

What to do next?

Example

Maybe most usefully, you can also run an R script noninteractively.

Here's an example that I wrote on my laptop.

```
library(plyr)
library(dplyr)
library(tidyr)
library(ggplot2)

print("This is an example of an R Script")
setwd("~/")
mdf <- read.csv("example_metadata.csv", header=TRUE, row.names=1)
mdf.summary <- mdf %>% group_by(Species, Age, Sex, Reprod) %>% tally()
mdf.summary <- data.frame(mdf.summary)
print("I'm running a summary")
write.csv(mdf.summary, "mdfsummary.csv")

print("I'm printing a graphic")
theme_set(theme_classic(base_size=12, base_family="serif"))
ggplot(mdf.summary, aes(x=Species, y=n, fill=Sex)) + geom_bar(stat="identity") + scale_fill_manual(values=c("black", "gray"))

ggsave("mdftallies.png", width=5, height=5, units="in", dpi=300)

print("Script completed succesfully!")
```

If you want to follow along in this section, download the R script and metadata here: <https://github.com/mgaley-004/MiSeq-Analysis/tree/main/Help>

Before running it, I need to make sure I have installed any libraries I use on MSI and then upload the script. I also need to upload “example_metadata.csv” since my script reads it in.

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Example

To upload files, you **can** use a GUI like WinFCP or FileZilla, but I would really encourage you to try using sftp directly through the terminal.

In a new window: Connect using either ssh (mac/linux) or pUTTy.

You must first navigate to the folder where your files are, like this:

```
cd /volumes/dean/chunlab/meetings
```

Then connect like this:

```
sftp yourx500@login.msi.umn.edu
```