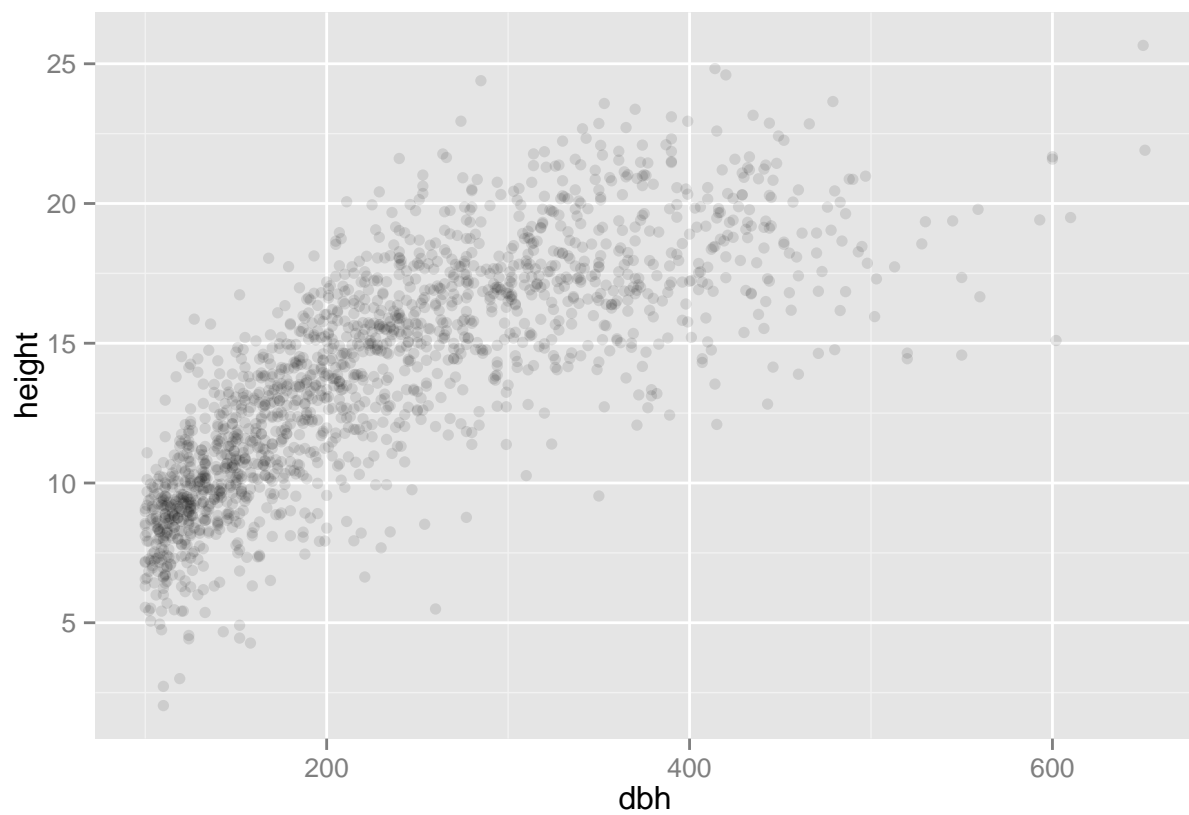


```
# saving to file
ggsave(filename = "test.pdf", plot = pl, width = 3, height = 4)
```

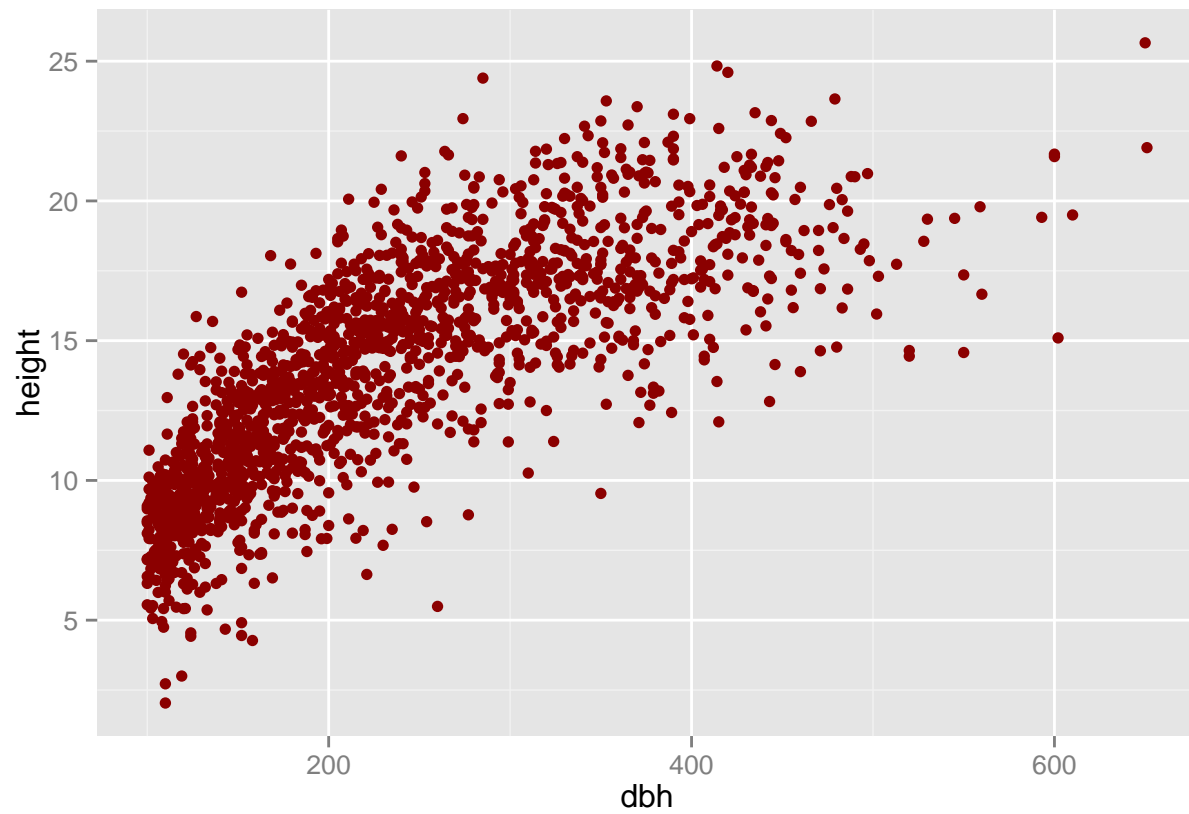
```
# setting a feature
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point()
```



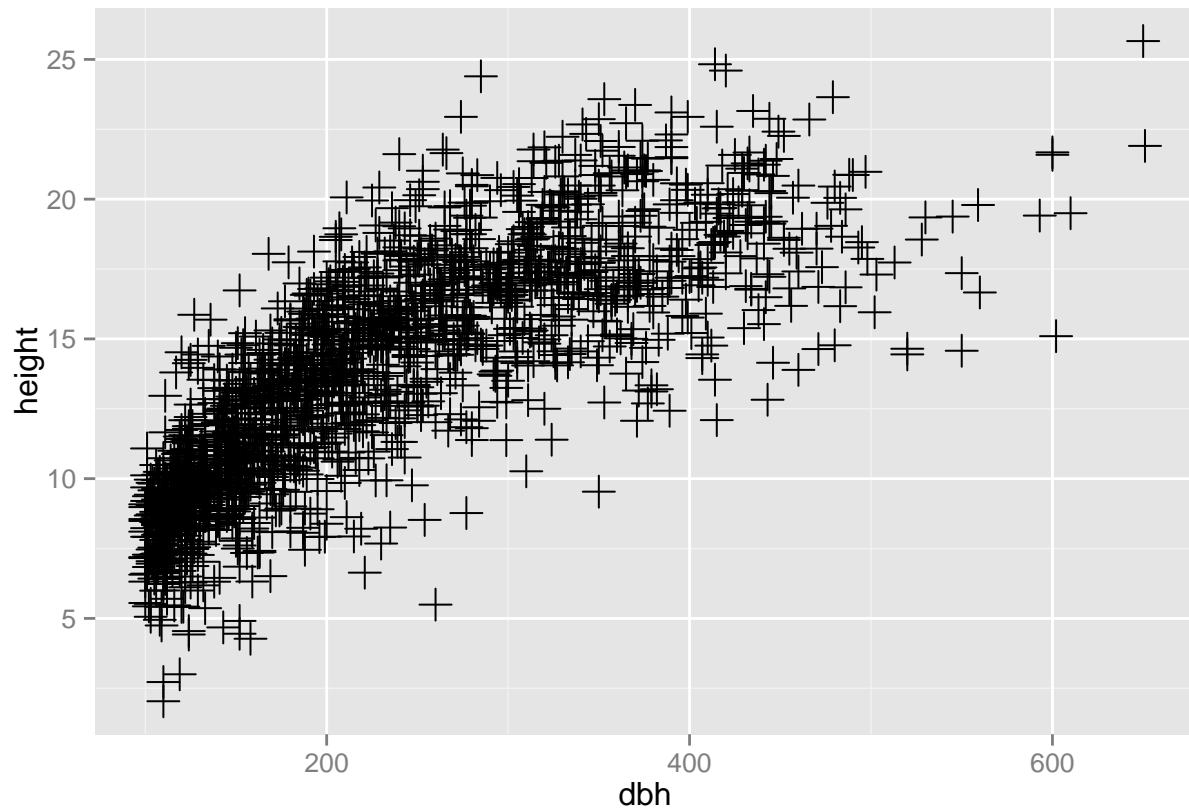
```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point(alpha = 0.1)
```



```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point(color = "darkred")
```



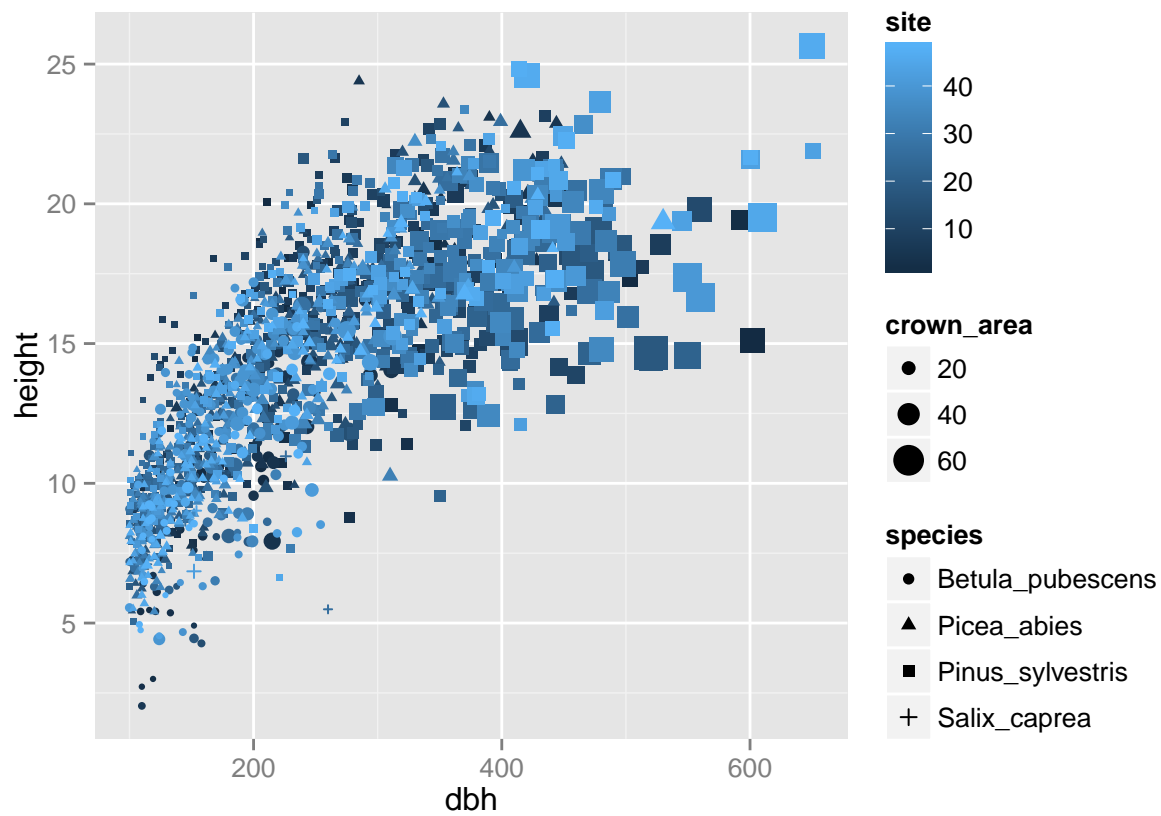
```
ggplot(data = dd, aes(x = dbh, y = height)) + geom_point(shape = 3, size = 4)
```



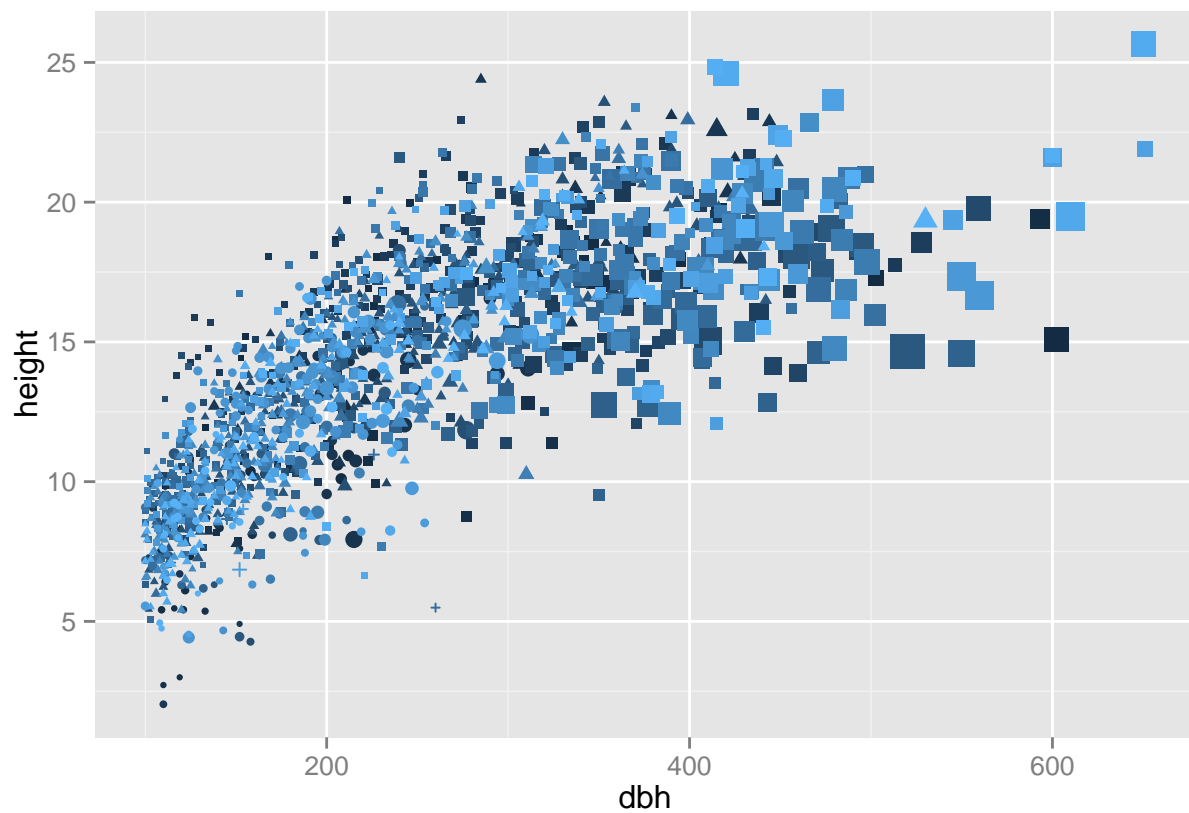
```
# switching legends off
```

```
pl <- ggplot(data = dd, aes(x = dbh, y = height, shape = species, color = site, size = crown_area)) + g  
pl
```

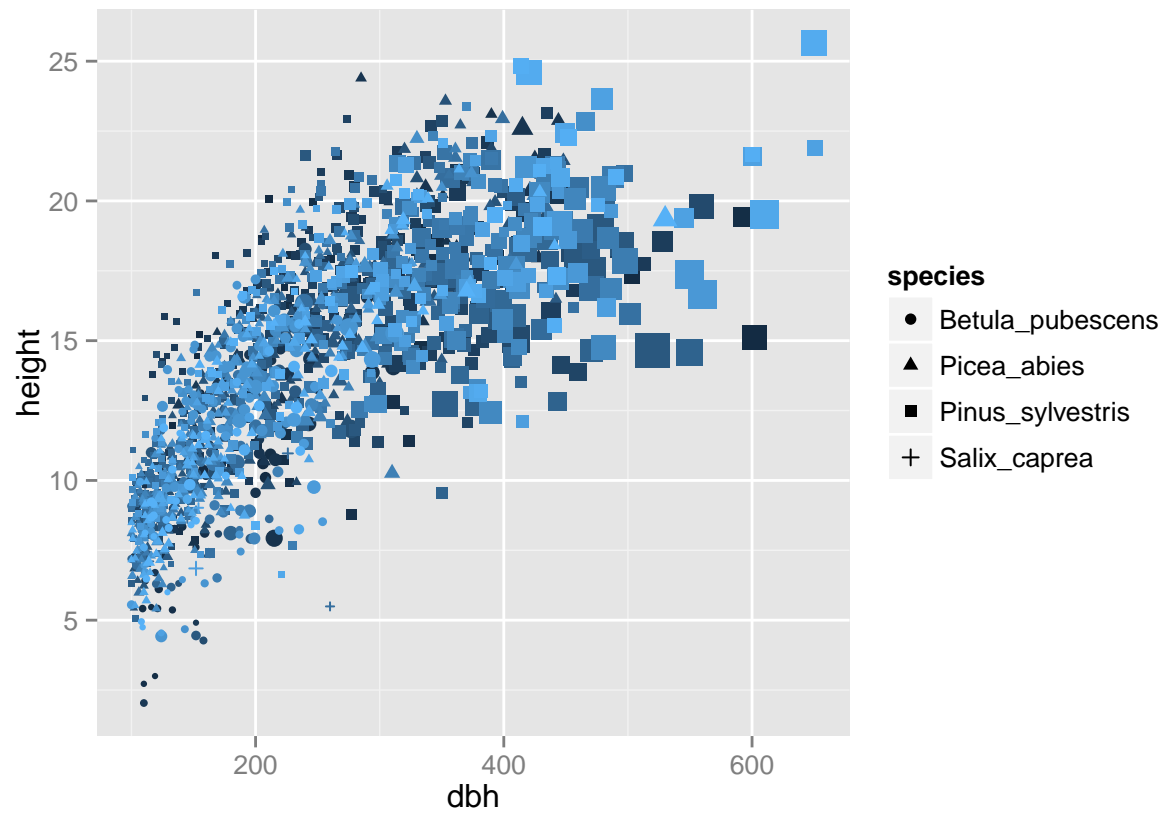




```
pl + theme(legend.position = "none") # switch off all legends
```



```
pl + guides(color = "none", size = "none") # switch off some legends
```



```
# zooming into a region  
pl + coord_cartesian(xlim = c(0,200), ylim = c(5, 10))
```

