Data Manipulation - Dplyr

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Questions

Perform the following operations on the attached file using methods available in the dplyr library

- 1) Select the first three columns
- 2) Select all columns except the species column
- 3) Select all the rows where both diameter and height are greater than 20
- 4) Arrange the rows by height
- 5) Arrange the rows by Species and then by height
- 6) Create a new column by dividing the leafarea with branchmass
- 7) Find the average diameter for each species
- 8) Create a new data frame containing 10th to 35th rows of the data

Code □ □ 4 p > x ? ● PRASHANTH S 19MID0020 ▼ Description ★ dplyr_library.R 🛭 Allometry.csv 🕄 Perform the following operations on the attached file using methods available in the dplyr library 4 df=read.csv("Allometry.csv") 6 ## 1st 3 columns 7 ans1 <- data f ans1 <- data.frame(df %>% select(c(1:3))) 8 #head(ans1) 10 ## exclude the species colum 2) Select all columns 11 ans2 <- data.frame(df %>% select(-species))
12 #head(ans2) ## take out the rows where the (diameter and height) > 20
ans3 <- (df %% filter(diameter > 20 & height > 20))
take out the rows where the (diameter and height) > 20
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take out the rows where rows where the rows where the rows where the rows where rows where the rows where 3) Select all the rows and height are greater than 20 4) Arrange the rows by height 5) Arrange the rows by Species and then by height by dividing the leafarea with branchmass 7) Find the average diameter for each species 8) Create a new data frame containing 10th to 35th rows of the data 34 35 ## 10 to 35 row of the data 36 ans8 = df %>% slice(10:35) 37 #ans8 https://moovit.vit.ac.in/



Mam, I implemented the code in moodle as-well as in RStudio also. In-order to avoid confusion with continuous output, I am including my implementation in RStudio also.

Data Manipulation - Dplyr

Importing the libraries

	Hide
library(dplyr)	
Attaching package: 'dplyr'	
The following objects are masked from 'package:stats':	
filter, lag	
The following objects are masked from 'package:base':	
intersect, setdiff, setequal, union	

Importing the data-sets

				1.11.00
<pre>df = read.csv('Allometry head(df)</pre>	/.CSV')			
species	diameter	height	leafarea	branchmass
<chr></chr>	<qp>></qp>	<dp>></dp>	<qp>></qp>	<qpl></qpl>
1 PSME	54.61	27.04	338.485622	410.24638
2 PSME	34.80	27.42	122.157864	83.65030
3 PSME	24.89	21.23	3.958274	3.51270
4 PSME	28.70	24.96	86.350653	73.13027
5 PSME	34.80	29.99	63.350906	62.39044
6 PSME	37.85	28.07	61.372765	53.86594
6 rows				

1) Select the first three columns

			Hide
	<pre>1 <- data.frame(df %>% select(c(1:3))) d(ans1)</pre>		
	species <chr></chr>	diameter <db ></db >	height <dbl></dbl>
1	PSME	54.61	27.04
2	PSME	34.80	27.42
3	PSME	24.89	21.23
4	PSME	28.70	24.96
5	PSME	34.80	29.99
6	PSME	37.85	28.07
6 rov	NS		

2) Select all columns except the species column

				Hide
ans2 <- data head(ans2)	a.frame(df %>% select(-sp	pecies))		
	diameter	height	leafarea	branchmass
	<qpl></qpl>	<dpl></dpl>	<dbl></dbl>	< db >
1	54.61	27.04	338.485622	410.24638
2	34.80	27.42	122.157864	83.65030
3	24.89	21.23	3.958274	3.51270
4	28.70	24.96	86.350653	73.13027
5	34.80	29.99	63.350906	62.39044
6	37.85	28.07	61.372765	53.86594
6 rows				

than 20

3) Select all the rows where both diameter and height are greater

			Hide
diameter > 20 & height >	20))		
diameter	height	leafarea	branchmass
<qpl></qpl>	<dbl></dbl>	<qpl></qpl>	<dpl></dpl>
54.61	27.04	338.485622	410.24638
34.80	27.42	122.157864	83.65030
24.89	21.23	3.958274	3.51270
28.70	24.96	86.350653	73.13027
34.80	29.99	63.350906	62.39044
37.85	28.07	61.372765	53.86594
	diameter <dbl> 54.61 34.80 24.89 28.70 34.80</dbl>	<dbl></dbl> 54.61 27.04 34.80 27.42 24.89 21.23 28.70 24.96 34.80 29.99	diameter height leafarea <dbl> <dbl> 54.61 27.04 338.485622 34.80 27.42 122.157864 24.89 21.23 3.958274 28.70 24.96 86.350653 34.80 29.99 63.350906</dbl></dbl>

ans4 = df %>% arrange(height)

4) Arrange the rows by height

species <chr></chr>	diameter <dbl></dbl>	height <dbl></dbl>	leafarea <dbl></dbl>	branchmas: <dbl:< th=""></dbl:<>
1 PIPO	4.83	3.57	2.636336	1.7781
2 PSME	5.33	4.95	4.851567	2.6706
3 PIMO	8.38	4.95	6.551044	4.3696
4 PSME	6.10	5.26	7.595163	3.5714
5 PIMO	6.48	5.42	7.650902	3.5062
6 PSME	7.37	5.58	11.502851	4.5891
rows				

Hide

Hide

ans5 = df %>% arrange(species, height) head(ans5)

species	diameter	height	leafarea	branchmass
<chr></chr>	<dpl></dpl>	<dbl></dbl>	<dbl></dbl>	<dpl></dpl>
\t \	NA	NA	NA	NA
PIMO	8.38	4.95	6.551044	4.36969
PIMO	6.48	5.42	7.650902	3.50621
PIMO	18.29	12.98	82.093031	28.04785
PIMO	12.95	13.44	18.855867	8.71068
PIMO	18.54	21.29	44.934469	16.54457
rows				

ans6 = df %>% mutate(leftarea_divide_branchmass = leafarea / branchmass) head(ans6)

species <chr></chr>	diameter <dbl></dbl>	height <dbl></dbl>	leafarea <dbl></dbl>	branchmass <db ></db >	leftarea_divide_branchmass <dbl></dbl>
1 PSME	54.61	27.04	338.485622	410.24638	0.8250789
2 PSME	34.80	27.42	122.157864	83.65030	1.4603398
3 PSME	24.89	21.23	3.958274	3.51270	1.1268466
4 PSME	28.70	24.96	86.350653	73.13027	1.1807785
5 PSME	34.80	29.99	63.350906	62.39044	1.0153944
6 PSME	37.85	28.07	61.372765	53.86594	1.1393613
6 rows					
7) Find th	ie avera	ge diar	neter for e	each species	
					Hide

ans7 = df %>% group_by(species) %>% summarize(avg_diameter = mean(diameter)) head(ans7)

species <chr></chr>	avg_diameter <dbl></dbl>
t \t	NA
PIMO	37.28842
PIPO	36.56500
PSME	33.05500
rows	

species	diameter		leafarea	branchmass
<chr></chr>	<dbl></dbl>	<dpl></dpl>	<qp>></qp>	<db< th=""></db<>
1 PSME	26.16	25.85	45.02004	45.3309
2 PSME	43.69	31.83	145.80980	96.3231
3 PSME	69.85	31.35	349.05701	543.9733
4 PSME	44.45	32.61	176.02921	110.1247
5 PSME	56.64	31.70	319.50711	260.487
6 PSME	54.61	30.18	234.36878	281.123