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## In this unit we will learn ...

- How commonly used distance measurements encode different notions of "close"
- How to measure similarity of highdimensional vectors

## Distances

Multivariate statistical methods require a notion of pairwise distance between objects. -Dissimilarity Non-negative:  $d(x,y) \ge 0$ Symmetric: d(x,y)=d(y,x)Monotone: d(x,y) > d(x,z) if z more similar to x -Metric (additional conditions) Definite: d(x,y)=0 iff x=yTriangle inequality:  $d(x,y)+d(y,z) \ge d(x,z)$ 

### **Distance Metrics**

• Manhattan distance (Hamming for binary data)

$$d(x,y) = \sum_{i} |x_i - y_i| \in (0,\infty)$$

• Euclidean distance

#### Examples of the Minkowski metric

## **Correlation Distances**

$$d(x,y) = 1 - r(x,y) \in (0,2)$$

Sample correlation measures r(x,y):

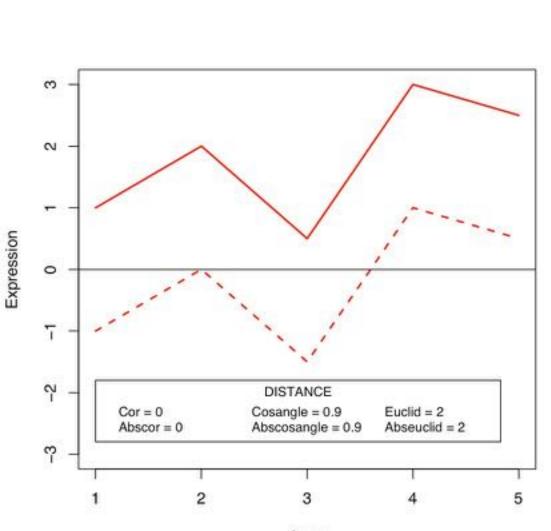
- Pearson
- Uncentered (cosine-angle distance)
- Spearman
- Kendall's Tau
- Maximal Information Coefficient

## More on Distances

- Minkowski metrics: magnitude
- Correlation distances: pattern (or both)
- The absolute value of any distance can also be used, e.g.

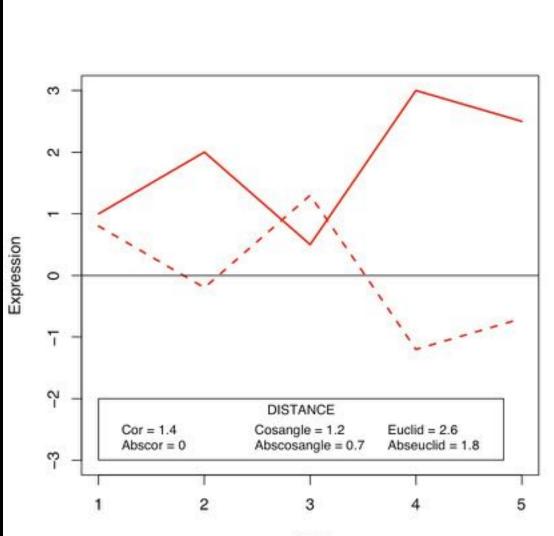
• Distances between distributions are a different concept, e.g., Kullback-Leibler  $D_{KL}(p(X)||q(X)) = -\sum_{x} p(x) \log\{q(x)/p(x)\}\$  $= \sum_{x} p(x) \log\{p(x)/q(x)\}$ 

# Perfectly Correlated



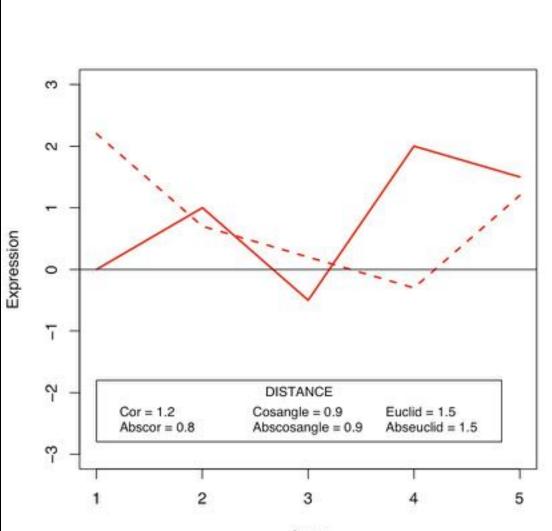
Array

## Anti-Correlated



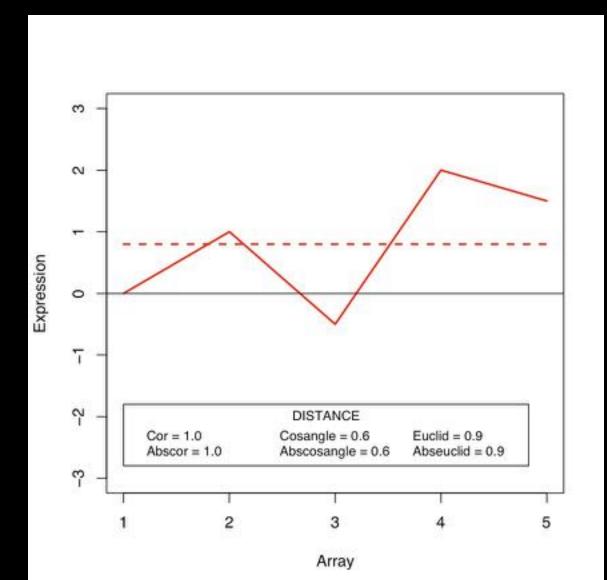
Array

### Same Mean, Uncorrelated



Array

### Same Mean, No Variation



# Distances in R

Package	Distances
stats	Euclidean, Manhattan, Canberra, max, binary
cluster	Euclidean,
bioDist	Manhattan
hopach	Euclidean, cor, cosine-angle (abs versions)
	cluster bioDist