

# Module 18 Multivariate Analysis for Genetic data

## Session 10 Cluster Analysis II

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# Model-based clustering

- Previous approaches do not make any **distributional assumptions**
- Probabilistic models can be used in clustering and this is called **model-based clustering**
- Finite mixture model

$$g(x|\boldsymbol{\pi}, \boldsymbol{\theta}) = \pi_1 f_1(x|\boldsymbol{\theta}_1) + \pi_2 f_2(x|\boldsymbol{\theta}_2) + \cdots + \pi_k f_k(x|\boldsymbol{\theta}_k)$$

- With  $\pi_i > 0$  and  $\sum_{i=1}^k \pi_i = 1$
- Each  $f_i$  is a probability distribution for the  $i$ th cluster.
- Usually  $f_i \sim N(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ , but not necessarily so.
- The **posterior probabilities** that observation  $x_j$  pertains to the  $i$ th cluster can be calculated

$$\frac{\pi_i f_i(x_j|\boldsymbol{\theta}_i)}{\sum_{i=1}^k \pi_i f_i(x_j|\boldsymbol{\theta}_i)}$$

# Procedure

- A value or estimate of the number of clusters  $k$  is needed
- The finite mixture model is estimated by maximum likelihood
- For each observation, the posterior probabilities of pertaining to  $j$  cluster are calculated
- Each observation is assigned to the cluster for which it has the largest posterior probability

# NIST autosomal STRs

	CSF1PO		D10S1248		D12S391		D13S317		D16S539		D18S51		D19S433		D1S1656		*	*	*
1	11	12	14	14	17	21	11	12	11	11	17	18	14	14	12		*	*	*
2	9	11	12	13	16	16	11	13	11	12	16	16	11	15	14		*	*	*
3	10	12	14	15	16	20	12	12	11	12	12	17	13	13	16		*	*	*
4	11	12	11	14	16	19	12	13	9	12	15	17	14	16	10		*	*	*
5	8	12	14	14	15	18	11	12	9	11	17	19	14	14	14		*	*	*
6	12	12	14	16	18	19	11	13	11	12	15	16	14	15	14		*	*	*
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Hill, C. et al. (2013) U.S. population data for 29 autosomal STR loci. *Forensic science international: Genetics* 497 7(3):e82–3.

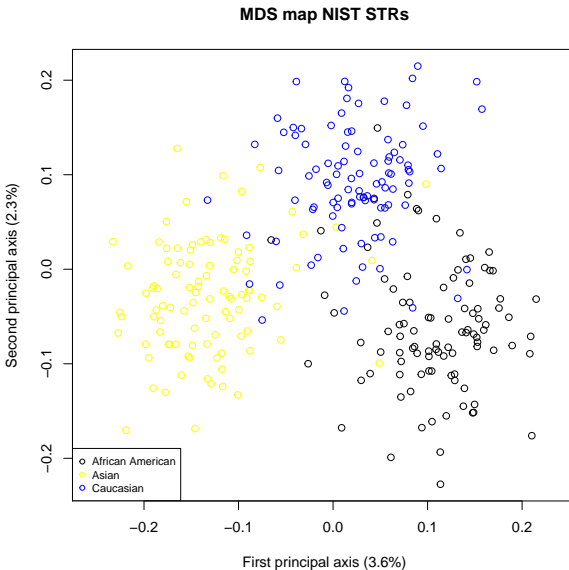
The data:

- 29 autosomal STRs
- Consider individuals with African-American, Asian and Caucasian ancestry
- Sample sizes balanced by subsampling

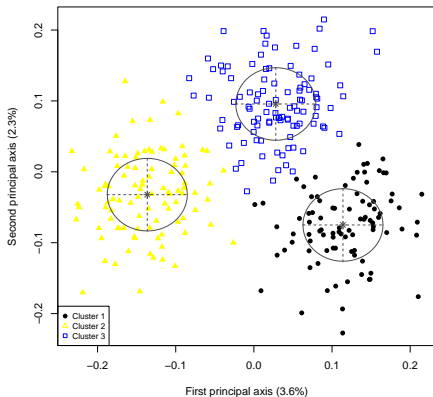
Prior to model-based clustering:

- STRs coded as binary variables
- **Quantification** of the data by MDS based on Jaccard metric

# MDS map of NIST STRs



# Model-based clustering with NIST STRs



	cluster		
	1	2	3
Prob	0.31	0.36	0.33
$x_1$	0.11	0.03	-0.14
$x_2$	-0.07	0.10	-0.03

Ancestry	Cluster		
	1	2	3
Afr. Am.	85	10	2
Asian	1	6	90
Caucasian	4	87	6

# Cluster validity indices

- Choose the optimal number of clusters according to some (numerical) criterion
- Several criteria have been developed
- Some popular criteria:
  - Total within-cluster sum-of-squares (WSS)
  - Pseudo  $F$ -statistics (Calinski-Harabasz, 1974)
  - Silhouette coefficient (Rousseeuw, 1987)
  - ....
- Multiple indices can be calculated and used together to decide upon a number of clusters



# Pseudo F statistics

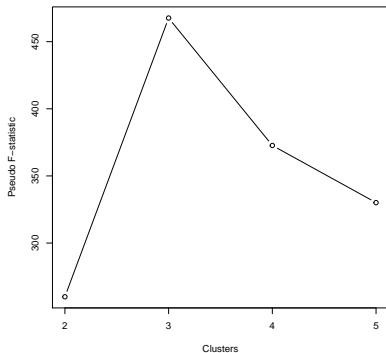
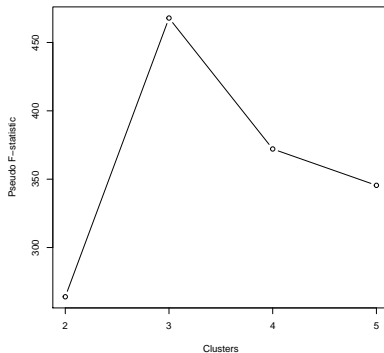
$$F = \frac{GSS/(K - 1)}{WSS/(N - 1)}$$

with:

- $K$  = number of groups
- $N$  = sample size
- $GSS$  = between-group sum-of-squares
- $WSS$  = within-group sum-of-squares

Choose the number of clusters that maximizes  $F$

# Example $F$ statistics

**F-statistics NIST STRs; model-based****F-statistics NIST STRs; k-means**

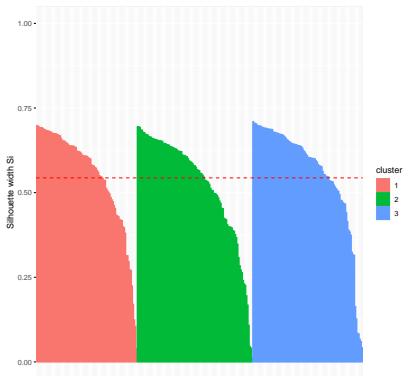
# Silhouette scores and silhouette coefficient

- Let  $a_i$  be the **average distance** between observation  $i$  and all other points in the **same cluster**.
- Let  $b_i$  be the **minimal average distance** between observation  $i$  and all other points in **another cluster**.
- The silhouette score is defined as

$$s_i = \frac{b_i - a_i}{\max(a_i, b_i)} \text{ and satisfies } -1 \leq s_i \leq 1$$

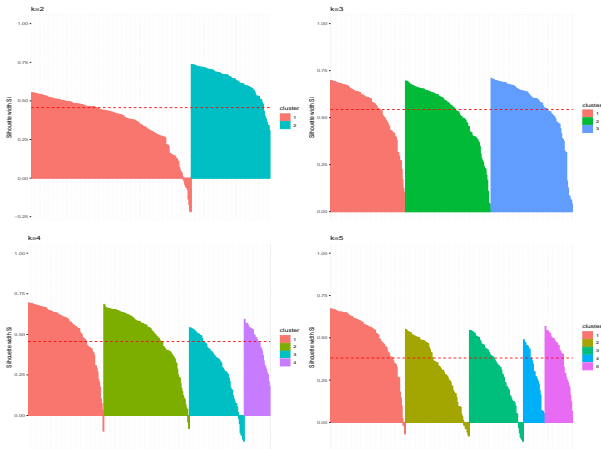
- $s_i$  measures **how well a case matches its own cluster**.
- $s_i$  can be averaged over all observations to give the **average silhouette score**.
- Choose the number of clusters that maximizes this average.

# Silhouette scores NIST data ( $k = 3$ with model-based clustering)

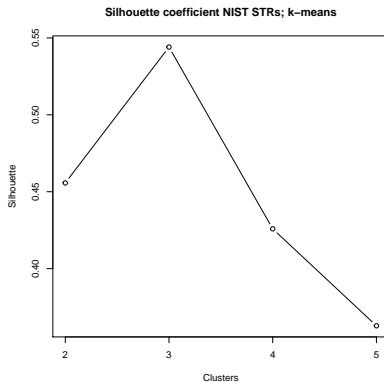
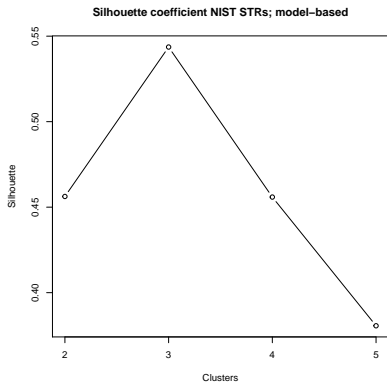


	All	1	2	3
s	0.54	0.55	0.52	0.56

# For varying $k$



# Average silhouette scores for varying $k$



# After a cluster analysis

After obtaining the clusters:

- Are the clusters really different? (manova/anova)
- How homogeneous is each cluster?
- Which variables discriminate the clusters? (descriptive statistics per group, LDA/QDA)

# Final remarks

In cluster analysis, the user has to make several choices:

- 1 the variables to include
- 2 possible transformations
- 3 the algorithm to use (hierarchical, divisive, model-based, ...)
- 4 the distance measure to use (Euclidean, City-Block, Mahalanobis, ...)
- 5 a measure of distance between clusters
- 6 metrics to assess the obtained clustering
- 7 ....



# References

- Manly, B.F.J. (1989) Multivariate statistical methods: a primer. 3rd edition. Chapman and Hall, London.
- Johnson & Wichern (2002) Applied Multivariate Statistical Analysis. 5th edition. Prentice Hall, Chapter 12.
- Everitt, B.S., Landau, S., Lees, M. & Stahl, D. (2011) Cluster Analysis. 5th edition. Wiley.