

ds4biomed

Summative

Pre-Workshop Exercise

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This is the `cmv` dataset you will load:

ID	ag	prior.radiation	aK...	cm	donor_negati				
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>				
1	61	0	1	1	recipient_posit				
2	62	1	5	0	recipient_nega				
3	63	0	3	0	NA				
4	33	1	2	0	recipient_posit				
5	54	0	6	0	NA				
6	55	0	2	1	NA				
7	67	0	1	0	NA				
8	51	0	2	0	NA				
9	44	1	2	1	NA				
10	59	0	4	0	recipient_nega				
1-1...	Previous	1	2	3	4	5	6	7	Next

1. Use the `readxl` library to load the `data/cmv.xlsx` into a variable, `cmv`.
2. Filter the `cmv` dataset such that only age > 65 are remaining. Save this to a variable, `cmv_subset`.
3. Save the `cmv_subset` variable to a `csv` file in `"data/cmv_subset.csv"`.

R Code

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Run Code

```
1 library(readxl)
2 read_xlsx()
3
```

4. Tidy the `cmv` dataset such that it looks like the `clean` dataset below. Save the tidy dataset into a variable, `cmv_tidy`.

ID	age	prior.radiation	aK...	cm	donor_status
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
1	61	0	1	1	donor_negativ
2	62	1	5	0	donor_negativ

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ID	age	prior.radiation	aK...	cmv	donor_status
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
3	63	0	3	0	donor_positive
4	33	1	2	0	donor_negative
5	54	0	6	0	donor_positive
6	55	0	2	1	donor_positive
7	67	0	1	0	donor_positive
8	51	0	2	0	donor_positive
9	44	1	2	1	donor_positive
10	59	0	4	0	donor_negative

1-1... Previous 1 2 3 4 5 6 7 Next

R Code

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 Run Code

```
1 |
2 |
3 |
```

5. In the `cmv_tidy` dataset, calculate the average
age for each value of `cmv`.

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```
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```

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