# Cluster Analysis and COVID-19 Immigration Policies

Thu Pham

thupham@college.harvard.edu Harvard Statistics Department

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#### Introduction

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- ► COVID-19 and the onset of many travel restrictions
- ▶ What makes immigration policies "similar?"
- ► Interesting to find similarities between countries with "similar" policies

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- ► COVID-19 and the onset of many travel restrictions
- What makes immigration policies "similar?"
- Interesting to find similarities between countries with "similar" policies

Research Question: Using cluster analysis, can we find demographic patterns in countries' COVID-19 immigration policies?

# Clustering Methods

 Cluster analysis: unsupervised machine learning method to group observations, with little to no prior knowledge of what the groups should look like Cluster Analysis and COVID-19 Immigration Policies

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## Clustering Methods

- Cluster analysis: unsupervised machine learning method to group observations, with little to no prior knowledge of what the groups should look like
- Common application: market analysis

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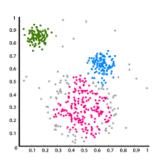
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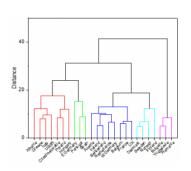
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## Clustering Methods

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## K-Means

Hartigan-Wong method: less prone to converge to a local optima <sup>1</sup> Thu Pham

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<sup>&</sup>lt;sup>1</sup>Morissette, Laurence and Sylvain Chartier. The k-means clustering technique: General considerations and implementation in Mathematica

K-Means

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Randomly initializes point to K clusters

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K-Means

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- ▶ Randomly initializes point to *K* clusters
- ► Repeat until clusters converge:

Hartigan-Wong method: less prone to converge to a local optima <sup>1</sup>

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- Hartigan-Wong method: less prone to converge to a local optima <sup>1</sup>
- ▶ Randomly initializes point to *K* clusters
- Repeat until clusters converge:
  - Calculate the within-cluster sum of squares error

$$SSE = \sum_{k}^{K} \sum_{x_i \in c_k} (x_i - \mu_k)^2$$

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- Repeat until clusters converge:
  - ► Calculate the within-cluster sum of squares error

$$SSE = \sum_{k}^{K} \sum_{x_i \in c_k} (x_i - \mu_k)^2$$

▶ Re-assign  $x_i$  to the cluster  $c_\ell$  that has the lowest SSE with the inclusion of  $x_i$ 

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 Deterministic, and does not require a choice of K clusters ahead of time

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<sup>&</sup>lt;sup>2</sup>Saraçli, Sinan, et al.: Comparison of hierarchical cluster analysis methods by cophenetic correlation

- Deterministic, and does not require a choice of K clusters ahead of time
- Each observation belongs to its own cluster

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- Each observation belongs to its own cluster
- Repeat until we have a single cluster:
  - Closest clusters are merged (by some linkage and metric criteria)
  - Clustering at each step is recorded

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  - Clustering at each step is recorded
- Construct and cut dendrogram
- Choosing a linkage criteria with the cophenetic correlation <sup>2</sup>:

$$c = \frac{\sum_{i < j} [d(x_i, x_j) - \bar{d}][t(x_i, x_j) - \bar{t}]}{\sqrt{\sum_{i < j} [x(i, j) - \bar{x}]^2 \sum_{i < j} [t(i, j) - \bar{t}]^2}}$$

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# Choosing the Number of Clusters

Gap statistic, the difference of total intra-cluster variation between observed data and reference data <sup>3</sup>

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<sup>&</sup>lt;sup>3</sup>Tibshirani, Robert et al. Estimating the number of clusters in a data set via the gap statistic.

## Choosing the Number of Clusters

Gap statistic, the difference of total intra-cluster variation between observed data and reference data <sup>3</sup>

For *K* clusters, calculate the intra-cluster variation:

$$W_K = \sum_{k=1}^K \frac{1}{2n_k} \sum_{i,i' \in C_k} d_{i,i'},$$

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$$W_K = \sum_{k=1}^K \frac{1}{2n_k} \sum_{i,i' \in C_k} d_{i,i'},$$

- Generate N reference distributions and cluster
- ► Compute the gap statistic:

$$\mathsf{Gap}(K) = \frac{1}{N} \sum_{n=1}^{N} [\log(W_{K,n}) - \log(W_K)]$$

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- Generate N reference distributions and cluster
- ► Compute the gap statistic:

$$\mathsf{Gap}(K) = \frac{1}{N} \sum_{n=1}^{N} [\log(W_{K,n}) - \log(W_K)]$$

► Choose the number of clusters as the smallest value of k such that  $Gap(k) \ge Gap(k+1) - \sigma(k+1)$ .

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# Methods of Analysis

 Multiple sample T-test (ANOVA) across each chosen demographic factor Cluster Analysis and COVID-19 Immigration Policies

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- Multiple sample T-test (ANOVA) across each chosen demographic factor
- ► Rand index to compare clustering

$$R = \frac{a+b}{\binom{n}{2}},$$

where for a partition X and Y of some set  $\widetilde{S}$  of n elements, a is the number of pairs in S that are in the same subset in both X and Y, and b is the number of pairs that are in different subsets in X and Y

# Data and Data Cleaning

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► COVID Border Accountability Project

➤ Variables Visa bans, history of travel bans, citizen bans, policy length, policy type, travel blockage (air, land, sea), refugee bans, country exceptions, work exceptions

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COVID Border Accountability Project

- Variables Visa bans, history of travel bans, citizen bans, policy length, policy type, travel blockage (air, land, sea), refugee bans, country exceptions, work exceptions
- ▶ Data cleaning: NA values, one-hot encoding, assumptions, aggregating by country

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- COVID Border Accountability Project
- Variables Visa bans, history of travel bans, citizen bans, policy length, policy type, travel blockage (air, land, sea), refugee bans, country exceptions, work exceptions
- Data cleaning: NA values, one-hot encoding, assumptions, aggregating by country
- World Bank data: GDP, population, life expectancy, fertility rate, and adult literacy rate (2020)

# Chosen Hyperparameters

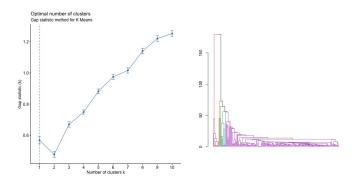


Figure: Gap statistic for K-Means (left), final dendrogram (right).

The cophonetic correlation was highest for minimum linkage (0.862).

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## ANOVA and Rand Index

Demographic	K-Means	HAC
GDP	0.485	0.334
Population	0.155	0.984
Life Expectancy	0.00542	0.039
Fertility Rate	0.0067	0.089
Literacy Rate	0.0273	0.149

Table: Significant p-values are bolded.

Policy Clustering	Continent	Development Level
K-Means	0.640	0.612
HAC	0.300	0.342

Table: Another interesting result: the rand index for K-Means vs HAC was 0.405.

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## **ANOVA**

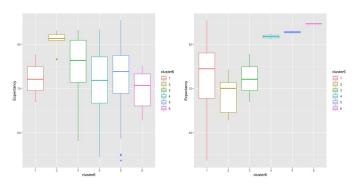


Figure: K-Means (left) and HAC (right)

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## **ANOVA**

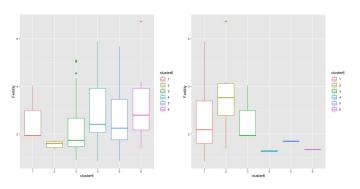


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## Rand Index

▶ Minimum distance linkage ⇒ stringier clusters; may merge clusters whose centroids are far apart Cluster Analysis and COVID-19 Immigration Policies

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## Rand Index

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- ▶ Minimum distance linkage ⇒ stringier clusters; may merge clusters whose centroids are far apart
- ► K-Means are more compact; takes into account the size of the clusters and the internal variance

## Rand Index

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▶ Minimum distance linkage ⇒ stringier clusters; may merge clusters whose centroids are far apart

- K-Means are more compact; takes into account the size of the clusters and the internal variance
- K-Means had more similar clustering to our "natural" metrics – why?

Continents: 43, 41, 50, 15, 40

Development level: 33, 29, 48, 61

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► More effective visualizations

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- More effective visualizations
- ► Some clusters seem "intuitive:" Belgium, Denmark, Greece, Iceland, Poland, and Sweden
- Others, not so much: Iraq, United States, Egypt, Mexico

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- ► More effective visualizations
- Some clusters seem "intuitive:" Belgium, Denmark, Greece, Iceland, Poland, and Sweden
- Others, not so much: Iraq, United States, Egypt, Mexico
- Impact of choosing cluster method