Regression Tree and Clustering for Distributions, and Homogeneous Structure of Population Characteristics

Mihoko Minami (Keio University)

Joint work with Cleridy E. Lennert-Cody of
Inter-American Tropical Tuna Commission (IATTC)

Introduction

We often collect samples on characteristics of different observation units and wonder Whether the characteristics of the observation units have similar distributional structure?

We consider methods to find homogeneous subpopulations

- using regression tree and clustering for distributions approaches
- based on a modified Jensen–Shannon divergence

and present

- a testing procedure for homogeneity of a cluster and
- a hierarchical testing procedure to find the minimal homogeneous/near–homogeneous tree structure of the distributions of a population characteristic.

Motivational Example

Yellowfin tuna fork length data

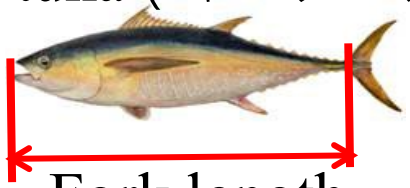
- collected from the tuna catch of purse-seine vessels operated
- in the eastern Pacific Ocean during 2003 – 2007

A total of 797 samples were available.

Each sample contains

- the fork lengths (cm) of about 50 yellowfin tunas, and
- the date and the location of the fishing operations associated with the tuna catch

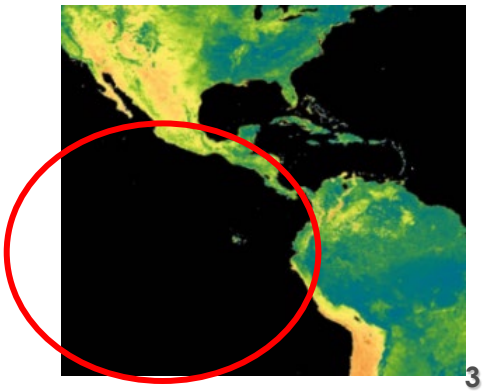
Yellowfin tuna (キハダマグロ



Fork length

Purse-seine set (巻網漁)

The eastern Pacific Ocean



The fork length data

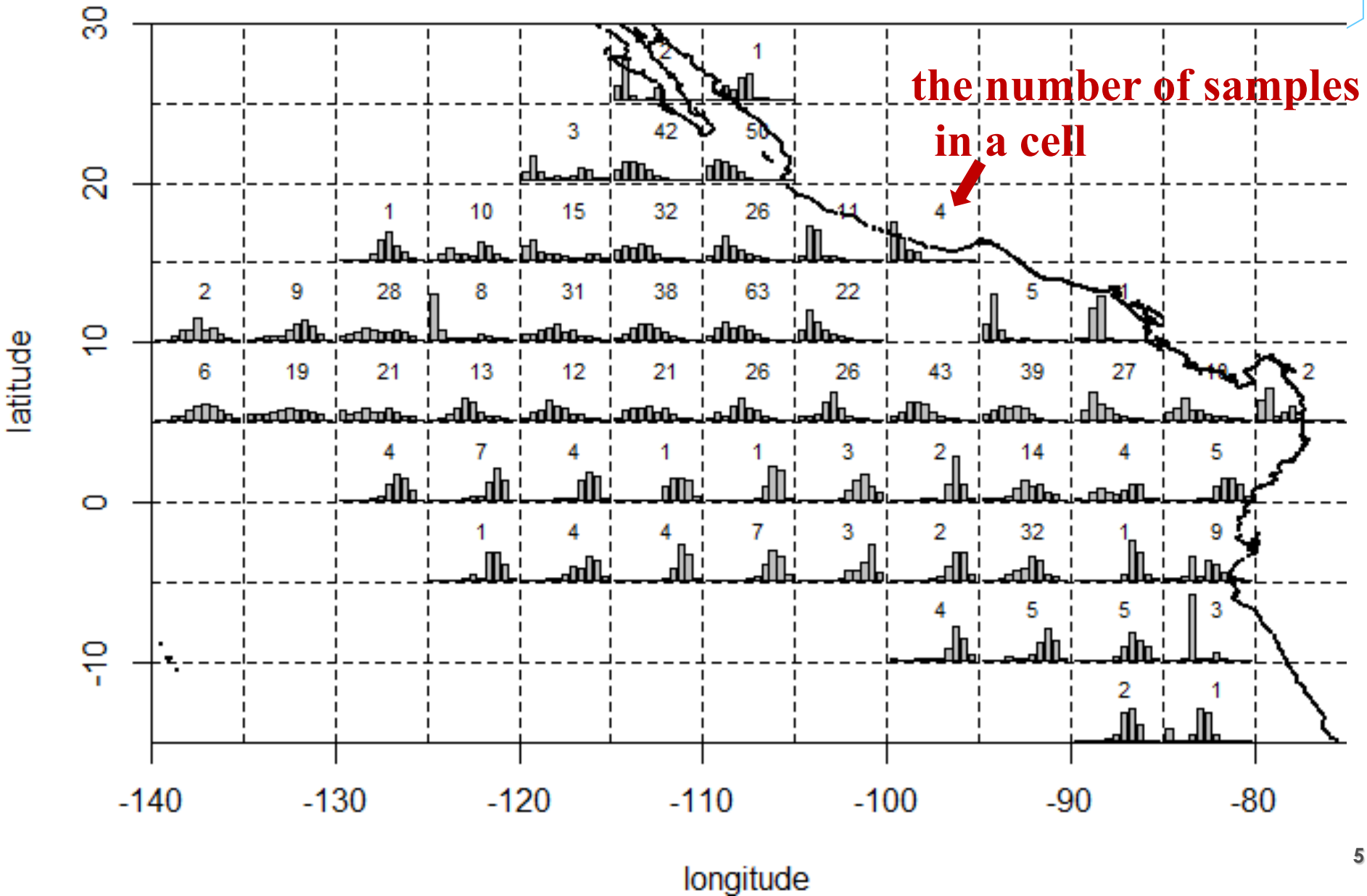
Data on the area and time period corresponding to the fishing operations are obtained from data recorded by onboard observers or from fishermen's logbooks.

The samples were collected by the port-sampling program of the Inter-American Tropical Tuna Commission (IATTC; www.iattc.org), which is the regional fishery management agency responsible for the conservation of tuna and other marine resources in the eastern Pacific Ocean

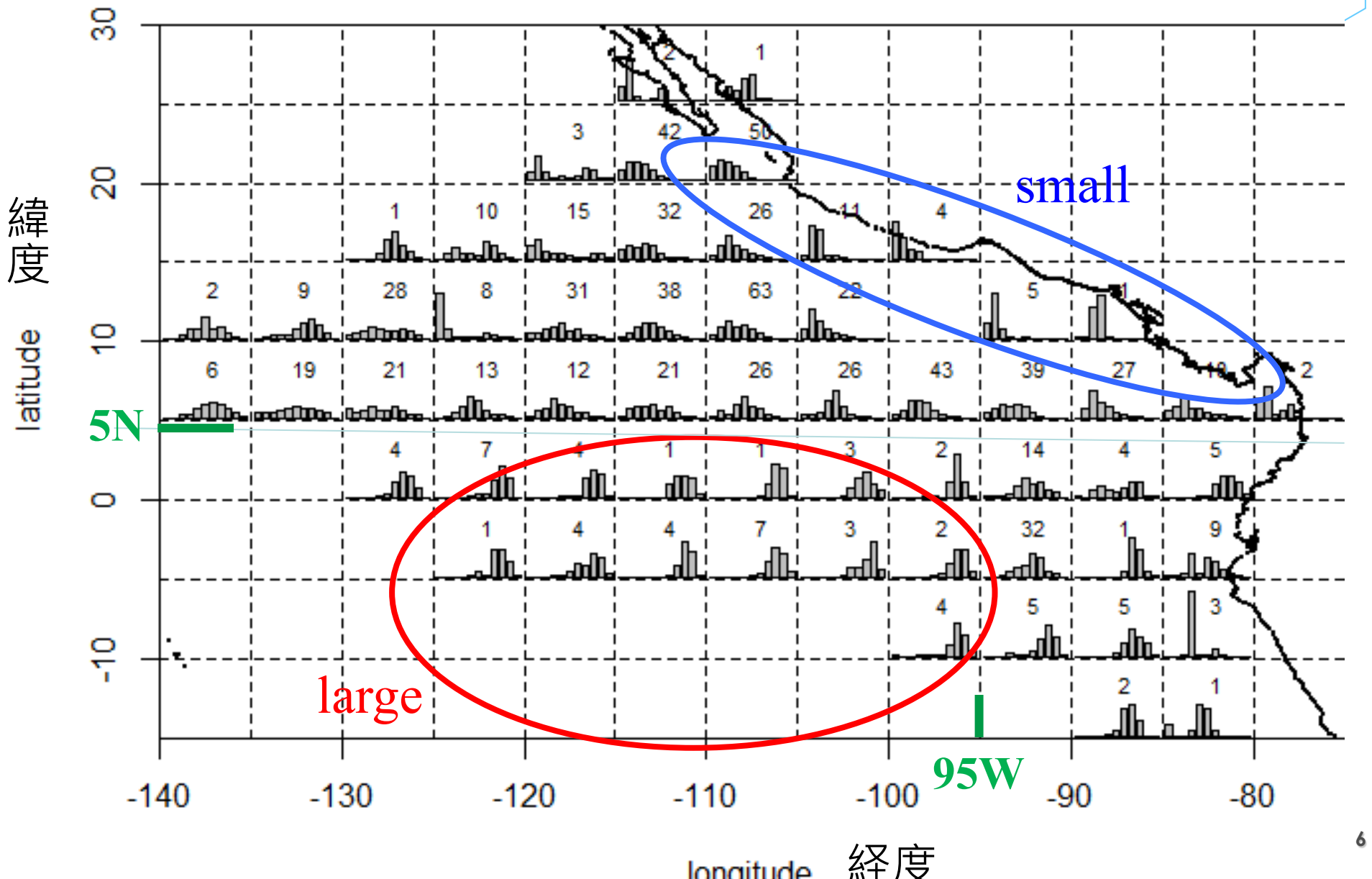
In our analysis, the fork length data were aggregated by location

- over time into 5° by 5° cells
- so that 797 samples were combined into 60 spatial cells.

Histograms and numbers of samples in cells



Histograms and numbers of samples in cells



Outline of Talk

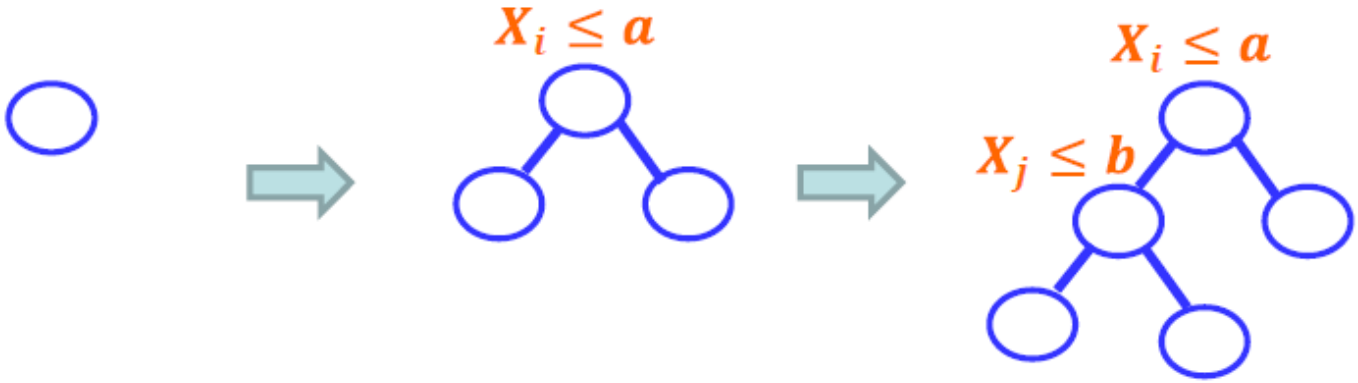
- Regression Tree and Hierarchical Clustering
- Modified Jensen–Shannon divergence, related distance and Impurity measures
- Regression Tree and Clustering for the Yellowfin tuna fork length data
  - With histograms
  - With density estimates
- Testing procedures for homogeneity and the minimum homogeneous tree structure
  - Near–homogeneous tree structure
- Summary and Future Work

Regression Tree
and
Hierarchical Clustering

Regression Tree

Classification and regression tree (CART, Breiman et al. (1984))

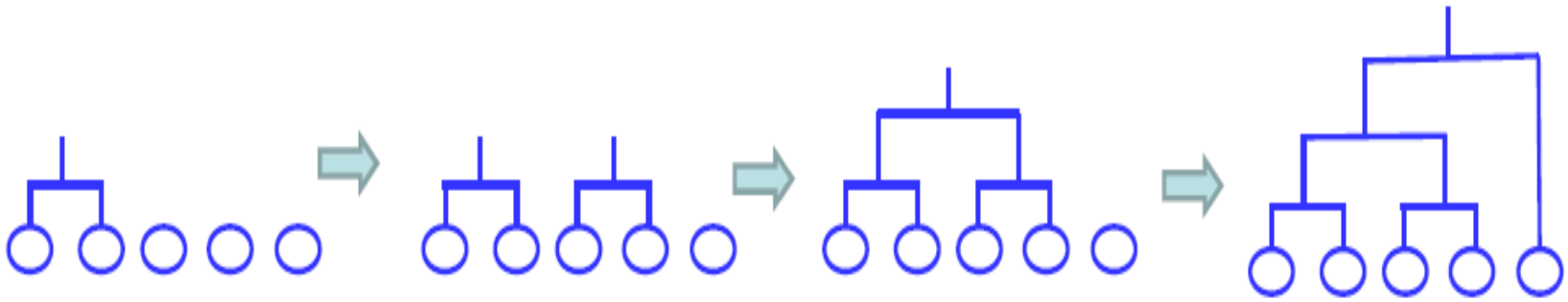
- starts from a set of all units and
- repeatedly subdivides that set using binary partitions defined by the values of an explanatory variable selected to provide the greatest decrease of the values of a response variable in a measure of impurity until all divided nodes satisfy the termination rule.



Hierarchical Clustering

Hierarchical clustering (cf. Gordon (1999))

- It is an agglomerative approach
- Each unit starts in its own cluster,
  - The method repeatedly combines the two closest clusters by some metric for distance among units
  - At the end, all units form one large cluster.



Modified Jensen–Shannon divergence, related distance, and impurity measures

Distance/Similarity Measures between distributions

- S.H. Cha (2007) listed a total of 42 measures in 7 types: 1) L_p Minkowski type, 2) L_1 family, 3) Intersection family, 4) Inner Product family, 5) Fidelity family or Squared-chord family, 6) Squared L2 family or $\chi 2$ family, 7) Shannon's entropy family
- The modified Jensen-Shannon Divergence (Dhillon et al. 2003)
- Clustering of histograms using Wasserstein metric (Ispiro and Lechevallier, 2006, Ispiro et al. 2014)
- k-Means using Mixed α-Divergences (Nielsen et al. 2014)
- Fuzzy clustering using L_1 measure (Phamtoan et al., 2022, Nguyen-Trang et al. 2023)
- Earth Mover's distance (Henderson et al., 2015)

The Modified Jensen–Shannon divergence

Modified Jensen–Shannon divergence (distance)

For distributions f_1 and f_2 with confidences m_1 and m_2 (> 0), respectively, let $\bar{f}_{\{1,2\}}$ be their weighted average distribution

$$\bar{f}_{\{1,2\}} = \frac{1}{m_1 + m_2}\left(m_1 f_1(x) + m_2 f_2(x)\right).$$

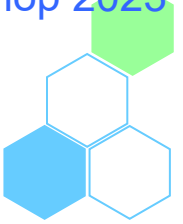
Then, the modified Jensen–Shannon divergence is defined as

$$\mathrm{D_{MJS}}\left((f_1, m_1), (f_2, m_2)\right) = m_1\ \mathrm{KL}\left(f_1 | \bar{f}_{\{1,2\}}\right) + m_2 \mathrm{KL}\left(f_2 | \bar{f}_{\{1,2\}}\right)$$

where $KL(f|g) = \int_{\Omega} f\left(x\right) log \frac{f(x)}{g(x)} dx$

(cf. Dhillon et al., 2003)

The Modified Jensen–Shannon divergence



- It is symmetric

$$\mathrm{D}_{\mathrm{MJS}}\big((f_1, m_1), (f_2, m_2)\big) = \mathrm{D}_{\mathrm{MJS}}\big((f_2, m_2), (f_1, m_1)\big)$$

- No support problem arises since

$$\{\mathrm{x}: \bar{f}_{\{1,2\}}(x) > 0\} = \{\mathrm{x}: f_1(x) > 0\} \cup \{x: f_2(\mathrm{x}) > 0\}$$

- It can be expressed with the information entropy

$$\mathrm{D}_{\mathrm{MJS}}\big((f_1, m_1), (f_2, m_2)\big)$$
$$= (m_1 + m_2)\, H\big(\bar{f}_{\{1,2\}}\big) - m_1 H(f_1) - m_2 H(f_2)$$

where $H(\cdot)$ is the information entropy,

$$H(f) = -\int_{\Omega} f(x) \log f(x) dx$$

- In the case of multinomial distributions (and histograms), $\mathrm{D}_{\mathrm{MJS}}\left(\left(\hat{f}_1, m_1\right), \left(\hat{f}_2, m_2\right)\right)$ is the log-likelihood ratio.

Impurity of a group of distributions

(Lennert-Cody et. Al, 2010, 2013)

At each step of CART, the binary split that produces the largest decrease in impurity is chosen.

Impurity of a group of distributions

For a group of distributions $\mathcal{G} = \{(f_i, m_i), i \in G\}$, let $m_{\mathcal{G}}$ and $\bar{f}_{\mathcal{G}}$ be its confidence and weighted average distribution, respectively,

$$m_{\mathcal{G}} = \sum_{i \in G} m_i \,, \bar{f}_{\mathcal{G}} = \frac{\sum_{i \in G} m_i \, f_i}{m_{\mathcal{G}}}.$$

We define the KL-impurity of $\mathcal{G} = \{(f_i, m_i), i \in G\}$ as

$$\mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}) = \sum_{i \in G} m_i \, \mathrm{KL}(f_i | \bar{f}_{\mathcal{G}})$$

An Expression with the information entropy

KL-impurity can be expressed with the information entropy

$$\mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}) = m_{\mathcal{G}}\, H\left(\bar{f}_{\mathcal{G}}\right) - \sum_{i \in G} m_i\, H(f_i)$$

because

$$\begin{aligned}
\mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}) &= \textstyle\sum_{i \in G} m_i\ \mathrm{KL}(f_i \,|\, \bar{f}_{\mathcal{G}}) \\
&= \textstyle\sum_{i \in G} m_i \int_{\Omega} f_i\,(x) \log \frac{f_i(x)}{\bar{f}_{\mathcal{G}}(x)}\ dx \\
&= -\textstyle\int_{\Omega} \sum_{i \in G}(x)\, m_i f_i(x) \log \bar{f}_{\mathcal{G}}(x) dx \\
&\qquad + \textstyle\sum_{i \in G} \int_{\Omega} m_i f_i(x) \log f_i(x) dx \\
&= m_{\mathcal{G}}\, H\left(\bar{f}_{\mathcal{G}}\right) - \textstyle\sum_{i \in G} m_i\, H(f_i)
\end{aligned}$$

Distance between two groups of distributions

Hierarchical clustering repeatedly combines two closest clusters as measured by some measure of "distance"

Distance between two groups of distributions

$$\mathrm{D}_{\mathrm{MJS}}(\mathcal{G}_1, \mathcal{G}_2) = \mathrm{D}_{\mathrm{MJS}}\left(\left(\bar{f}(\mathcal{G}_1), \textstyle\sum_{i\in G_1} m_i\right),\ \left(\bar{f}(\mathcal{G}_2), \textstyle\sum_{i\in G_2} m_i\right)\right)$$

where

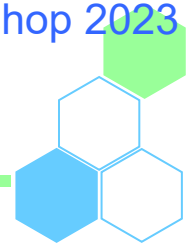
$$\bar{f}_{\mathcal{G}_j} = \frac{\sum_{i\in G_j} m_i\, f_i}{m_{\mathcal{G}_j}}, j = 1,2$$

It can be shown that

$$\mathrm{D}_{\mathrm{MJS}}(\mathcal{G}_1, \mathcal{G}_2) = m_{\mathcal{G}_1\cup\mathcal{G}_2}\mathrm{H}(\mathcal{G}_1 \cup \mathcal{G}_2) - m_{\mathcal{G}_1}\mathrm{H}(\mathcal{G}_1) - m_{\mathcal{G}_2}\mathrm{H}(\mathcal{G}_2)$$

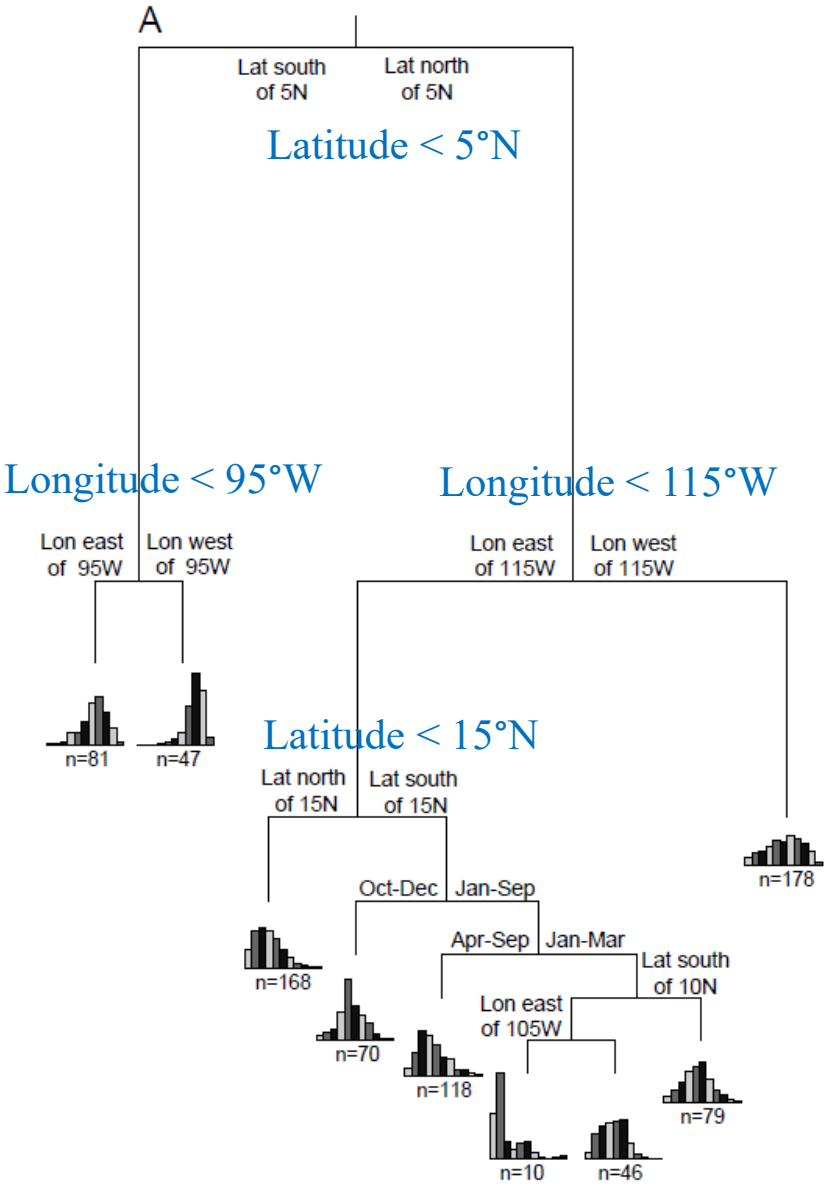
$$= \mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}_1 \cup \mathcal{G}_2) - \mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}_1) - \mathrm{Imp}_{\mathrm{KL}}(\mathcal{G}_2)$$

Increase of impurity by the merge / Decrease of impurity by partition



Regression Tree for Histograms of Yellowfin tuna fork length

Regression tree for histograms of tuna body length



Responses :

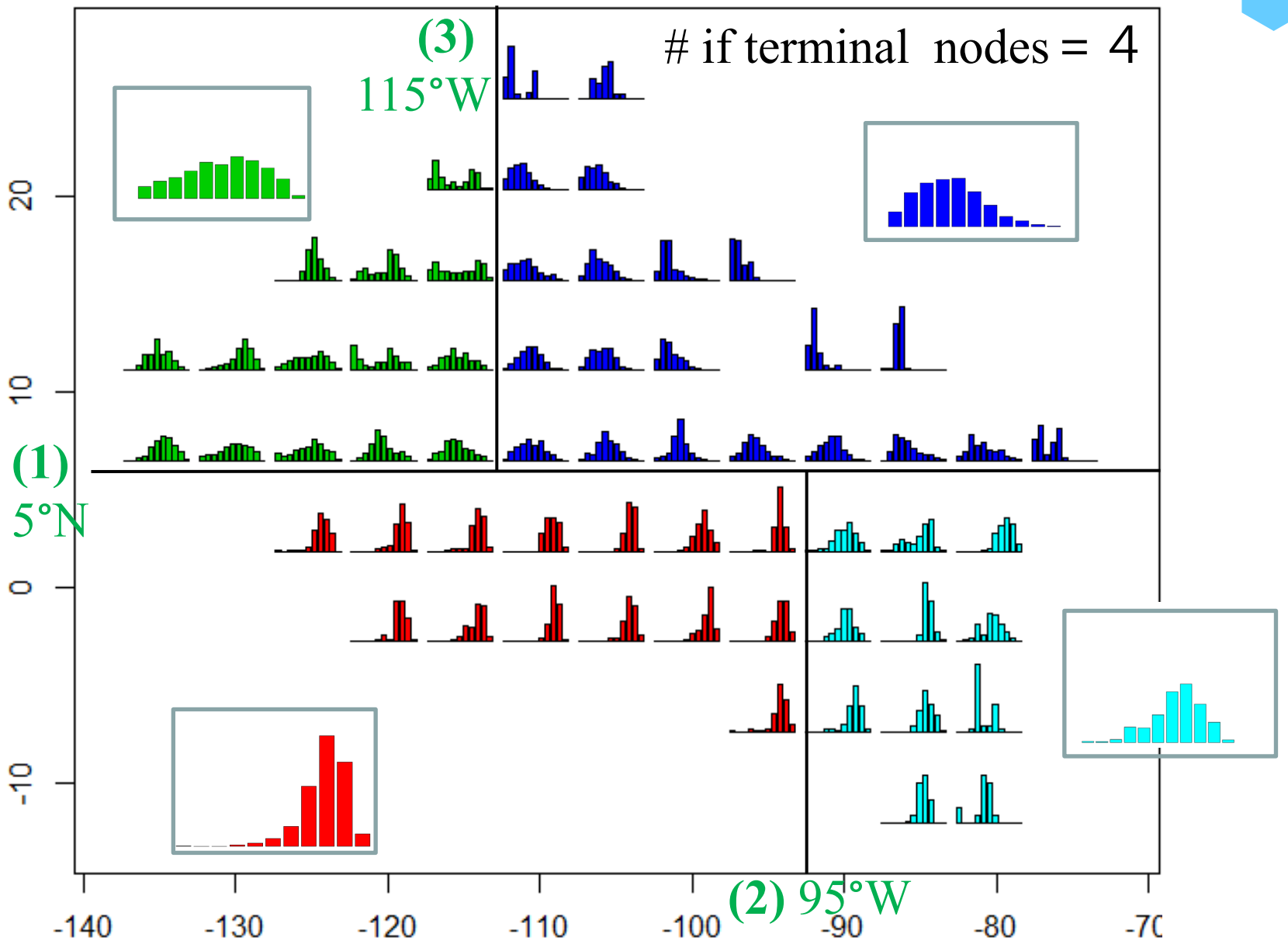
distributions of body length

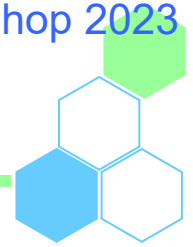
Explanatory variables :

season, latitude, longitude

Cleridy E. Lennert-Cody, Mihoko Minami, Patrick K. Tomlinson, Mark N. Maunder, Fisheries Research (2010)

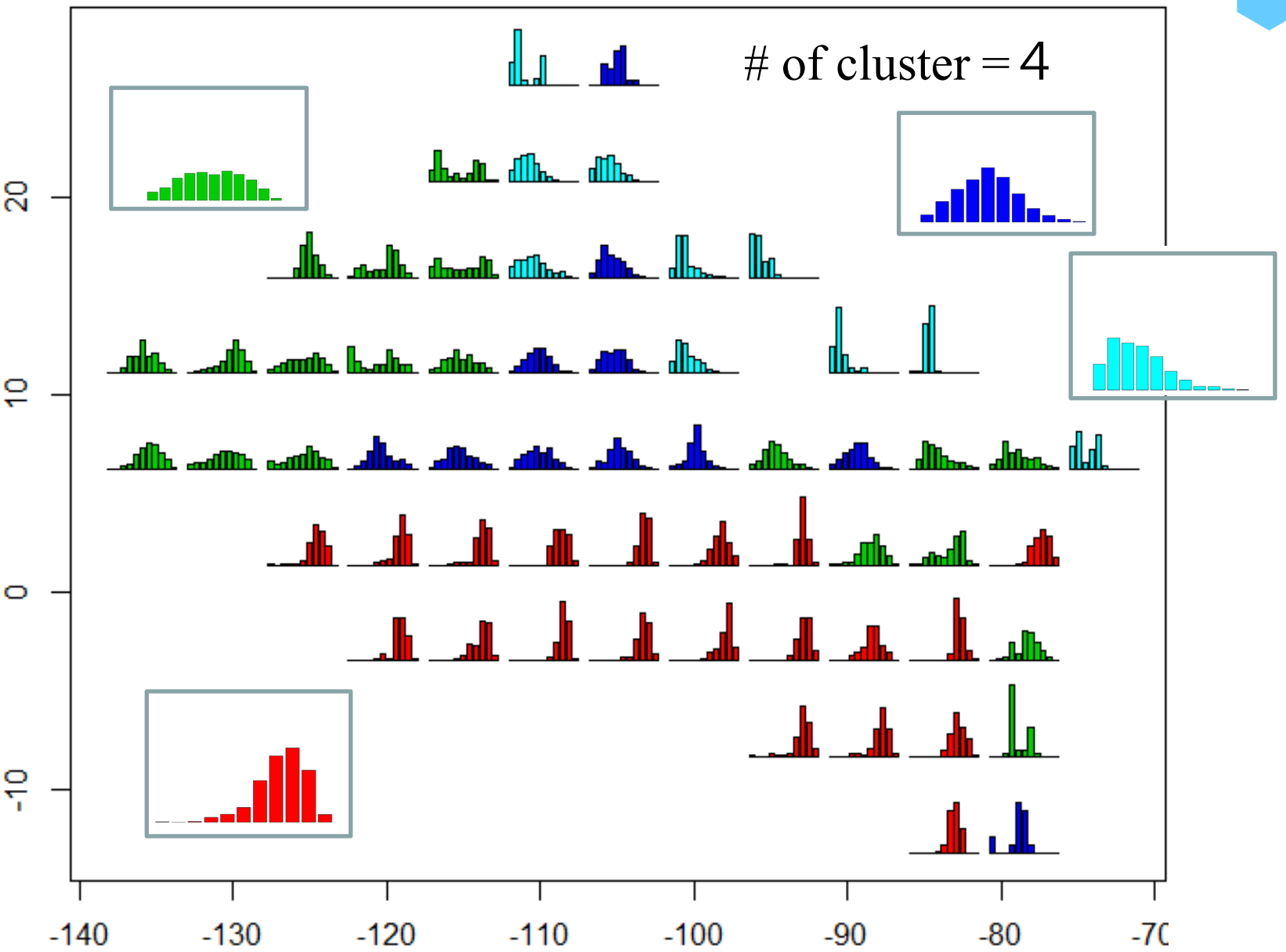
Partition of the Eastern Pacific Ocean by Regression Tree



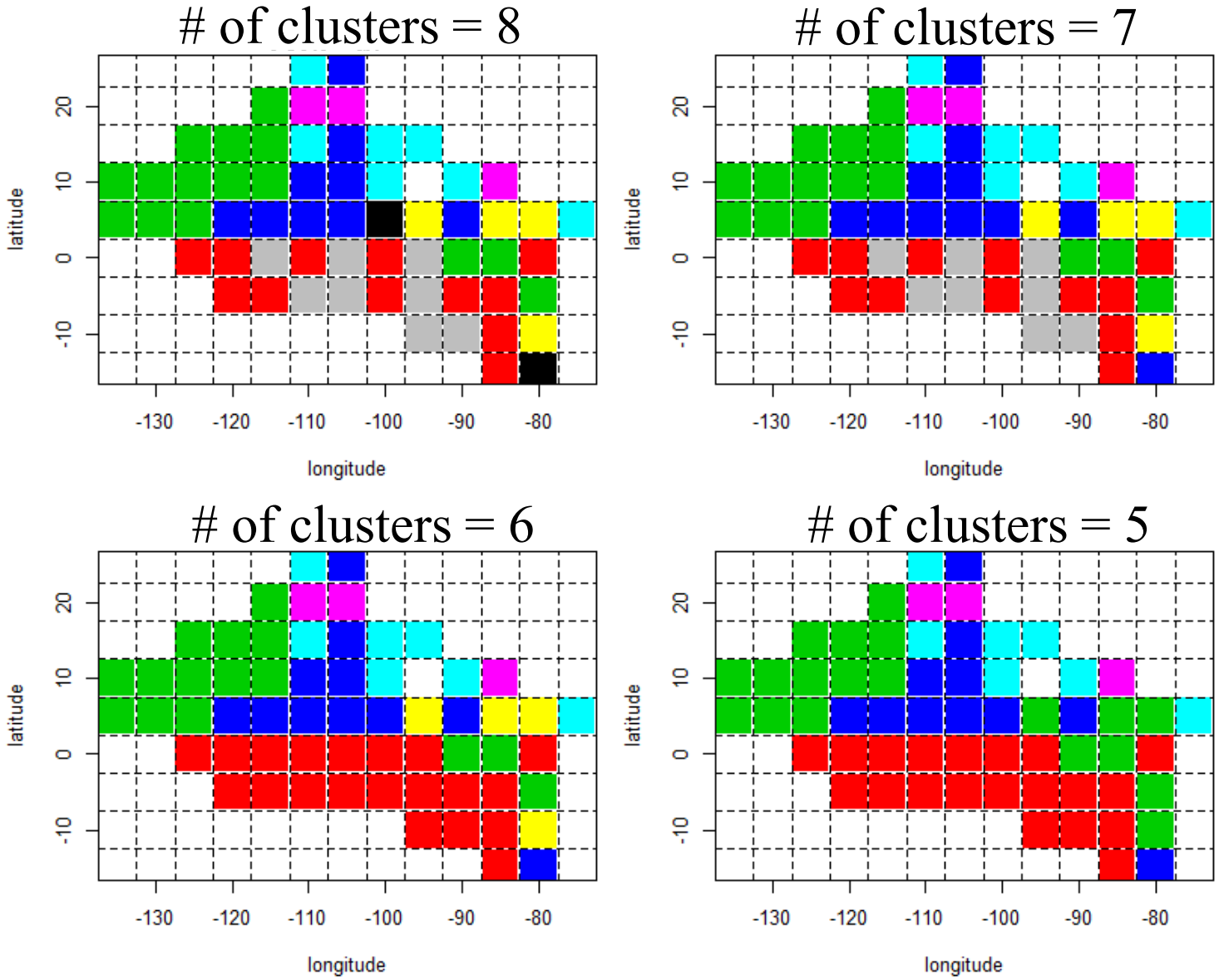


Hierarchical Clustering for Histograms of Yellowfin tuna fork length

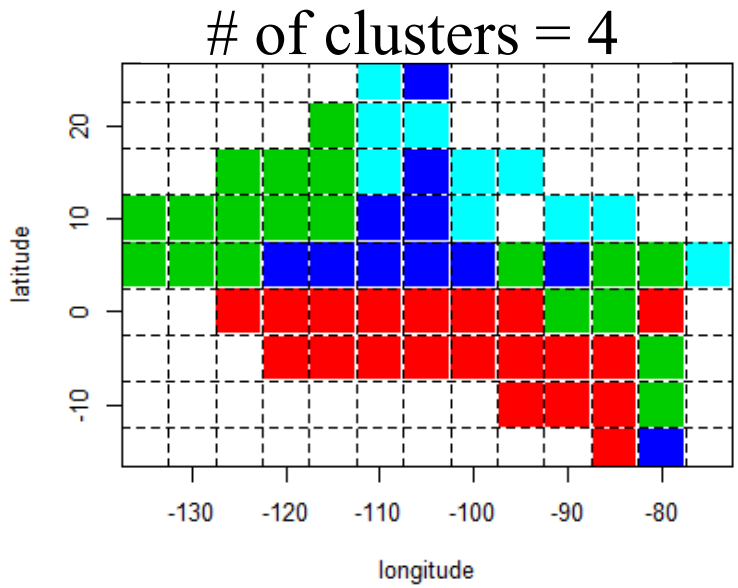
Partition of the Eastern Pacific Ocean by Regression Tree

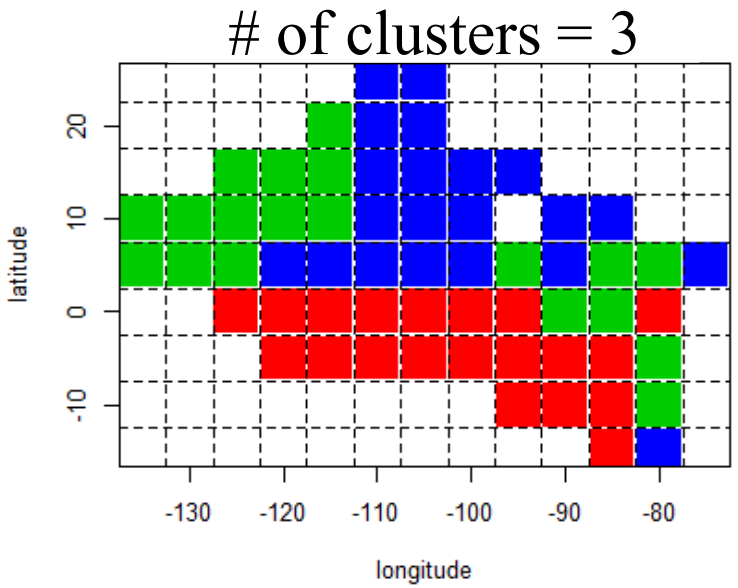


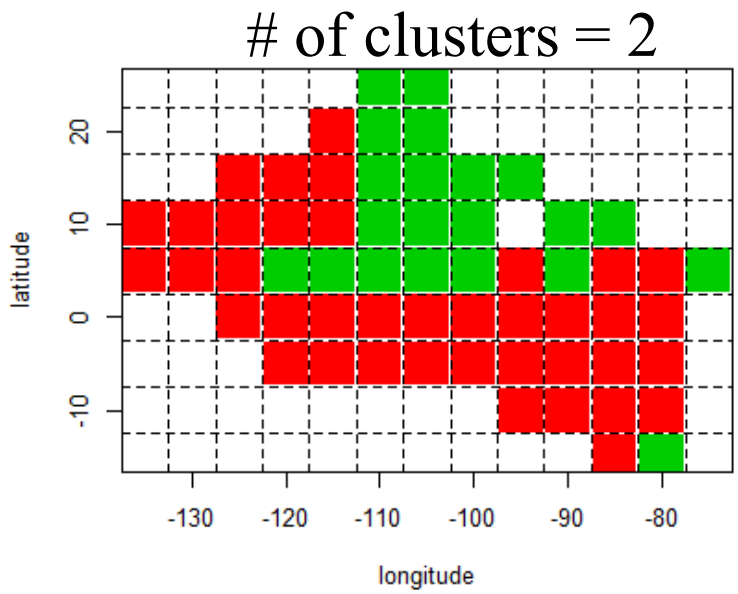
Partitions with different numbers of clusters



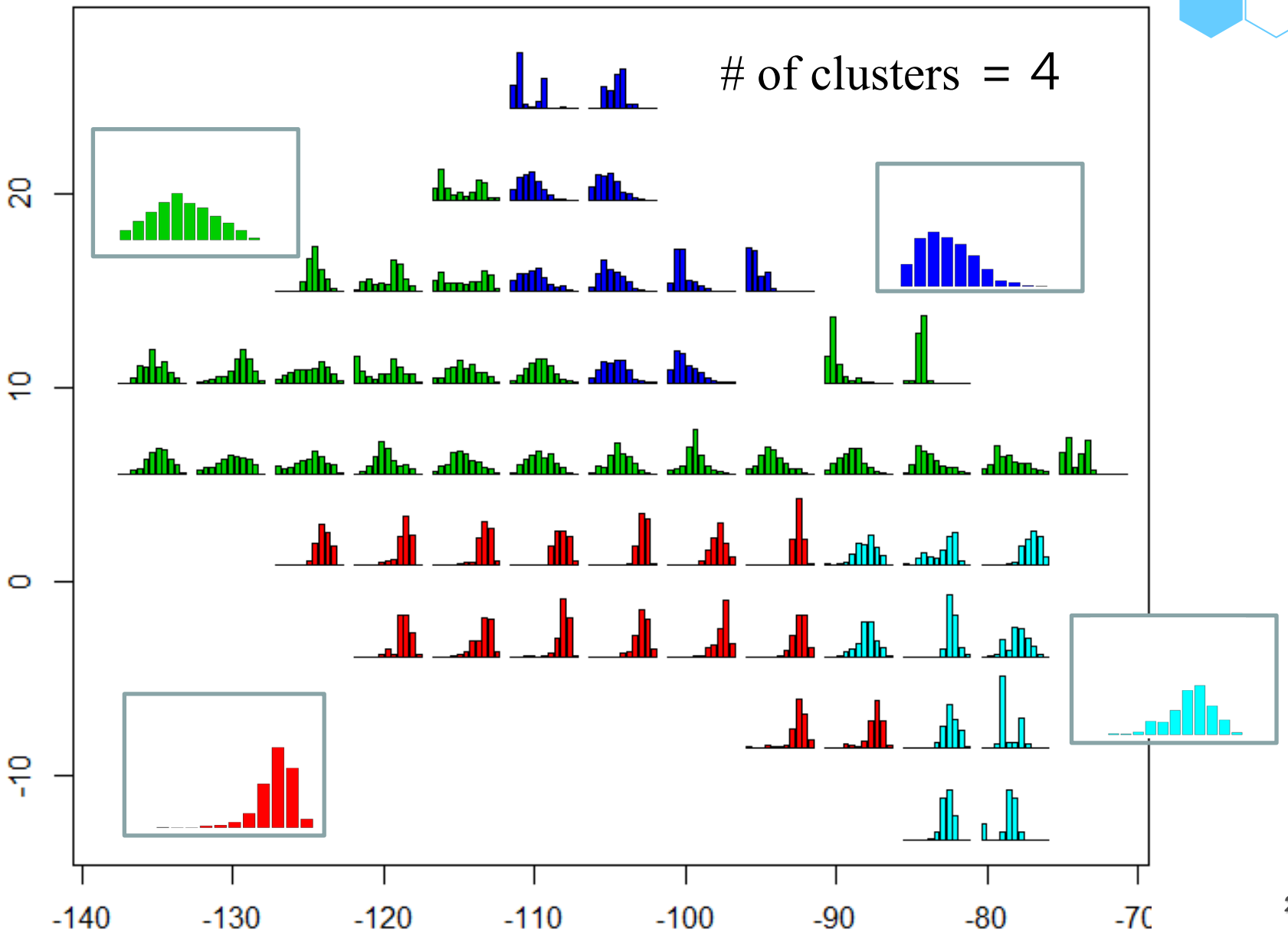
Partitions with different numbers of clusters







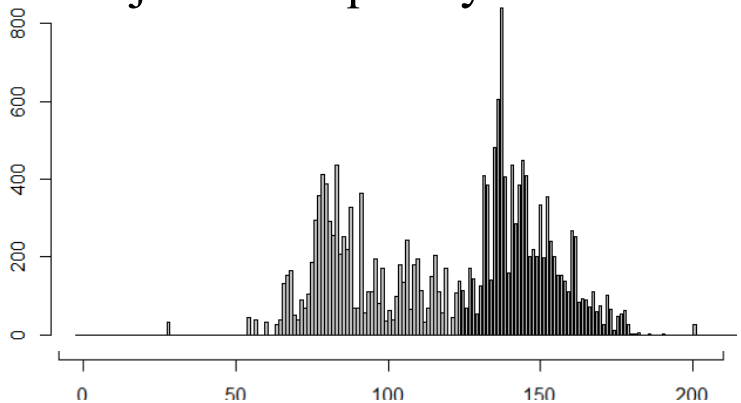
Clustering under connectivity restriction



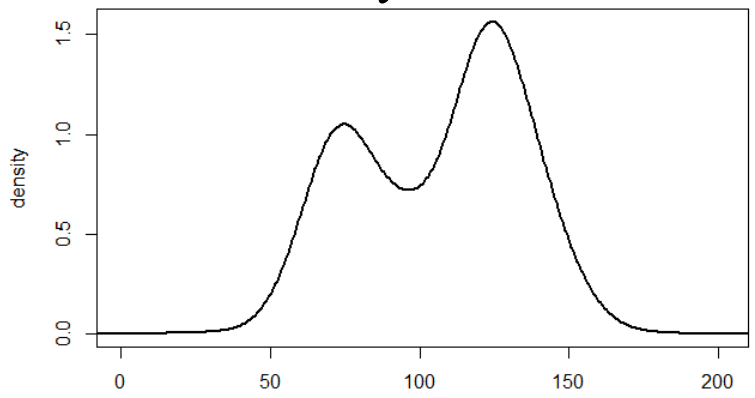
Regression Tree for Density Estimates of Yellowfin tuna fork length

Kernel density estimation for tuna fork length

Adjusted frequency of cell i



Kernel density estimate



Kernel density estimation of tuna body length for cell i

$$\widehat{f}_i(x) = \frac{1}{h\, m_i} \sum_{j=1}^{M} b_{ij} K\left(\frac{x - x_j}{h}\right)$$

where

$$K(x) = \frac{1}{\sqrt{2\pi}} e^{-x^2/2} \quad \text{Gauss kernel}$$

x_j body length of size j $(j = 1, 2, \ldots, M)$

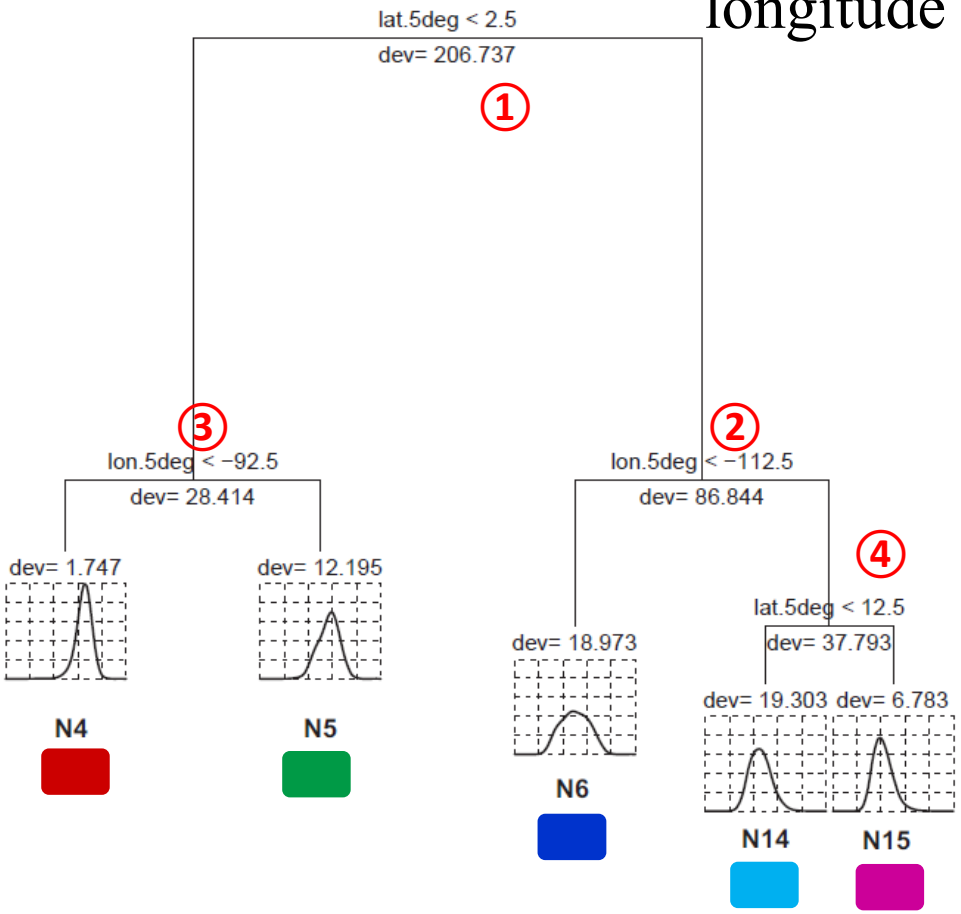
b_{ij} adjusted frequency of size j in cell i

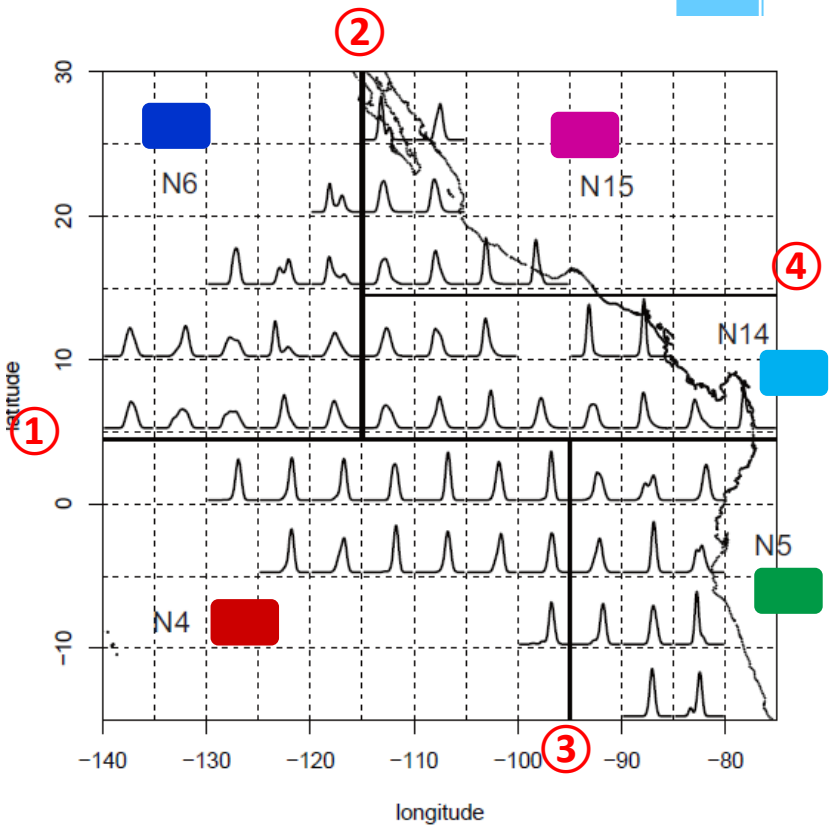
$$m_i = \sum_{j=1}^{M} b_{ij} \quad \text{Total frequency of cell } i$$

sample size = "confidence"

Regression tree and partitions of the Ocean

Response variable: density estimates
Explanatory variables : latitude, longitude





(c.f. Lennert-Cody et. al, 2010, 2013)

Stopping rule:
(1) leaf impurity < 0.1×root impurity
(2) confidence < 20

Clustering for Density Estimates of Yellowfin tuna fork length

Distance measures between clusters of distributions

For comparison, we performed clustering with three distances:

◆ Modified Jensen–Shannon divergence (MJS)

$$\mathrm{D}_{\mathrm{MJS}}(\mathcal{G}_1, \mathcal{G}_2) = m_1 \,\mathrm{KL}\left(\bar{f}_1 | \bar{f}_{\{1,2\}}\right) + m_2 \mathrm{KL}\left(\bar{f}_2 | \bar{f}_{\{1,2\}}\right)$$

◆ Earth Mover's distance (EMD) (Henderson et al. 2015)

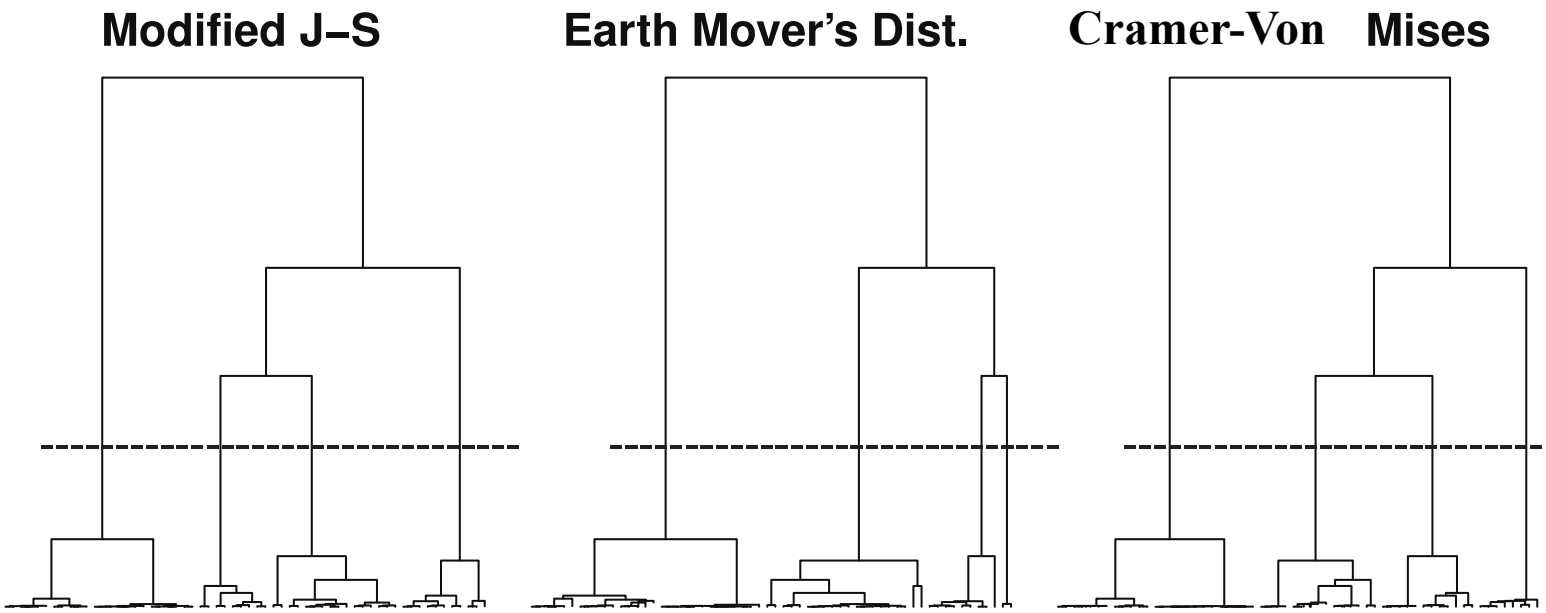
$$\mathrm{D}_{\mathrm{EMD}}(\mathcal{G}_1, \mathcal{G}_2) \equiv \int_0^1 \left|\bar{F}_1^{-1}(y) - \bar{F}_2^{-1}(y)\right| dy = \int_{-\infty}^{\infty} \left|\bar{F}_1(x) - \bar{F}_2(x)\right| dx$$

◆ Cramér–Von Mises type distance

$$\mathrm{D}_{\mathrm{CVM}}(\mathcal{G}_1, \mathcal{G}_2) \equiv \frac{m_1 \cdot m_2}{(m_1 + m_2)} \int_{-\infty}^{\infty} \left(\bar{F}_1(x) - \bar{F}_2(x)\right)^2 dF^b(x)$$

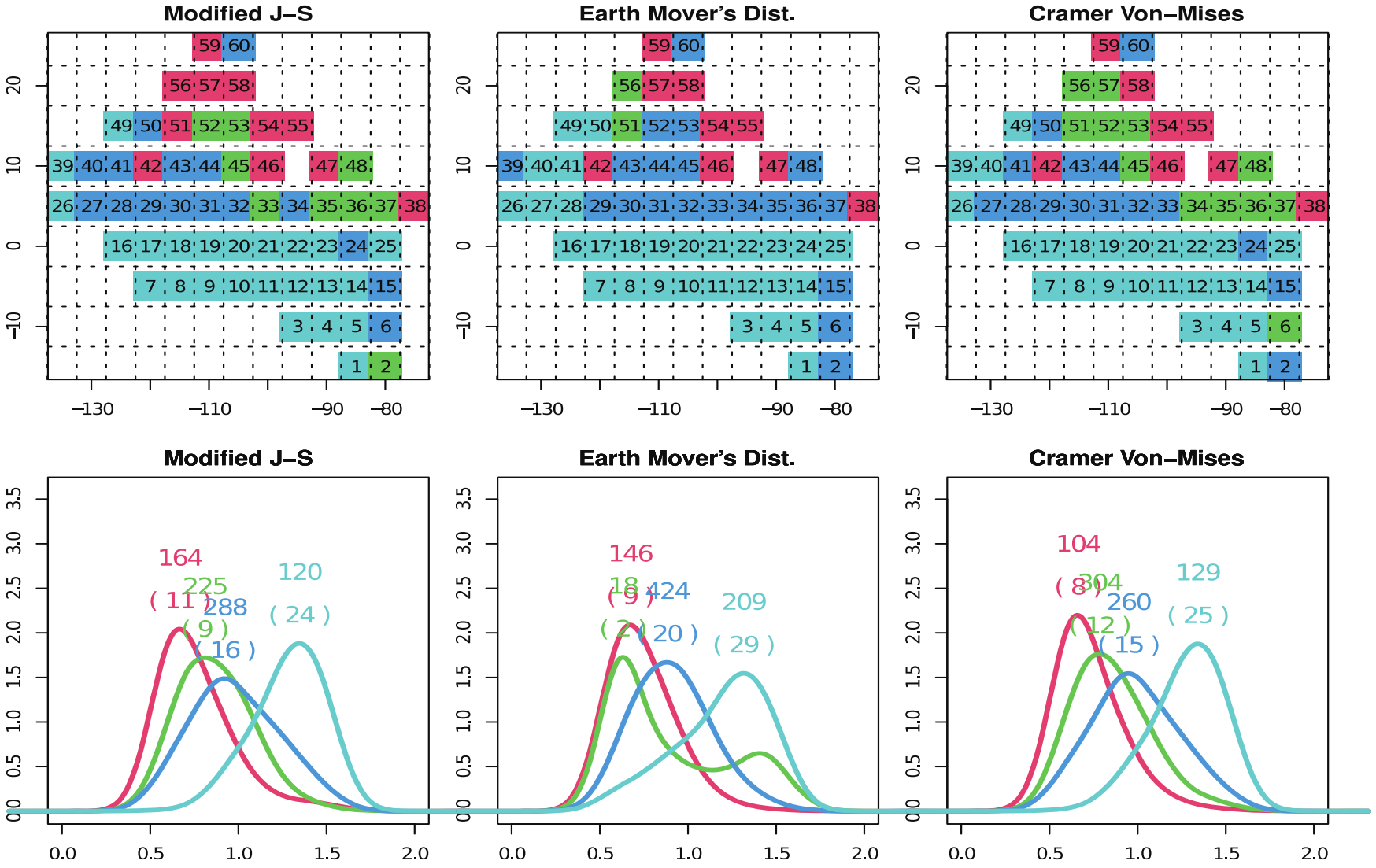
where F^b is the overall average distribution function as F^b

Dendrograms of 5° × 5° cells



- clusters by modified J-S divergence and Cramer Von-Mises distance are somehow similar compared to the clusters by Earth Mover's distance
- Earth Mover's distance produced a cluster with a small confidence (sample size)

Clusters and distributions of $5° \times 5°$ cells



Comparison of results by three distances

- Modified Jensen–Shannon divergence (MJS)

$$\mathrm{D_{MJS}}(\mathcal{G}_1, \mathcal{G}_2) = m_1\ \mathrm{KL}\left(\bar{f}_1 | \bar{f}_{\{1,2\}}\right) + m_2 \mathrm{KL}\left(\bar{f}_2 | \bar{f}_{\{1,2\}}\right)$$

- Earth Mover's distance (EMD) (Henderson et al. 2015)

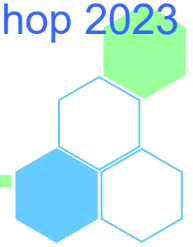
$$\mathrm{D_{EMD}}(\mathcal{G}_1, \mathcal{G}_2) \equiv \int_0^1 \left|\bar{F}_1^{-1}(y) - \bar{F}_2^{-1}(y)\right| dy = \int_{-\infty}^{\infty} \left|\bar{F}_1(x) - \bar{F}_2(x)\right| dx$$

c.f. $\mathrm{L}_1(\mathcal{G}_1, \mathcal{G}_2) \equiv \int_{-\infty}^{\infty} \left|\bar{f}_1(x) - \bar{f}_2(x)\right| dx$ (T. Nguyen-Trang et al. 2022)

- Cramér–Von Mises type distance

$$\mathrm{D_{CVM}}(\mathcal{G}_1, \mathcal{G}_2) \equiv \frac{m_1 \cdot m_2}{(m_1 + m_2)} \int_{-\infty}^{\infty} \left(\bar{F}_1(x) - \bar{F}_2(x)\right)^2 dF^b(x)$$

Measure	Modified J-S			Earth Mover's Dist.			Cramér Von-Mises		
	# of cells	# of sets	mean length(m)	# of cells	# of sets	mean body length(m)	# of cells	# of sets	mean body length(m)
cluster 1	11	164	0.771	9	146	0.754	8	104	0.741
cluster 2	9	225	0.881	2	18	0.913	12	304	0.866
cluster 3	16	288	0.994	20	424	0.919	15	260	0.999
cluster 4	24	120	1.294	29	209	1.197	25	129	1.289



Testing procedures for homogeneity and the minimal homogeneous tree structure

Testing homogeneity of kernel density estimates

Cao and Keilegom (2006) considered the problem to test

$$H_0: F_1 = F_2$$

using the kernel density estimates $\hat{f}_1$ and $\hat{f}_2$ obtained from two independent random samples,

$$X_1, \ldots X_n \sim^{i.i.d.} F_1, \quad Y_1, \ldots Y_m \sim^{i.i.d.} F_2.$$

They defined a test statistics, showed its asymptotic distribution and proposed a testing procedure for $H_0: F_1 = F_2$

However, their testing procedure cannot be applied to test the homogeneity of a cluster because member distributions or samples are results of previous merges and are not independent.

Randomization sample for testing homogeneity

Suppose $\mathcal{G} = \{(\widehat{f}_i, m_i), i \in G\}$, $\mathcal{G} = \mathcal{G}_L \cup \mathcal{G}_R$ an $\mathrm{D}_{\mathrm{MJS}}(\mathcal{G}_L, \mathcal{G}_R) = d$.

H_0: $\mathcal{G}$ is homogeneous (i.e., all samples used to estimate $\widehat{f}_i$ are from the same distribution)

◆ Generation of randomization sample $\boldsymbol{t} = (t_1, t_2, \cdots, t_K)$

For $k = 1,2, \cdots, K$, repeat the following steps

1. Generate a sample $\boldsymbol{x}_i^k$ of size m_i from $\bar{f}_{\mathcal{G}}$ for all $i \in G$
2. Compute density estimate $\hat{g}_i^k$ with $\boldsymbol{x}_i^k$ for all $i \in G$
3. Perform clustering with $\mathcal{G}^k = \{(\hat{g}_i^k, \mathrm{m_i}), i \in G\}$.
4. Let $t_k = \mathrm{D}_{\mathrm{MJS}}(\mathcal{G}_L^k, \mathcal{G}_R^k)$ where $\mathcal{G}_L^k$ and $\mathcal{G}_R^k$ are two clusters combined at the last step, that is, $\mathcal{G} = \mathcal{G}_L^k \cup \mathcal{G}_R^k$.

Testing procedure for homogeneity of a cluster

- Generate a randomization sample $\boldsymbol{t}$ of small size K_1 $(\mathrm{e.g.}\,100)$
- If $\#\{t_k | t_k > d, k = 1,2,\cdots,K_1\} \geq N_{d1}$ $(\mathrm{e.g.}\,10)$
  then, $[p$ value for $d]$ is greater than $\frac{N_{d1}}{K_1}$ $(\mathrm{e.g.}\,0.1)$
- If $\#\{t_k | t_k > d, k = 1,2,\cdots,K_1\} < N_{d1}$ $(\mathrm{e.g.}\,10)$
  then, compute the Chebyshev's upper bound U of $P(X \geq d)$ under H_0 computed with sample mean and variance of sample $\boldsymbol{t}$
  - If the upper bound U $\leq \epsilon$ $(\mathrm{e.g.}\,0.001)$
    then, $[p$ value for $d]$ is less than U
    $\left(U = \frac{svar(t)}{(d-\bar{t})^2} \right)$
  - If the upper bound U $> \epsilon$ $(\mathrm{e.g.}\,0.001)$
    then, generate a randomization sample of large size K_2 $(e.g.1000)$ and let $N_{d2} = \#\{t_k | t_k > d, k = 1,2,\cdots,K_2\}$
    $[p$ value for d$]$ = $\inf\{p | P(W \leq N_{d2}) \leq 0.05,\ W \sim \mathrm{Bin}(K_2, p)\}$

Hierarchical testing procedure for homogeneity

Let $H_0^{(j)}$ be "Cluster $\mathcal{G}_j$ is homogeneous".

Because the null hypotheses have the Hierarchical structure,

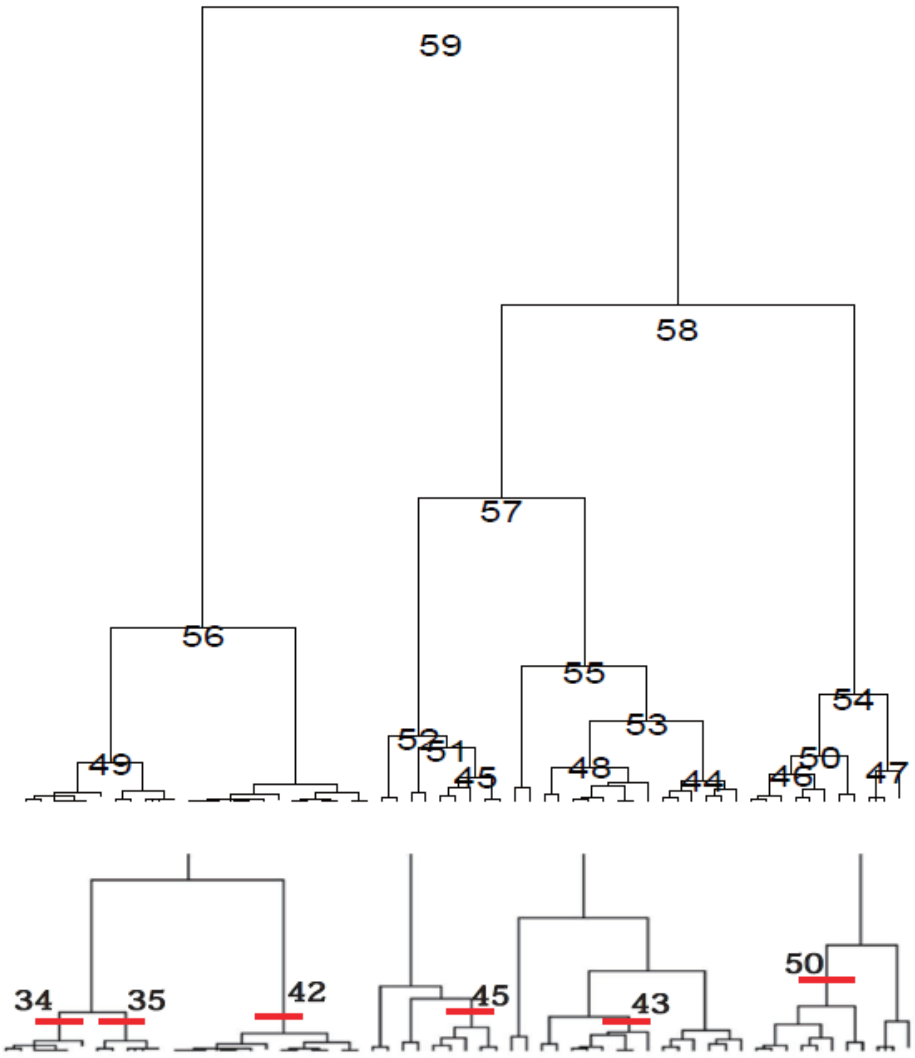
$$\mathcal{G}_i \supset \mathcal{G}_j \text{ implies } H_0^{(i)} \Rightarrow H_0^{(j)},$$

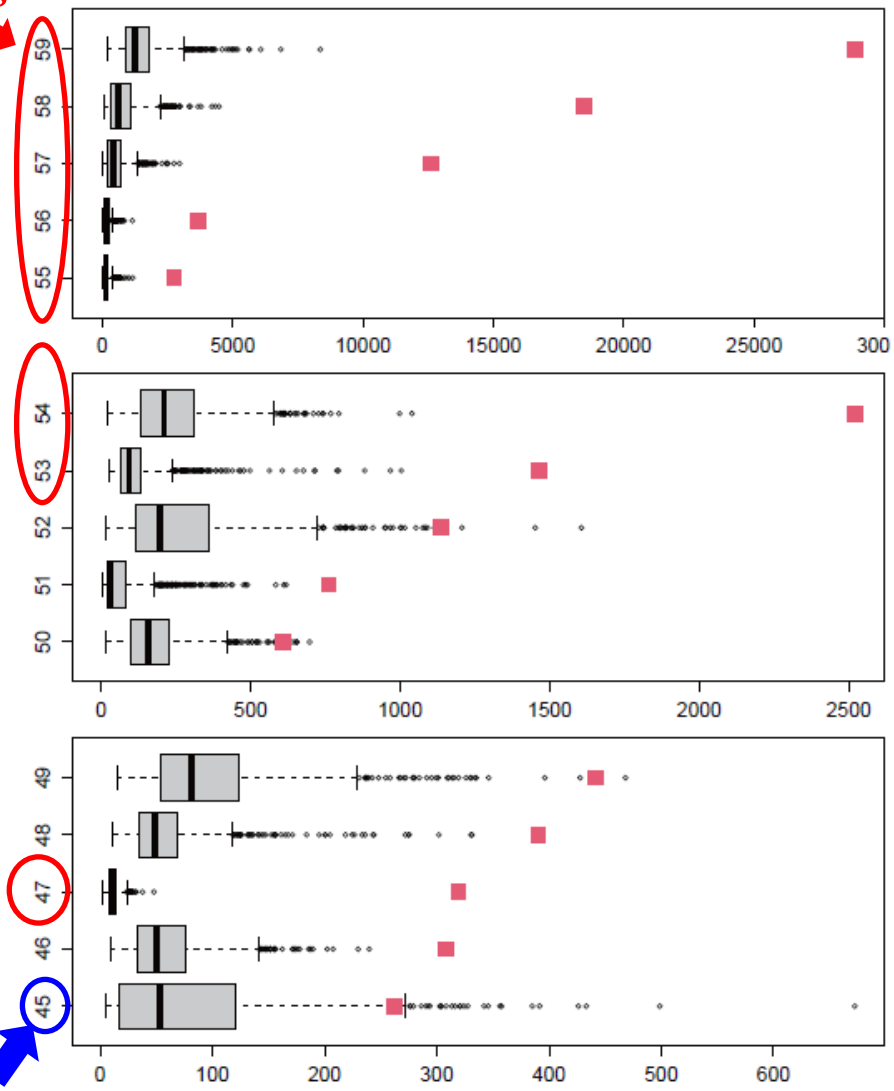
the family-wise error rate is controlled at the significance level α with the following hierarchical testing procedure:

- Test starts from the top, the cluster of all distributions
- If the hypothesis is significant at α,
  then, the hypothesis "the cluster is homogeneous" is rejected
  The test proceeds to child clusters.
- If the hypothesis is not significant at α,
  then, the hypothesis "the cluster is homogeneous" is accepted
  The child clusters are not tested.

Boxplot of randomization samples with size K_1

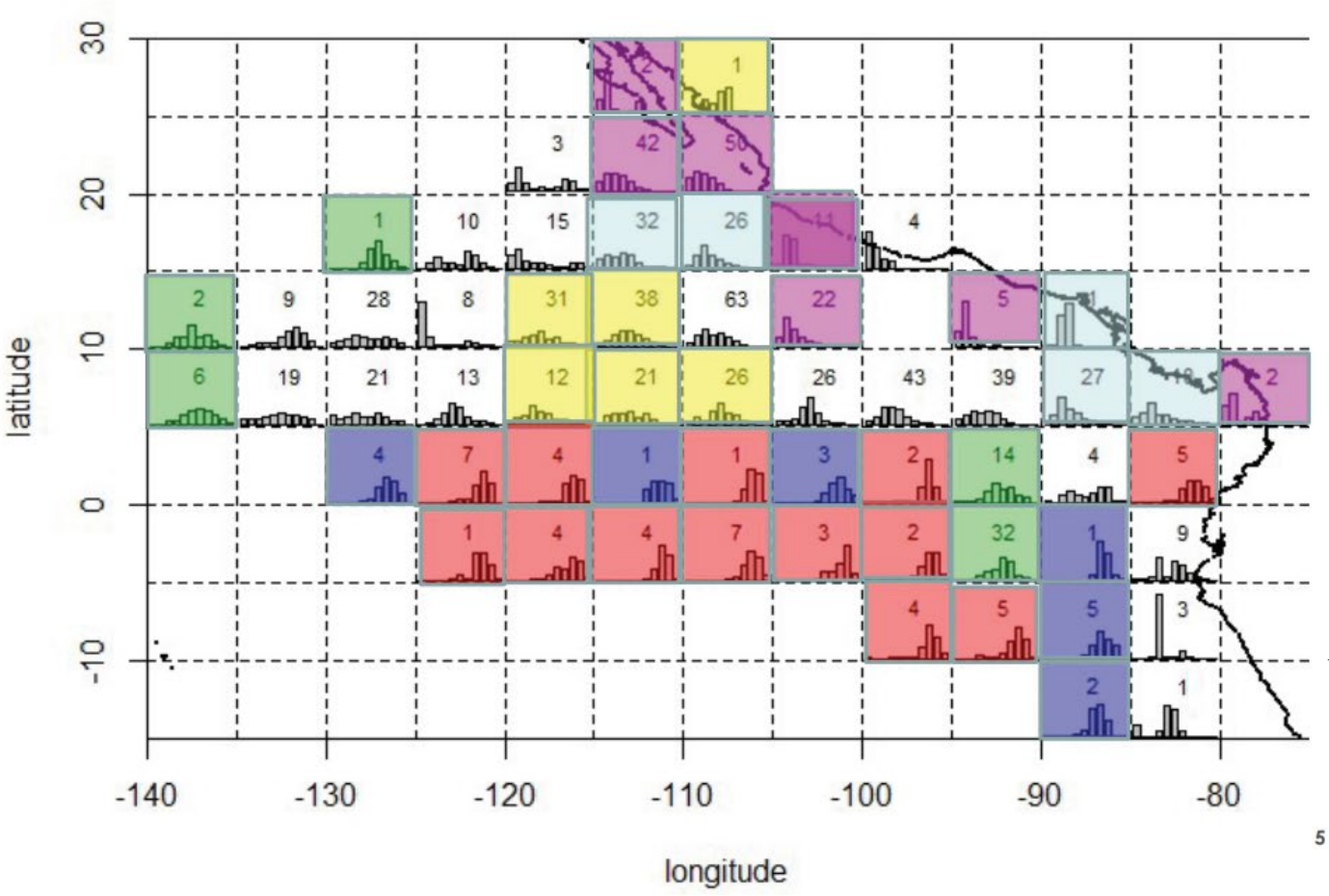
Not homogeneous at $\alpha = 0.01$





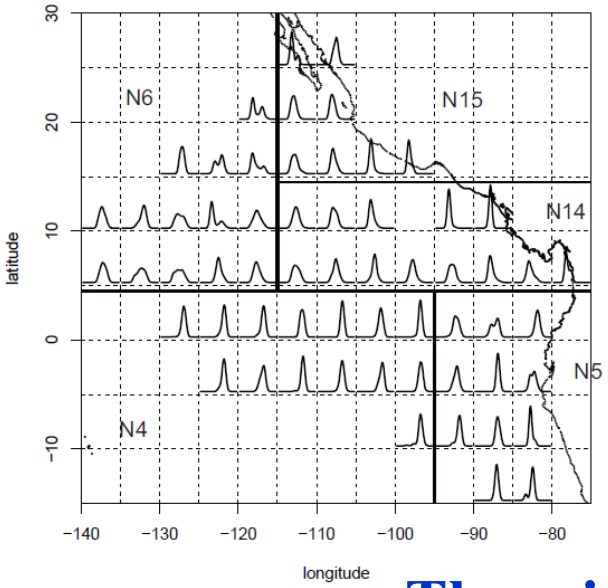
Cannot be said "Not homogeneous"

The minimal Homogeneous tree structure with $\alpha = 0.01$

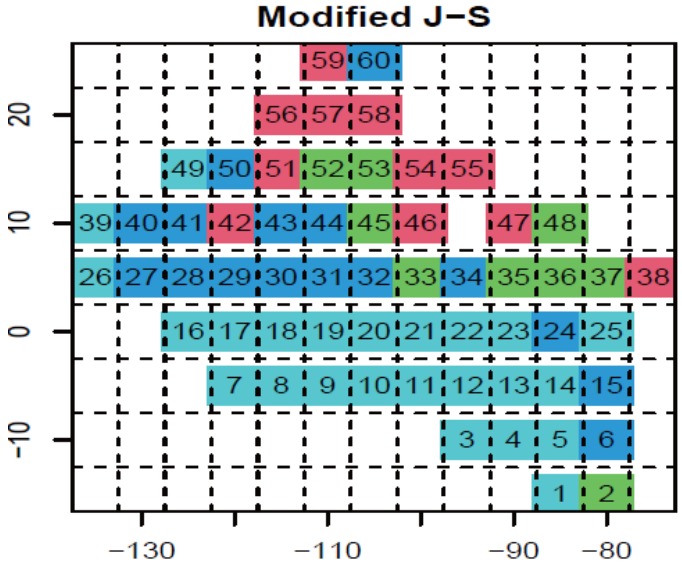


Comparison of the results

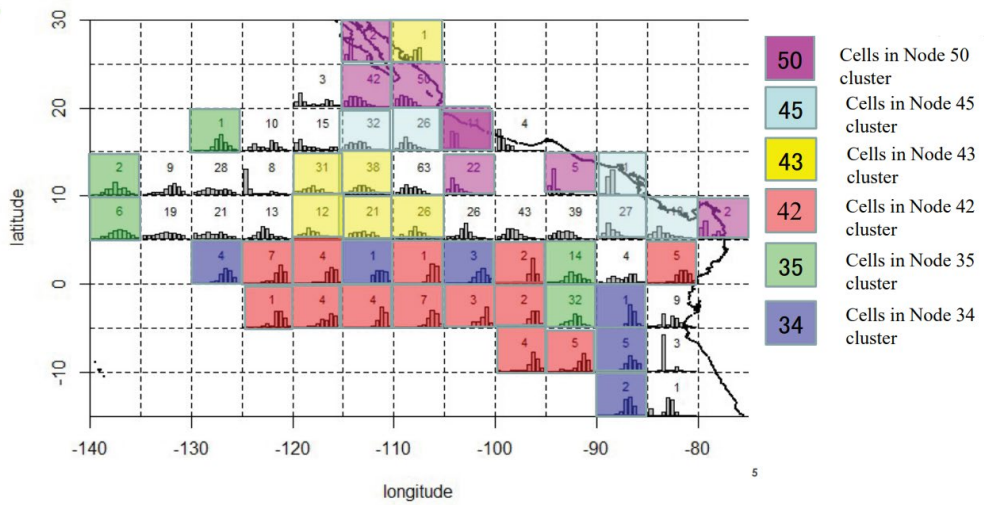
Regression tree



Hierarchical clustering



The minimal homogeneous structure



Near-homogeneous tree structure

Homogeneity might be too demanding for defining a cluster.

As a relaxed concept, we regard a cluster whose Chebyshev's upper bound U obtained with random sample is less than θ, is near-homogeneous with cut-off value θ.

Cut-off value interval	# of nodes	Terminal nodes in the minimal near-homogeneious tree
$[31.32, \infty]$	1	59
[26.81, 31.32)	3	58, 49, 42
[15.08, 26.81)	5	55, 54, 52, 49, 42
[14.20, 15.08)	7	55, 52, 50, 49, 42, (42), 21
[9.94, 14.20)	10	52, 50, 49, 48, 44, 42, (42), (6), (34), 21
[9.41, 9.94)	11	52, 50, 49, 44, 43, 42, (42), (6), (34), 21, 30
[6.50, 9.41)	12	52, 50, 49, 44, 43, 42, (42), (6), (34), 21, (15), (29)
[9.41, 9.94)	16	52, 50, 49, 43, 42, (42), (6), (34), 21, (15), (29), 23, (40), (28), (27), (41)

Numbers without parenthesis are node(merge) numbers and numbers in parenthesis are original cell numbers

Summary and future work

- We consider regression tree and hierarchical clustering methods for distributions based on the modified Jensen–Shannon divergence.
- We presented a testing procedure for homogeneity of a cluster and a hierarchical testing procedure to find the minimal homogeneous/near–homogeneous tree structure of distributions.
- These methods and procedures are applied to the yellowfin tuna fork length data

Future work

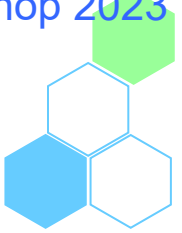
- We would like to extend the method to Bayesian clustering for distributions with prior for partitions.

Reference

- Breiman, L. and Friedman, J. H. and Olshen, R. A. and Stone, C. J. (1984). *Classification and Regression Trees,* Wadsworth and Brooks, Monterey, CA.
- Cao, R. and van Keilegom I. (2006) Empirical Likelihood Tests for Two-Sample Problems via Nonparametric Density Estimation, Can J Stat 34, 61-77
- Cha, S.-H. (2007). Comprehensive survey on distance/similarity measures between probability density functions. Int. J. Math. Model. Meth. Appl. Sci.(1), 300—307
- Dhillon, I. S., S. Mallela, and R. Kumar (2003). A divisive information-theoretic feature clustering algorithm for text classification. *Journal of Machine Learning Research*(3), 1265—1287.
- Henderson, K., Gallagher, B., Eliassi-Rad, T. (2015). EP-MEANS: An Efficient Nonparametric Clustering of Empirical Probability Distributions. *SAC '15* Proceedings of the 30th Annual ACM Symposium on Applied Computing, 893-900.
- Gordon, A.D. (1999). *Classification,* 2nd Edition, CRC Press,
- Irpino, A. and Lechevallier, Y. 2006. Dynamic clustering of histograms using Wasserstein metric. In COMPSTAT 2006 – Advances in Computational Statistics pp 869-876.
- Irpino, A., Verde, R., de Carvalho, F. de A.T. 2014. Dynamic clustering of histogram data base don adaptive squared Wasserstein distances. Expert Systems with Applications 41: 3351-3366. **DOI** | 10.1016/j.eswa.2013.12.001

Reference

- Jiang, B., J. Pei, Y. Tao and X. Lin(2013) Clustering uncertain data based on probability distribution similarity. IEEE Transactions on Knowledge and Data Engineering, 25(4), 751--763.
- Lennert-Cody、C. E., Minami, M. Patrick K. Tomlinson, Mark N. Maunder (2010), Exploratory analysis of spatial-temporal patterns in length-frequency data: An example of distributional regression trees, *Fisheries Research,* 102, 323-326
- Lennert-Cody, C. E., Maunder, M. N., Aires-da-Silva, A., & Minami, M. (2013). Defining population spatial units: Simultaneous analysis of frequency distributions and time series. *Fisheries Research*, 139, 85-92.
- Minami, M. and Lennert-Cody, C.E. (2023). Regression Tree and Clustering for Distributions, and Homogeneous Structure of Population Characteristics, submitted
- Nielsen, F., Nock, R. and Amari, S-I. 2014. On clustering histograms with k-Means by using Mixed alpha-Divergences. Entropy 16 (6): 3273-3301.
- Thao Nguyen-Trang, Trung Nguyen-Thoi1, Tai Vo-Van (2023) Globally automatic fuzzy clustering for probability density functions and its application for image data, Applied Intelligence,
- Dinh Phamtoan, Tai Vovan (2022), Automatic fuzzy clustering for probability density functions using the genetic algorithm, Neural Computing and Applications (2022) 34:14609-14625.



Thank you for your attention

Standardized mJS of Nodes

Node ID	Std. mJS	Upper bound	out of 100	out of 1000	p-value	parent node	child nodes	Signicance
59	31.32	0.0010	0		< 0.0010	–	56, 58	**
58	26.81	0.0014	0		< 0.0014	59	57, 54	**
57	28.99	0.0012	0		< 0.0007	58	52, 55	**
56	36.61	0.0007	0		< 0.0007	59	49, 42	**
55	14.20	0.0050	0		< 0.0050	57	40, 53	**
54	15.08	0.0044	0		< 0.0044	58	50, 47	**
53	18.14	0.0030	0		< 0.0030	55	48, 44	**
52	4.28	0.0547	1	3	0.0077	57	20, 51	**
51	9.35	0.0114	0	0	0.0030	52	32, 45	**
50†	4.47	0.0502	1	6	0.0118	54	46, 31	*
49	6.03	0.0275	0	1	0.0047	56	34, 35	**
48	9.94	0.0101	0	0	0.0030	53	30, 43	**
47	59.27	0.0003	0		< 0.0003	54	−42†, 21	**
46_	9.01	0.0123	0	0	0.0030	50	25, 38	*
45†	2.38	0.1759	5	31	0.0416	51	39,19	*
44	6.50	0.0237	0	0	0.0030	53	36, 37	**
43†	2.45	0.1662	6	37	0.0484	48	41, -43	*
42†	2.59	0.1490	1	19	0.0278	56	29, 33	*
41	9.64	0.0108	0	0	0.0030	43	22, 9	*