STAT 215A Fall 2017 Week 5

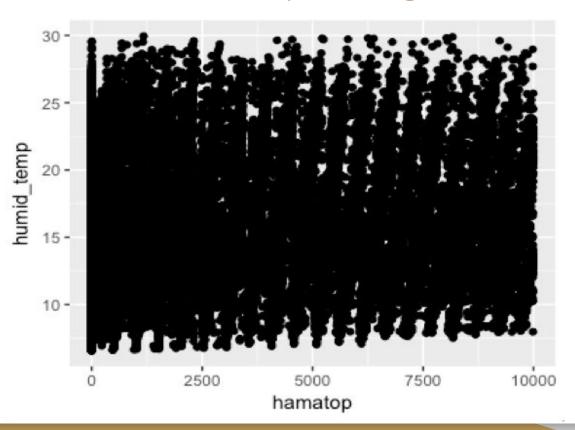
Rebecca Barter 09/22/2017

Peer review



Image source: http://bit.ly/x2pms8

Overplotting



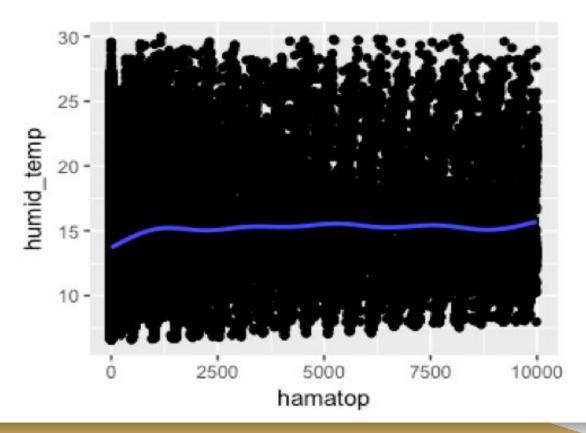
Overplotting

Some report file sizes were so large that I couldn't open them!

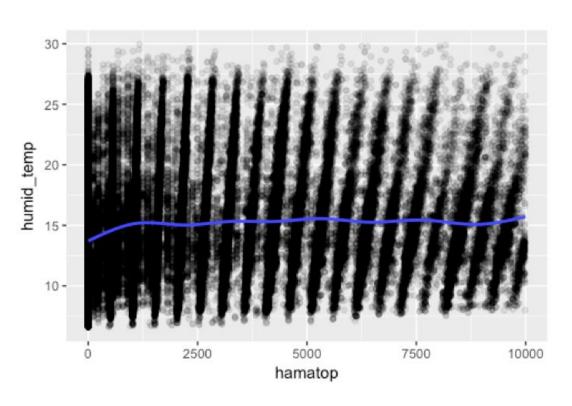
You need to make sure that your figures are rendered as png rather than pdf...

```
<<dev = "png", dpi = 300>>=
ggplot(big_df) + ...
@
```

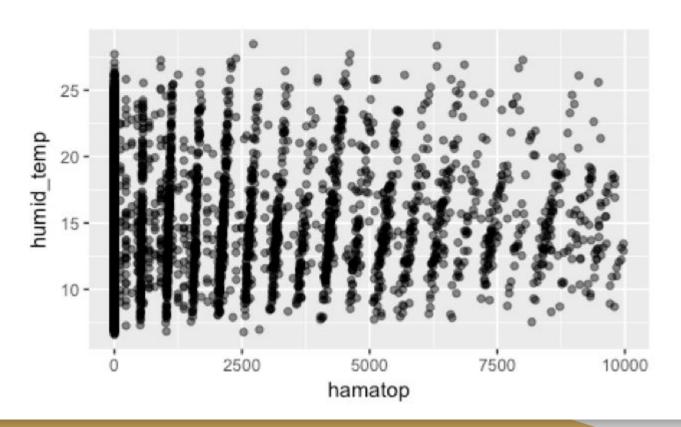
Overplotting: add a trendline?



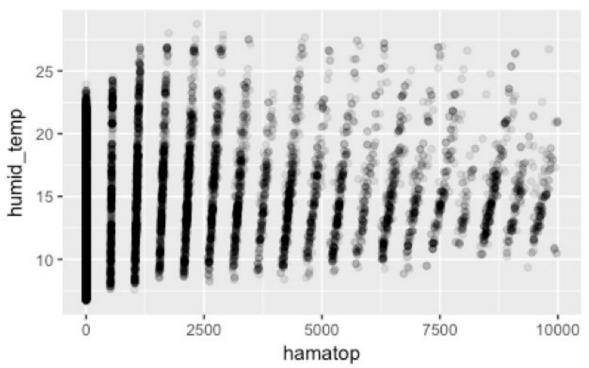
Overplotting: add transparency?



Overplotting: subsampling 10,000 points?

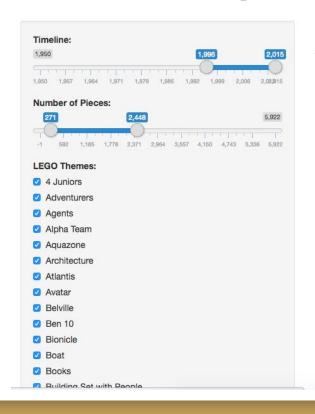


Overplotting: meaningful subsampling (plotting only a single node)?



Interactive plotting: shiny apps

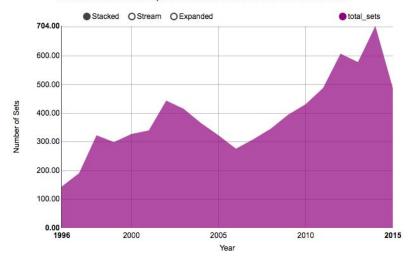
https://shiny.rstudio.com/gallery/lego-set.html



■ Dataset
✓ Visualize the Data

Number of Sets by Year

Please hover over each point to see the Year and Total Number of Sets.



Number of Themes by Year

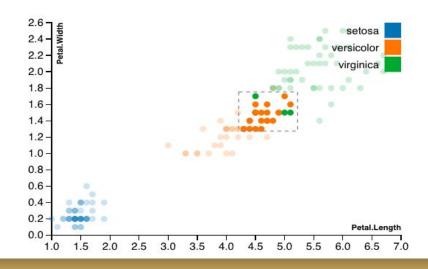
Please hover over each bar to see the Year and Total Number of Themes.

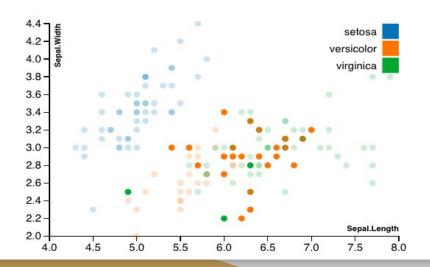
Interactive plotting: linked brushing via crosstalk

https://rstudio.github.io/crosstalk/using.html

```
library(crosstalk)

shared_iris <- SharedData$new(iris)
bscols(
   d3scatter(shared_iris, ~Petal.Length, ~Petal.Width, ~Species, width="100%", height=300),
   d3scatter(shared_iris, ~Sepal.Length, ~Sepal.Width, ~Species, width="100%", height=300)
)</pre>
```

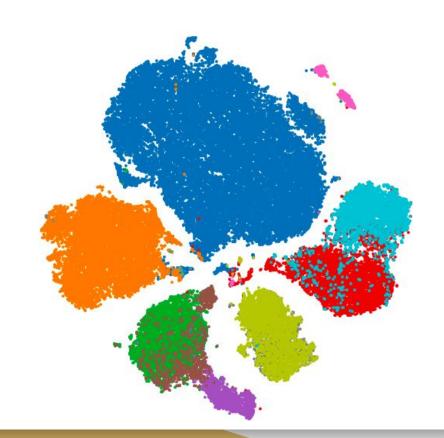




Clustering

K-means Hierarchical clustering Spectral clustering

• • •



Silhouette plots

A measure of the separation between clusters

$$s(i) = rac{b(i) - a(i)}{\max\{a(i), b(i)\}}$$

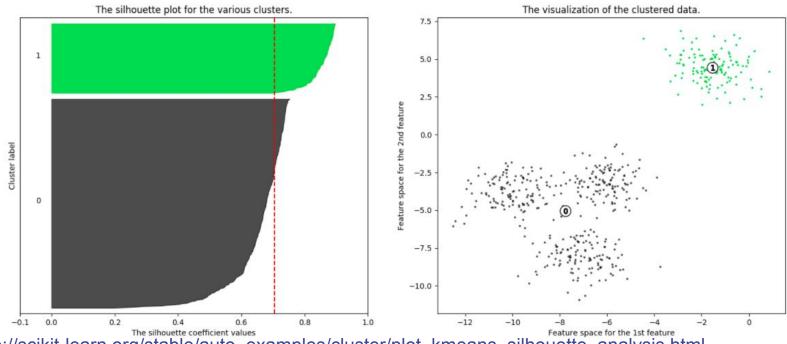
average dissimilarity of data point *i* with all other data within the same cluster

lowest average dissimilarity of data point *i* to any other cluster

Silhouette plots (average sil = 0.70)

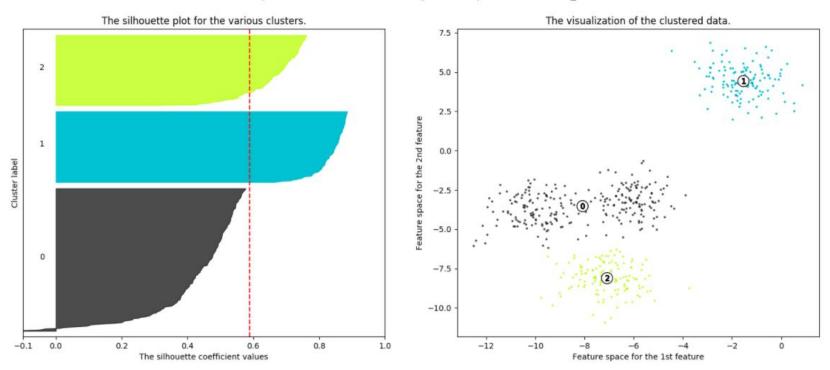
Plot silhouette widths in decreasing order, grouped by cluster

Silhouette analysis for KMeans clustering on sample data with n_clusters = 2



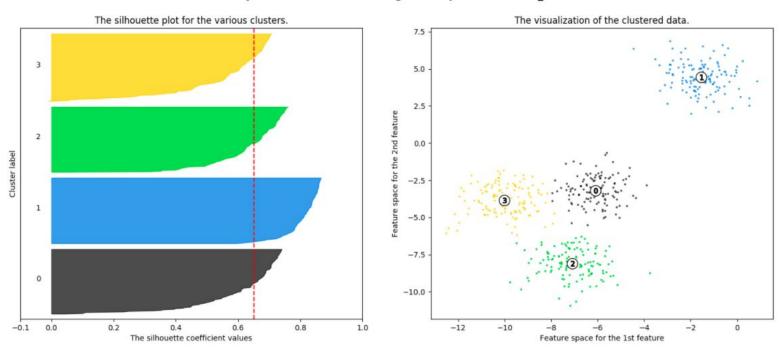
Silhouette plots (average sil = 0.59)

Silhouette analysis for KMeans clustering on sample data with n_clusters = 3



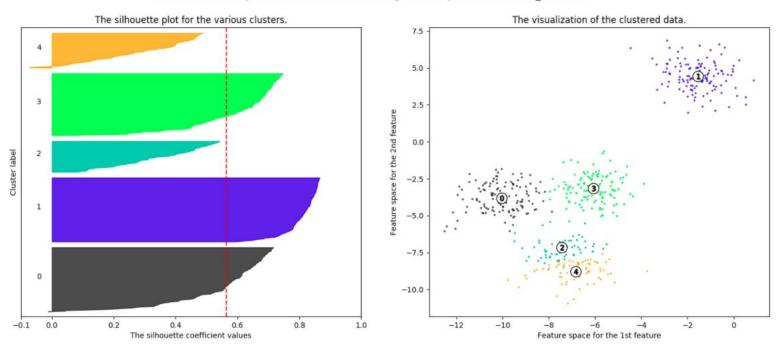
Silhouette plots (average sil = 0.65)

Silhouette analysis for KMeans clustering on sample data with n_clusters = 4



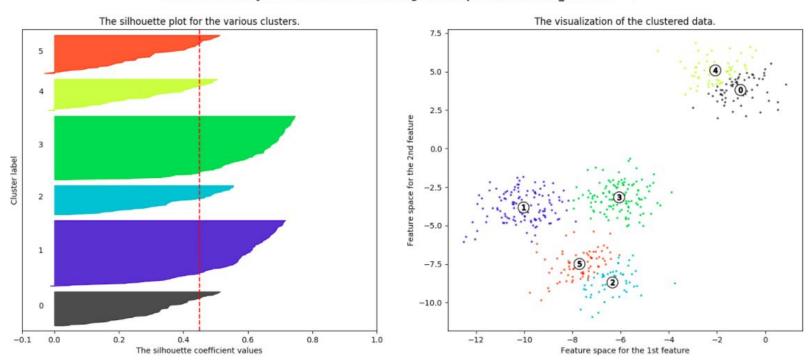
Silhouette plots (average sil = 0.56)

Silhouette analysis for KMeans clustering on sample data with n_c clusters = 5



Silhouette plots (average sil = 0.45)

Silhouette analysis for KMeans clustering on sample data with n clusters = 6



Silhouette plots (**k** = **2** is the best!)

```
For n_clusters = 2 The average <u>silhouette_score</u> is : 0.704978749608

For n_clusters = 3 The average <u>silhouette_score</u> is : 0.588200401213

For n_clusters = 4 The average <u>silhouette_score</u> is : 0.650518663273

For n_clusters = 5 The average <u>silhouette_score</u> is : 0.563764690262

For n_clusters = 6 The average <u>silhouette_score</u> is : 0.450466629437
```

- 1. Load wine.csv (14 characteristics of 178 wines from 3 different cultivars)
- 2. Plot the wines in the space defined by the first two principal components. Color each wine by its cultivar (type).

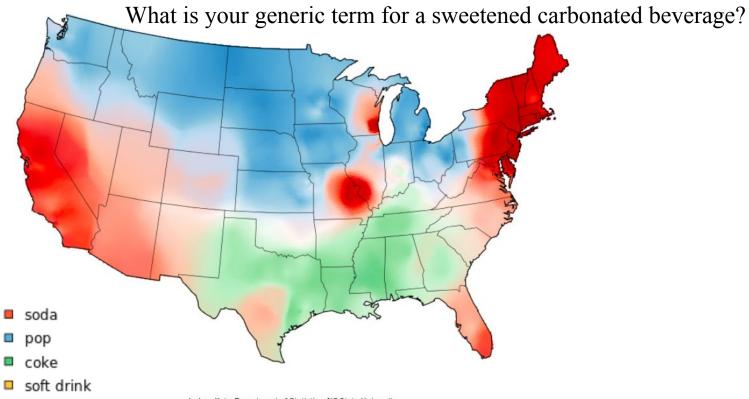
- 1. Load wine.csv (14 characteristics of 178 wines from 3 different cultivars)
- 2. Plot the wines in the space defined by the first two principal components. Color each wine by its cultivar.
- 3. Run k-means with 3 cluster centers using all variables (except cultivar). Color each point in your previous plot by cluster.

- 1. Load wine.csv (14 characteristics of 178 wines from 3 different cultivars)
- 2. Plot the wines in the space defined by the first two principal components. Color each wine by its cultivar.
- 3. Run k-means with 3 cluster centers using all variables (except cultivar). Color each point in your previous plot by cluster.
- 4. Run k-means using the first two principal components only. Color each point in your plot by cluster. Compare the spectral clustering to the standard k-means clustering.

- 1. Load wine.csv (14 characteristics of 178 wines from 3 different cultivars)
- 2. Plot the wines in the space defined by the first two principal components. Color each wine by its cultivar.
- 3. Run k-means with 3 cluster centers using all variables (except cultivar). Color each point in your previous plot by cluster.
- 4. Run k-means using the first two principal components only. Color each point in your plot by cluster. Compare the spectral clustering to the standard k-means clustering.
- 5. Re-run steps 3 and 4 each four times. Do the results change?

- 1. Load wine.csv (14 characteristics of 178 wines from 3 different cultivars)
- 2. Plot the wines in the space defined by the first two principal components. Color each wine by its cultivar.
- 3. Run k-means with 3 cluster centers using all variables (except cultivar). Color each point in your previous plot by cluster.
- 4. Run k-means using the first two principal components only. Color each point in your plot by cluster. Compare the spectral clustering to the standard k-means clustering.
- 5. Re-run steps 3 and 4 each four times. Do the results change?
- 6. Re-run steps 3-5 with 10 cluster centers. Compare silhouette plots.

Introducing Lab 2



Joshua Katz, Department of Statistics, NC State University

http://www.businessinsider.com/22-maps-that-show-the-deepest-linguistic-conflicts-in-america-2013-6