

The screenshot shows the RStudio interface. The top pane displays the Environment window, which lists objects in the global environment. The objects are:

- cancer_data**: 218 obs. of 18 variables
- cancer_data_1**: 218 obs. of 4 variables
- cancer_data_escalado**: num [1:218, 1:4] 0.672 0.76 -1.717 -1.806 -1.806 ...
- conoc_activ_factor_ca...**: 218 obs. of 18 variables
- dist_link_cancer_data**: List of 7
- km_res**: List of 9

Below the Environment window, the Values section shows the value of **dist_cancer_data** as:

```
'dist' num [1:23653] 2.23 3.51 6.17 4.63 2 ...
```

The bottom pane shows the Packages window, which lists installed and available packages. The 'User Library' section is visible, showing a list of installed packages with their versions and update status (indicated by checkboxes and icons).

Name	Description	Version
<input type="checkbox"/> abind	Combine Multidimensional Arrays	1.4-8
<input type="checkbox"/> askpass	Password Entry Utilities for R, Git, and SSH	1.2.1
<input type="checkbox"/> backports	Reimplementations of Functions Introduced Since R-3.0.0	1.5.0
<input type="checkbox"/> base64enc	Tools for base64 encoding	0.1-3
<input type="checkbox"/> bayestestR	Understand and Describe Bayesian Models and Posterior Distributions	0.16.0
<input type="checkbox"/> bdsmatrix	Routines for Block Diagonal Symmetric Matrices	1.3-7
<input type="checkbox"/> BiasedUrn	Biased Urn Model Distributions	2.0.12
<input type="checkbox"/> bigD	Flexibly Format Dates and Times to a Given Locale	0.3.1
<input type="checkbox"/> bit	Classes and Methods for Fast Memory-Efficient Boolean Selections	4.6.0

EnvironmentHistoryConnectionsTutorial

Global Environment

18 MiB

Data

cancer_data	218 obs. of 18 variables
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Values

dist_cancer_data	'dist' num [1:23653] 2.23 3.51 6.17 4.63 2 ...
------------------	--

Ahora con el escalado:

```
{r}
head(cancer_data_escalado)
```

	edad	edad_relacion_sexual	parejas_sex	num_hijos
1	0.6716910	1.5824717	-0.2996692	0.71040667
2	0.7601676	-0.5709542	-0.8882088	0.71040667
3	-1.7171751	-0.5709542	0.8774100	-0.04505018
4	-1.8056516	-0.5709542	4.4086475	-1.55596388
5	-1.8056516	-0.5709542	2.0544892	-1.55596388
6	-0.6554568	0.2904162	-0.2996692	-0.04505018

Calculo de distancias:

```
{r}
dist_cancer_data <- dist(cancer_data_escalado, method = "euclidean")
```

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18 MiB

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------------------	--

Visualizamos las distancias euclidianas en un mapa de calor:

```
{r}
fviz_dist(dist_cancer_data)
```

Nuestro mapa de calor donde se visualiza la matriz de distancias euclidianas de nuestras muestras de

(Top Level)

EnvironmentHistoryConnectionsTutorial

Global Environment

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Nuestro mapa de calor donde se visualiza la matriz de distancias euclidianas de nuestras muestras de

datos de "dist_cancer_data". Los tonos más claros (naranja/blanco) indican distancias menores (mayor

similitud), mientras que los tonos más oscuros (violeta/azul) representan distancias mayores (menor

similitud). Se observa una estructura de bloques, sugiriendo la **presencia de clústeres o agrupaciones**

naturales dentro de los datos, donde **las muestras dentro de un bloque son más similares entre sí**

que con las muestras de otros bloques.

Usamos el metodo de agrupamiento: Funcion de enlace (linkage)

```
{r}
dist_link_cancer_data <- hclust(d = dist_cancer_data, method = "ward.D2")
```

Empleamos los dendogramas par la visualizacion de los patrones:

```
{r}
fviz_dend(dist_link_cancer_data, cex = 0.7)
```

Cluster Dendrogram

20 -

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins

Untitled1* cancer_data_escalado cancer_data_1 conoc_actit_factor_cancer_cervical

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Empleamos los dendrogramas par la visualizacion de los patrones:

```
{r}
fviz_dend(dist_link_cancer_data, cex = 0.7)
```

Cluster Dendrogram

Height

(Top Level) Quarto

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En nuestro dendrograma, vemos la representación gráfica del análisis de clúster jerárquico. En el eje Y, "Height", indica la distancia o disimilitud a la que los clústeres se fusionan. Las ramas que se unen a alturas bajas representan muestras o grupos de muestras muy similares. A medida que se asciende en el dendrograma, las uniones ocurren a mayores distancias, indicando la formación de clústeres más grandes y heterogéneos. La estructura ramificada revela la jerarquía de las agrupaciones, permitiendo identificar subgrupos dentro de los datos.

Revisamos los grupos que se formaron en el dendrograma:

```
{r}
fviz_dend(dist_link_cancer_data,
  k = 3,
  cex = 0.5,
  k_colors = c("#e700a9", "#00ce70", "#e70400"),
  color_labels_by_k = TRUE,
  rect = TRUE)
```

Cluster Dendrogram

Height

(Top Level) Quarto

Console

Go to file/function Addins

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Cluster Dendrogram

Height

Project (None)

Environment History Connections Tutorial

Import Dataset 17 MiB

R Global Environment

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Untitled1* cancer_data_escalado cancer_data_1 conoc_actit_factor_cancer_cervical

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Se muestran los resultados de un análisis de clúster jerárquico, donde se han identificado y visualizado K=3 grupos distintos, según la instrucción del código (k=3). Cada color (magenta, verde, rojo) representa uno de los tres clústeres. Las líneas punteadas verticales indican los límites de estos clústeres. La "Height" en el eje Y sigue representando la disimilitud. La segmentación visual facilita la interpretación de las agrupaciones de las muestras, revelando patrones y relaciones inherentes dentro del conjunto de datos.

Estimamos el numero optimo de clusters:

1º escalamos los datos:

```
{r}
cancer_data_escalado = scale(cancer_data_1)
```

2º Graficamos la suma de cuadrados dentro de los graficos:

```
{r}
fviz_nbclust(cancer_data_escalado, kmeans, nstart = 25, method = "wss") +
  geom_vline(xintercept = 3, linetype = 2)
```

Optimal number of clusters

(Top Level) Quarto Console

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<input type="checkbox"/> bit	Classes and Methods for Fast Memory-Efficient Boolean Selections	4.6.0
<input type="checkbox"/> bit64	A S3 Class for Vectors of 64bit Integers	4.6.0-1

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```
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Optimal number of clusters

(Top Level) Quarto Console

Se muestra la "Total Within Sum of Square" (WCSS) en función del número de clústeres (k). Se busca el

Environment History Connections Tutorial

Import Dataset 17 MiB

R Global Environment

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Se muestra la "Total Within Sum of Square" (WCSS) en función del número de clústeres (k). Se busca el punto de inflexión, o "codo", donde la disminución marginal de WCSS se estanca. La línea punteada indica k=3 como el número óptimo, sugiriendo que más de tres clústeres no aportan una reducción significativa en la varianza intra-clúster.

Calculamos el agrupamiento de los k-means:

```
{r}
set.seed(123)
km_res <- kmeans(cancer_data_escalado, 3, nstart = 25)
```

```
{r}
km_res
```

K-means clustering with 3 clusters of sizes 163, 49, 6

Cluster means:

	edad	edad_relacion_sexual	parejas_sex	num_hijos
1	0.4735688	0.01298091	-0.1191356	0.3303609
2	-1.4535511	0.03552084	-0.1675481	-1.0626043
3	-0.9946168	-0.64273506	4.6048274	-0.2968691

Clustering_vector:

Environment History Connections Tutorial

Import Dataset 18 MiB

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```
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km_res <- kmeans(cancer_data_escalado, 3, nstart = 25)
```

```
{r}
km_res
```

K-means clustering with 3 clusters of sizes 163, 49, 6

Cluster means:

	edad	edad_relacion_sexual	parejas_sex	num_hijos
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3	-0.9946168	-0.64273506	4.6048274	-0.2968691

Clustering vector:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
21	22	23	1	1	2	3	2	1	2	1	1	2	2	2	2	2	1	2	1	2
2	1	2	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41
42	43	44	45	46	3	2	3	2	2	2	2	2	2	2	2	2	1	1	1	1
1	1	1	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	1	1	1	1	2	2	1	1	1	1	1	1	1	2	1	2
2	2	2	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87
88	89	90	91	92	1	2	1	1	1	2	1	1	2	1	2	3	2	1	1	1
1	2	3	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
111	112	113	114	115																

Chunk 14

Console

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113 114 115

1	1	1	1	1	1	2	1	1	1	1	2	2	1	1	1	2	1	1	1
1	1	1	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132
133	134	135	136	137	138	1	1	1	1	1	1	1	1	1	1	1	1	1	1
1	1	1	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155
156	157	158	159	160	161	1	1	1	1	1	1	1	1	1	2	1	1	1	1
1	1	1	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178
179	180	181	182	183	184	1	1	3	1	1	1	1	1	1	1	1	1	1	1
1	1	1	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201
202	203	204	205	206	207	1	1	1	1	1	1	1	1	1	1	1	1	1	2
1	2	1	208	209	210	211	212	213	214	215	216	217	218	1	1	1	1	1	1

Within cluster sum of squares by cluster:

[1]	331.35589	142.43927	41.05674
-----	-----------	-----------	----------

(between_SS / total_SS = 40.7 %)

Available components:

[1]	"cluster"	"centers"	"totss"	"withinss"	"tot.withinss"
[6]	"betweenss"	"size"	"iter"	"ifault"	

Console

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Visualizamos los clusters k-means

```
{r}
fviz_cluster(
  km_res,
  data = cancer_data_escalado,
  palette = c("#0064E7", "#E67E22", "#F1C40F"),
  ellipse.type = "euclid",
  repel = TRUE,
  ggtheme = theme_minimal()
)
```

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Console

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R Global Environment

Data

cancer_data	218 obs. of 18 variables
cancer_data_1	218 obs. of 4 variables
cancer_data_escalado	num [1:218, 1:4] 0.672 0.76 -1.717 -1.806 -1.806 ...
conoc_activ_factor_cancer...	218 obs. of 18 variables
dist_link_cancer_data	List of 7
km_res	List of 9

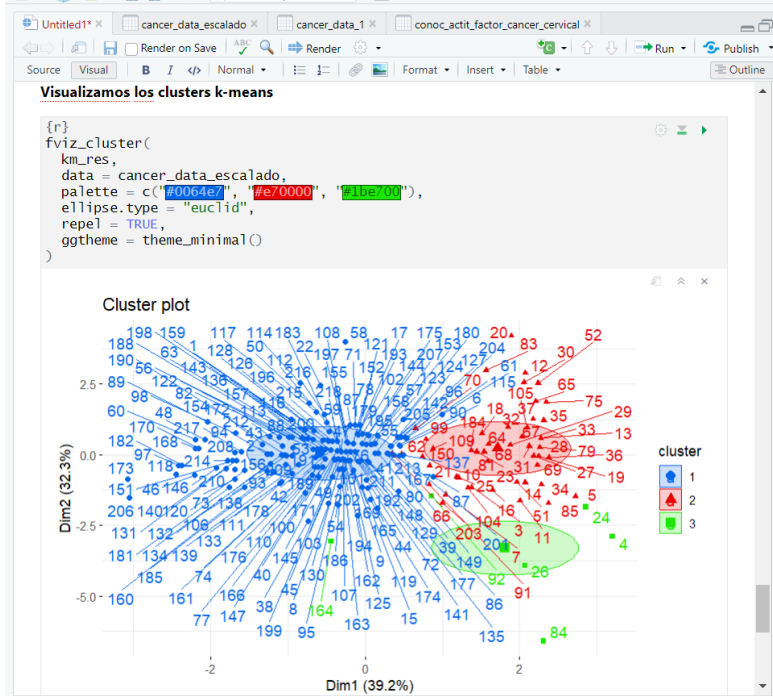
Values

dist_cancer_data	'dist' num [1:23653] 2.23 3.51 6.17 4.63 2 ...
------------------	--

Files Plots Packages Help Viewer Presentation

Install Update

Name	Description	Version
User Library		
abind	Combine Multidimensional Arrays	1.4-8
askpass	Password Entry Utilities for R, Git, and SSH	1.2.1
backports	Reimplementations of Functions Introduced Since R-3.0.0	1.5.0
base64enc	Tools for base64 encoding	0.1-3
bayestestR	Understand and Describe Bayesian Models and Posterior Distributions	0.16.0
bdsmatrix	Routines for Block Diagonal Symmetric Matrices	1.3-7
BiasedUrn	Biased Urn Model Distributions	2.0.12
bigD	Flexibly Format Dates and Times to a Given Locale	0.3.1
bit	Classes and Methods for Fast Memory-Efficient Boolean Selections	4.6.0



Environment History Connections Tutorial

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CONCLUSION:

The screenshot shows the RStudio interface. The top pane is the Environment pane, displaying a list of objects in the Global Environment. The objects are:

- `cancer_data`: 218 obs. of 18 variables
- `cancer_data_1`: 218 obs. of 4 variables
- `cancer_data_escalado`: num [1:218, 1:4] 0.672 0.76 -1.717 -1.806 -1.806 ...
- `conoc_activ_factor_ca...`: 218 obs. of 18 variables
- `dist_link_cancer_data`: List of 7
- `km_res`: List of 9

Below the Environment pane is the Files pane, which shows the User Library. The library contains the following packages:

Package	Description	Version
<code>abind</code>	Combine Multidimensional Arrays	1.4-8
<code>askpass</code>	Password Entry Utilities for R, Git, and SSH	1.2.1
<code>backports</code>	Reimplementations of Functions Introduced Since R-3.0.0	1.5.0
<code>base64enc</code>	Tools for base64 encoding	0.1-3
<code>bayestestR</code>	Understand and Describe Bayesian Models and Posterior Distributions	0.16.0
<code>bdsmatrix</code>	Routines for Block Diagonal Symmetric Matrices	1.3-7
<code>BiasedUrn</code>	Biased Urn Model Distributions	2.0.12

