Discharge

library(glue)  
library(readxl)  
library(tidyverse)

── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
✔ dplyr 1.1.2 ✔ readr 2.1.4  
✔ forcats 1.0.0 ✔ stringr 1.5.0  
✔ ggplot2 3.4.2 ✔ tibble 3.2.1  
✔ lubridate 1.9.2 ✔ tidyr 1.3.0  
✔ purrr 1.0.1   
── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
✖ dplyr::filter() masks stats::filter()  
✖ dplyr::lag() masks stats::lag()  
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library(gtsummary)

Warning: package 'gtsummary' was built under R version 4.3.1

library(rio)

Warning: package 'rio' was built under R version 4.3.1

Data <- import\_list("ENVIRONMENTAL.xlsx")  
  
species <- Data$Sheet2  
discharge <- Data$Sheet1  
  
species |> select(-1)

Species Sampling site  
1 Anguilla mossambica Midstream  
2 Anguilla bengalensis Midstream  
3 Anguilla bengalensis Downstream  
4 Anguilla marmorata Downstream  
5 Anguilla mossambica Downstream  
6 Anguilla mossambica Midstream  
7 Anguilla bengalensis Upstream  
8 Anguilla bengalensis Midstream  
9 Anguilla mossambica Midstream  
10 Anguilla mossambica Downstream  
11 Anguilla bengalensis Downstream  
12 Anguilla mossambica Downstream  
13 Anguilla bengalensis Midstream  
14 Anguilla bengalensis Midstream  
15 Anguilla bengalensis Midstream  
16 Anguilla mossambica Midstream  
17 Anguilla bengalensis Midstream  
18 Anguilla mossambica Midstream  
19 Anguilla bengalensis Upstream  
20 Anguilla bengalensis Upstream  
21 Anguilla mossambica Upstream  
22 Anguilla bengalensis Upstream  
23 Anguilla bengalensis Upstream  
24 Anguilla bengalensis Midstream  
25 Anguilla bengalensis Midstream  
26 Anguilla bengalensis Midstream  
27 Anguilla mossambica Midstream  
28 Anguilla bengalensis Midstream  
29 Anguilla bengalensis Downstream  
30 Anguilla bengalensis Downstream  
31 Anguilla bengalensis Downstream  
32 Anguilla mossambica Downstream  
33 Anguilla mossambica Downstream  
34 Anguilla mossambica Downstream  
35 Anguilla bengalensis Midstream  
36 Anguilla bengalensis Downstream  
37 Anguilla marmorata Downstream  
38 Anguilla bengalensis Downstream  
39 Anguilla bengalensis Downstream  
40 Anguilla mossambica Downstream  
41 Anguilla mossambica Midstream  
42 Anguilla bengalensis Midstream  
43 Anguilla mossambica Midstream  
44 Anguilla bengalensis Upstream  
45 Anguilla bengalensis Upstream  
46 Anguilla mossambica Upstream  
47 Anguilla mossambica Upstream  
48 Anguilla mossambica Upstream  
49 Anguilla bengalensis Upstream  
50 Anguilla bengalensis Upstream  
51 Anguilla bengalensis Downstream  
52 Anguilla bengalensis Downstream  
53 Anguilla bengalensis Downstream  
54 Anguilla mossambica Downstream  
55 Anguilla bengalensis Downstream  
56 Anguilla bengalensis Upstream  
57 Anguilla bengalensis Upstream  
58 Anguilla bengalensis Upstream  
59 Anguilla bengalensis Midstream  
60 Anguilla bengalensis Midstream  
61 Anguilla bengalensis Midstream  
62 Anguilla bengalensis Midstream  
63 Anguilla bengalensis Upstream  
64 Anguilla bengalensis Upstream  
65 Anguilla bengalensis Midstream  
66 Anguilla mossambica Downstream  
67 Anguilla bengalensis Downstream  
68 Anguilla bengalensis Midstream  
69 Anguilla bengalensis Midstream  
70 Anguilla bengalensis Midstream  
71 Anguilla bengalensis Midstream  
72 Anguilla mossambica Upstream  
73 Anguilla bengalensis Upstream  
74 Anguilla bengalensis Upstream  
75 Anguilla bengalensis Upstream  
76 Anguilla bengalensis Upstream

data <- discharge |>  
 select(`Sampling location`, `Discharge (m3/s)`) |>   
 left\_join(species, join\_by(`Sampling location`==`Sampling site`))

Warning in left\_join(select(discharge, `Sampling location`, `Discharge (m3/s)`), : Detected an unexpected many-to-many relationship between `x` and `y`.  
ℹ Row 1 of `x` matches multiple rows in `y`.  
ℹ Row 1 of `y` matches multiple rows in `x`.  
ℹ If a many-to-many relationship is expected, set `relationship =  
 "many-to-many"` to silence this warning.

## Discharge

data |> select(Species, `Discharge (m3/s)`) |>   
 tbl\_summary(by = Species,  
 statistic = `Discharge (m3/s)` ~ "{mean}") |> add\_p() |> as\_gt()

| **Characteristic** | **Anguilla bengalensis**, N = 251*1* | **Anguilla marmorata**, N = 4*1* | **Anguilla mossambica**, N = 100*1* | **p-value***2* |
| --- | --- | --- | --- | --- |
| Discharge (m3/s) | 8 | 1 | 8 | 0.10 |
| *1*Mean | | | | |
| *2*Kruskal-Wallis rank sum test | | | | |