\mathbf{R}

Tablular Data

Reading tables:

```
df = read.table("path/filename.csv") # default tab separated
df = read.csv("path/filename.csv") # default comma separated
df = data.table::fread("path/filename.csv", data.table = F) # fast -- preferred!
Writing tables:
write.csv(df, "path/filename.csv") # default comma separated
```

data.table::fwrite(df, "path/filename.csv") # fast -- preferred!

Remember that we examined three kinds of data in TCGA. Data stored as text (.csv) in bold

- 1. Clinical.
- 2. Transcriptomic.
- 3. Mutation.

SummarizedExperiments (Transcriptomics)

Our transcriptomic data was stored as a SummarizedExperiment. Before, we queried it every time, but there's a better way to store it using the HDF5Array package. It'll actually create a separate folder.

MAFs (Mutations)

We stored our MAF data as a giant csv. To convert the csv into a MAF object, we did the following:

Figures

We didn't really discuss how to save figures in R because the syntax is a bit weird, but here is an example below:

```
png("path/img.png")
product to generate your plot
dev.off()
```

Python

Tabular Data

We'll use pandas to open and write tables:

```
import pandas as pd

df = pd.read_csv("path/file.csv")

# do something with df

df.to_csv("path/file.csv")
```

Figures

Instead of using ${\tt plt.show()},$ we just use ${\tt plt.savefig()}:$

```
import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

# make your plot

plt.savefig("path/img.png")
```