Final Assignment

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Data set 1: Biomedical Data

Introduction

Data and Methods

m3	m2	m1	date	age
10.9	83.5	52	60079	22
11.0	77.0	20	80078	32
13.2	86.5	28	70078	36
22.6	104.0	30	110079	22
15.2	83.0	40	10078	23
9.6	78.8	24	50079	30
	10.9 11.0 13.2 22.6 15.2	83.5 10.9 77.0 11.0 86.5 13.2 104.0 22.6 83.0 15.2	52 83.5 10.9 20 77.0 11.0 28 86.5 13.2 30 104.0 22.6 40 83.0 15.2	60079 52 83.5 10.9 80078 20 77.0 11.0 70078 28 86.5 13.2 110079 30 104.0 22.6 10078 40 83.0 15.2

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age	date	m1	m2	m3	m4
30	100078	167	89	25.6	364
41	100078	104	81	26.8	245
22	80079	30	108	8.8	284
22	80079	44	104	17.4	172
20	100078	65	87	23.8	198
42	90078	440	107	20.2	239

Results

Conclusion

Data Set 2: DNA Data

Introduction

Data and Methods

 Results

Conclusion

Future Work

Appendix

```
## complete source code for this document can be found at:
## https://github.com/joelstrouts/PDS-week-9
## Reading Data
## =======
get_fpath <-
  {function (fname) paste("../resources/data-sets/", fname, sep="")}
read_transpose_df <-</pre>
  {function (fpath, ...) as.data.frame(t(read.table(fpath, ...)))}
df_blood_samples_n <- read.table(get_fpath("normals.txt"), header = TRUE)</pre>
df_blood_samples_c <- read.table(get_fpath("carriers.txt"), header = TRUE)</pre>
df_human_phage_dna <- read.table(get_fpath("human-phage.txt"))</pre>
knitr::kable(head(df_blood_samples_n))
knitr::kable(head(df_blood_samples_c))
knitr::kable(head(df_human_phage_dna))
## End of Document
## =======
```