Response function summary

RFxSum <- read_csv("Response_Fx_Summary.csv")</pre>

```
## Parsed with column specification:
## cols(
## Study = col_character(),
## Chemical = col_character(),
## Class = col_character(),
## Pathway = col_character(),
## Species = col_character(),
## Type = col_character(),
## Response = col_character()
```

table(RFxSum\$Chemical, RFxSum\$Pathway)

##							
##		${\tt bottom-up}$	direct	larvae	direct	${\tt snail}$	top-down
##	2,4-D	0		0		0	3
##	Ammonium Phosphate	0		2		1	0
##	Atrazine	3		3		3	0
##	Azinphos-methyl	0		0		1	0
##	Butachlor	0		2		1	1
##	Butralin	0		2		2	0
##	Carbaryl	0		0		0	5
##	Carbofuran	0		0		0	1
##	Chlorpyrifos	0		2		3	4
##	Cypermethrin	0		0		0	1
##	Deltamethrin	0		0		1	1
##	Diazinon	0		0		2	0
##	Dichlorvos	0		0		0	1
##	Dimethoate	0		0		0	1
##	Endosulfan	0		0		2	3
##	Esfenvalerate	0		0		0	1
##	Fenitrothion	0		0		0	3
##	Fertilizer	2		0		5	0
##	Fluazifop-p-butyl	0		2		1	0
##	Glyphosate	0		4		4	0
##	Lambda-cyhalothrin	0		0		0	2
##	Malathion	0		2		5	2
##	Methyldemeton	0		0		0	1
##	Metolachlor	0		1		0	0
##	Monocrotophos	0		0		0	1
##	MSMA	0		0		0	1
##	Oryzalin	0		0		0	1
##	Paraquat	0		0		1	0
##	Pendimethalin	0		2		2	0
##	Permethrin	0		0		0	1
##	Phosphamidon	0		0		0	1
##	Potassium Sulphate	0		0		1	0

```
##
    Profenofos
                           0
##
    Quinalphos
                          0
                                       0
                                                 0
                                                          1
    Terbufos
                          0
                                      0
                                                 0
                                                          2
##
##
    Tributyltin
                         0
                                      0
                                                 0
                                                          1
                                                          2
    Trifluralin
                          0
                                       0
                                                  0
##
                                                  1
                                                          0
##
    Urea
```

```
RFxSum %>%
  group_by(Chemical, Pathway) %>%
  summarise(n = n()) \%>\%
  spread(key = Pathway, value = n) %>%
  rename("bottom_up" = !!names(.[2]),
         "direct_larvae" = !!names(.[3]),
         "direct_snail" = !!names(.[4]),
         "top_down" = !!names(.[5]),) %>%
  mutate(num_records = sum(bottom_up, direct_larvae,
                           direct_snail, top_down, na.rm = TRUE)) %>%
  filter(num_records > 1) %>%
  select(-num_records) %>%
  replace_na(list("bottom_up" = 0,
                  "direct_larvae" = 0,
                  "direct_snail" = 0,
                  "top_down" = 0)) %>%
  knitr::kable()
```

Chemical	$bottom_up$	${\rm direct_larvae}$	${\rm direct_snail}$	top_down
2,4-D	0	0	0	3
Ammonium Phosphate	0	2	1	0
Atrazine	3	3	3	0
Butachlor	0	2	1	1
Butralin	0	2	2	0
Carbaryl	0	0	0	5
Chlorpyrifos	0	2	3	4
Deltamethrin	0	0	1	1
Diazinon	0	0	2	0
Endosulfan	0	0	2	3
Fenitrothion	0	0	0	3
Fertilizer	2	0	5	0
Fluazifop-p-butyl	0	2	1	0
Glyphosate	0	4	4	0
Lambda-cyhalothrin	0	0	0	2
Malathion	0	2	5	2
Pendimethalin	0	2	2	0
Profenofos	0	2	3	2
Terbufos	0	0	0	2
Trifluralin	0	0	0	2
Urea	0	2	1	0