Sankay Plots of Workshop Comments

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Contents

Introduction

CBEP recently received a grant from NSF's CIVIC Innovation Challenge to work on developing hydrodynamic models that address community needs in Portland Harbor. As part of the project, CBEP hosted three community workshops in November of 2022.

Facilitators produced both "live" notes during the meeting – visible to all on a screen at the front of the meeting room – and detailed meeting transcripts. CBEP staff then reviewed those notes paragraph by paragraph, and coded each paragraph in terms of six characteristics:

- Potential users and uses of hydrodynamic models,
- Data or information needs identified by community members,
- Implied extensions of the initial Casco Bay Model required to fully address those data needs, and
- Ideas for improving communications of model results (e.g., communications channels and user interface design),
- Specifications for model performance or capabilities such as resolution, geographic coverage or ability to conduct simulations.
- Suggestions about monitoring or data collection that could improve information availability.

If a paragraph or live note included something relevant to one or more of these categories, we summarized the related idea, and then assigned each paragraph or comment to categories. In this way we cn look at what ideas were expressed most commonly during the workshops.

Of course, not all paragraphs include information related to each of the five types of information, so there is not a perfect one-to-one correspondence between categories.

In this R Notebook, I explore these data principally by looking at cross-correlations among ideas in the different categories.

Load Packages

```
library(tidyverse)
#> -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
#> v ggplot2 3.4.0      v purrr   0.3.5
#> v tibble  3.1.8      v dplyr   1.0.10
#> v tidyr   1.2.1      v stringr 1.5.0
#> v readr   2.1.3      v forcats 0.5.2
```

```
#> -- Conflicts ---------------------------------------- tidyverse_conflicts() --
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag()    masks stats::lag()
library(readxl)
library(networkD3)  #an alternative might be the riverplot package

theme_set(theme_classic())
```

Create Figures Folder

```
dir.create(file.path(getwd(), 'figures'), showWarnings = FALSE)
```

Load Data

```
the_data <- read_excel("Data_Export_Query.xlsx" ) %>%
  mutate(ID = as.integer(ID)) %>%
  rename_with(function(x) sub(" Category_Category", '_Category', x)) %>%
  rename_with(function(x) sub(" ", '_', x))
head(the_data)
#> # A tibble: 6 x 16
#>      ID Category   Day   Comment User_~1 Inter~2 Inter~3 Data_~4 Data_~5 Exten~6
#>   <int> <chr>      <chr> <chr>   <chr>   <chr>   <chr>   <chr>     <dbl> <chr>
#> 1     1 Live Comm~ Day ~ How ca~ Urban ~ Simple  Exampl~ <NA>         NA Draina~
#> 2     2 Live Comm~ Day ~ Use of~ Harbor~ <NA>    <NA>    Waves         4 <NA>
#> 3     2 Live Comm~ Day ~ Use of~ Marine~ <NA>    <NA>    Waves         4 <NA>
#> 4     2 Live Comm~ Day ~ Use of~ Urban ~ <NA>    <NA>    Waves         4 <NA>
#> 5     3 Live Comm~ Day ~ MS4 pr~ Water ~ Inform~ Shared~ <NA>         NA Discha~
#> 6     3 Live Comm~ Day ~ MS4 pr~ Water ~ Inform~ Shared~ <NA>         NA Draina~
#> # ... with 6 more variables: Extension_Timing <dbl>, Monitoring_Category <chr>,
#> #   Monitoring_Data_Group <dbl>, Data_Quality_Category <chr>,
#> #   Data_Quality_Type <dbl>, Data_Quality_Timing <dbl>, and abbreviated
#> #   variable names 1: User_Category, 2: Interface_Category, 3: Interface_Group,
#> #   4: Data_Group, 5: Data_Timing, 6: Extension_Category
```

Our coding was generated in a somewhat sloppy `Access` database, and because of the way SQL works, it is easier to replace numerical values for some groups here, in `R`, rather than before we exported the data from `Access`. I read in the dictionaries here.

```
timing_table <- read_excel("Timing Category.xlsx",
    col_types = c("numeric", "text", "text"))
data_types_table <- read_excel("Data Type.xlsx",
    col_types = c("numeric", "text", "text"))
```

Numerical Values to Strings

And finally I correct the data table to all text entries.

```
the_data <- the_data %>%
  mutate(Data_Timing = timing_table$Timing[match(Data_Timing,
                                                 timing_table$ID)],
         Extension_Timing = timing_table$Timing[match(Extension_Timing,
                                                      timing_table$ID)],
         Data_Quality_Timing = timing_table$Timing[match(Data_Quality_Timing,
                                                      timing_table$ID)]) %>%
  mutate(Monitoring_Data_Group = data_types_table$Group[match(Monitoring_Data_Group,
                                                    data_types_table$ID)],
         Data_Quality_Type = data_types_table$Group[match(Data_Quality_Type,
                                                    data_types_table$ID)])
```

#A Warning about Uniqueness We have to be careful here, because each note or comment can be represented in this data table multiple times. Each paragraph in the meeting transcript might imply several different users, for example. But if there are multiple users and multiple data types, the records got duplicated (in part) in the SQL query. So for any analysis, we need to test for uniqueness of the data. always

We actually have over 400 records, built out of just over 200 unique comments.

```
cat("All rows in the data:\t\t")
#> All rows in the data:
nrow(the_data)
#> [1] 376

cat("Unique comments reviewed:\t")
#> Unique comments reviewed:
the_data %>%
  select(ID) %>%
  unique() %>%
  nrow()
#> [1] 207
```

Sankay Plot Methods

We need to create a network data set, which has to identify links between notes by `Source`, `Target` and `Value`. The `sankeyNetwork()` function from the `networkD3` package on which we rely wants the data in a very specific format.

- It wants to define NODES via a data frame of node labels (and, optionally, node groups that can be used to assign colors to nodes).
- It wants to define links via a data frame containing NUMERIC (integer?) values identifying nodes. The data frame can also include data on link groups for assigning colors to links.
- The integers defining each node must match the order of those nodes in the nodes data frame.

Data Wrangling

For clarity, I break the data wrangling up into discrete steps. That simplifies both explanation and checking intermediate results.

First, we select the user and data information.

We are headed for a display that shown User or Use groups on the left, and Data groups on the right. Both User and Data classifications included a category called simply "Other", for comments that clearly articulated a data request that I could not figure out how to categorize.

Sankey plots need not be unidirectional, so logically, nodes are neither sources nor targets. If I use the same name for both the "User Other" and the "Data Other" categories, the package sees them as the same category, which has unintended effects on plot geometry (since we can then have "Other" as either or both a source or a target.

TO avoid that problem, we have to edit the category names so the two "Other" categories don't look equivalent.

Finally, we convert the (string) data to factors, and sort them in decreasing order of frequency, which may help with later graphic design.

```
tmp <- the_data %>%
  select(ID, User_Category, Data_Group) %>%
  filter(! is.na(User_Category)) %>%
  filter(! is.na(Data_Group)) %>%
  mutate(User_Category = if_else(User_Category == 'Other',
                                 'Other User', User_Category),
         Data_Group = if_else(Data_Group == 'Other',
                                 'Other Data',Data_Group)) %>%
  mutate(User_Category = if_else(User_Category == 'Water Quality',
                                 'Water Quality User', User_Category),
         Data_Group = if_else(Data_Group == 'Water Quality',
                                 'Water Quality Data',Data_Group)) %>%
  mutate(User_Category = fct_infreq(User_Category),
         Data_Group = fct_infreq(Data_Group)) %>%
  unique()
```

We next calculate the number of links between each pair of source and target nodes.

```
tmp2 <- tmp %>%
  group_by(User_Category, Data_Group) %>%
  summarize(weight = n(),
            .groups = 'drop')
```

I add a `groups` variable, to allow me to control the color of the source and target nodes in the diagram.

```
nodes <- tibble(node_name = c(unique(tmp2$User_Category),
                              unique(tmp2$Data_Group)),
                groups = c(rep("A", length(unique(tmp2$User_Category))),
                           rep("B", length(unique(c(tmp2$Data_Group))))))
```

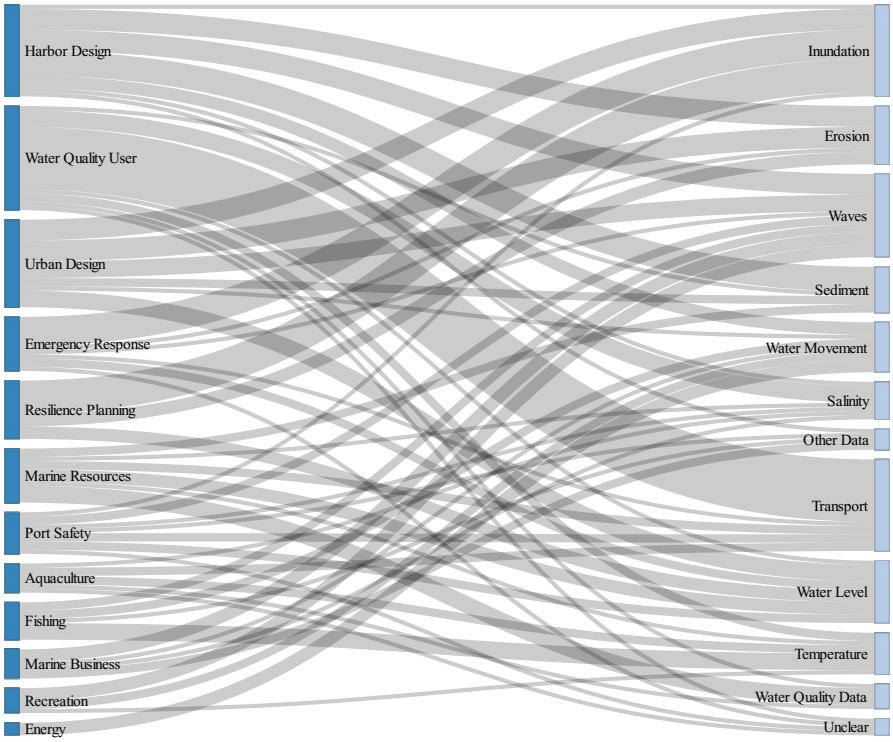
Then we have to convert the character string values in our links data frame (`tmp2`) to zero-valued numerical IDs, as required by the `networkD3` package.

`match()` here is a quick way of implicitly extracting the row number of a matching record from each vector (column) in the `tmp2` data frame.

```
tmp3 <- tmp2 %>%
  mutate(link_group = User_Category,
         User_Category = match(User_Category, nodes$node_name) - 1,
         Data_Group = match(Data_Group, nodes$node_name) - 1)
```

Initial Graphic

```
plt <- sankeyNetwork(Links = tmp3,
             Source = "User_Category",
             Target = "Data_Group",
             Value = "weight",
             Nodes = nodes,
             NodeID = "node_name",
             NodeGroup = 'groups',
             height = 800,
             fontSize = 16,
             iterations = 0)
#> Links is a tbl_df. Converting to a plain data frame.
#> Nodes is a tbl_df. Converting to a plain data frame.
plt
```



Custom Colors

It might be nice to color the nodes or links according to categories. This is surprisingly difficult, because the package uses one color scale for both notes and links.

I found it hard to figure out how colors were ordered, and then found it hard to assemble the correct color specification as required for `network3D`.

I generate new node group names. For the "Source" nodes, we use the name of the user category. For the "Target" nodes, we use an arbitrary string, here `"B"`.

```
users <- as.character(levels(tmp2$User_Category))
types <- as.character(levels(tmp2$Data_Group))

nodes <- tibble(node_name = c(users, types),
                groups = c(users,
                           rep("B", length(unique(c(tmp2$Data_Group))))))
```

We want the links to match the color of the source nodes, so we specify matching color group names for links based on the source (here, left hand) nodes.

```
tmp3 <- tmp2 %>%
  mutate(link_group = as.character(User_Category),
         User_Category = match(User_Category, nodes$node_name) - 1,
         Data_Group = match(Data_Group, nodes$node_name) - 1)
```

Now I have to define my color palette. This is more work than it should be because you have to encapsulate a D3 graphics command in a string so that the `sankeyNetwork()` function can pass it on to the underlying Java / D3 code.

The command requires you to define the names and the colors together as the domain and range of the palette.

I randomize color order to minimize conflict with adjacent nodes. I specify the last color – for the right hand nodes – as a medium purple gray.

```
domain = c(users, "B")
(grps <- length(domain))
#> [1] 13
range <- sample(hcl.colors(15, palette = "viridis"), grps - 1, replace = FALSE)
range <- c(range,"#9090c0")
range
#>  [1] "#25C771" "#1E4D85" "#3C3777" "#4B0055" "#FDE333" "#D4E02D" "#00BA82"
#>  [8] "#008A98" "#006290" "#A6DA42" "#007796" "#73D25B" "#9090c0"
```

In the next step I build a data frame containing the domain and range. It is probably not strictly necessary, but it did avoid some odd artifacts with escaped quotes.

```
cols <- tibble(d = domain, r = range)
cols
#> # A tibble: 13 x 2
#>    d                  r
#>    <chr>              <chr>
#>  1 Harbor Design      #25C771
```

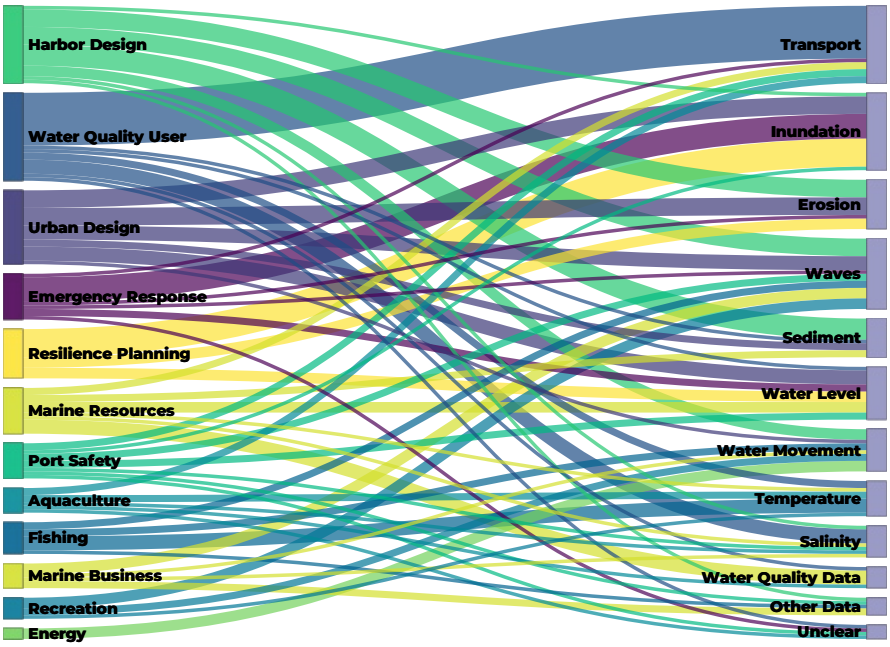
```
#>  2 Water Quality User  #1E4D85
#>  3 Urban Design        #3C3777
#>  4 Emergency Response  #4B0055
#>  5 Resilience Planning #FDE333
#>  6 Marine Resources    #D4E02D
#>  7 Port Safety         #00BA82
#>  8 Aquaculture         #008A98
#>  9 Fishing             #006290
#> 10 Marine Business     #A6DA42
#> 11 Recreation          #007796
#> 12 Energy              #73D25B
#> 13 B                   #9090c0
```

The colors are assembles as a string, which takes some fussy work to do programmatically using `paste()`. Basically, I concatenate the text needed for the D3 function call with the lists of domain and range I just built.

```
the_colors <- paste0('d3.scaleOrdinal() .domain(["',
                     paste(cols$d, collapse='", "'),
                     '"]) .range(["',
                      paste(cols$r, collapse='", "'),
                     '"])')
cat(the_colors)
#> d3.scaleOrdinal() .domain(["Harbor Design", "Water Quality User", "Urban Design", "Emergency Respons
```

Revised Graphic

```
plt <- sankeyNetwork(Links = tmp3,
             Source = "User_Category",
             Target = "Data_Group",
             Value = "weight",
             LinkGroup = "link_group",
             NodeGroup = "groups",
             Nodes = nodes,
             NodeID = "node_name",
             colourScale = the_colors,
             nodeWidth = 20,
             nodePadding = 10,
             height = 700,
             fontSize = 16,
             fontFamily = 'Montserrat ExtraBold',
             iterations = 0)
#> Links is a tbl_df. Converting to a plain data frame.
#> Nodes is a tbl_df. Converting to a plain data frame.
plt
```



Simplified Graphic

That graphic looks like a bowl of spaghetti. Most connections represent only one mention during the workshops. Since the data is based on both the live notes and the later transcript, one mention could show up either once or twice in my classification of the notes.

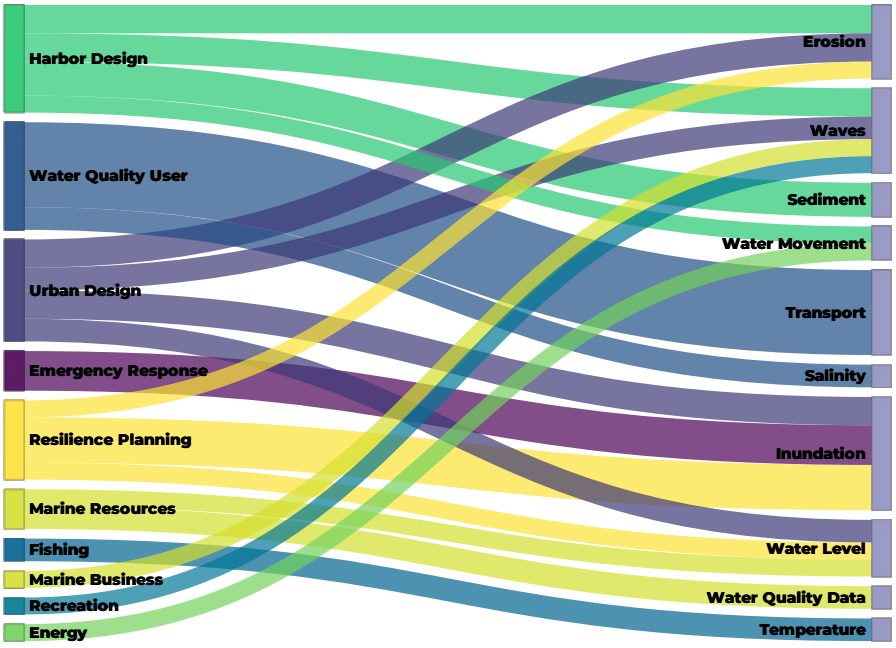
So, what I want to do is simplify the data by hiding all those "once or twice" links. It turns out if you drop rare links, a few nodes are never linked, so I want to drop them too.

```
tmp4 <- tmp2 %>%
  filter(weight > 2)
```

```
types <- unique(as.character(tmp4$Data_Group))
users <- unique(as.character(tmp4$User_Category))

nodes <- tibble(node_name = c(users, types),
                groups = c(users,
                           rep("B", length(types))))
```

```
tmp5 <- tmp4 %>%
  mutate(link_group = as.character(User_Category),
         User_Category = match(User_Category, nodes$node_name) - 1,
         Data_Group = match(Data_Group, nodes$node_name) - 1)
```

```r
plt <- sankeyNetwork(Links = tmp5,
              Source = "User_Category",
              Target = "Data_Group",
              Value = "weight",
              LinkGroup = "link_group",
              NodeGroup = "groups",
              Nodes = nodes,
              NodeID = "node_name",
              colourScale = the_colors,
              nodeWidth = 20,
              nodePadding = 10,
              height = 700,
              fontSize = 16,
              fontFamily = 'Montserrat ExtraBold',
              iterations = 0)
#> Links is a tbl_df. Converting to a plain data frame.
#> Nodes is a tbl_df. Converting to a plain data frame.
plt
```



Functions for Generating the Graphics

I develop three functions to encapsulate all of that logic. All three are local utility functions, so I eschew error checking. The three functions are:

1. A function to assemble the `D3` color function call
2. A function to convert our source data frames, with a column of source and target names, into the format required by `sankeyNetwork()`.
3. A function that actually generates the Sankey Plot (and calls the other two functions).

Define Color String

This function could be generalized to allow automated dropping of weak links.

```
d3_colors <- function(left_names, right_name, final_color = NULL) {
  #left_names is a vector of string node labels used for the source nodes.
  #right.name is the name for the (single) target node group.
  #final_color is a string defining a color for the right (target) nodes.

  domain = c(left_names, right_name)
  grps <- length(left_names) + 1
  #browser()
  if(! is.null(final_color)) {
    range <- sample(hcl.colors(grps-1, palette = "viridis"), grps - 1,
                    replace = FALSE)
    range <- c(range,final_color)
  }
  else
    #print(grps)
    range <- sample(hcl.colors(grps, palette = "viridis"), grps,
                    replace = FALSE)
  cols <- tibble(d = domain, r = range)
  the_colors <- paste0('d3.scaleOrdinal() .domain(["',
                       paste(cols$d, collapse='", "'),
                       '"]) .range(["',
                       paste(cols$r, collapse='", "'),
                       '"])')
  return(the_colors)
}
```

```
d3_colors(c("cat", "dog", "squirrel"), "foods", "#ffffff")
#> [1] "d3.scaleOrdinal() .domain([\"cat\", \"dog\", \"squirrel\", \"foods\"]) .range([\"#FDE333\", \"#
```

Assemble the Nodes and Links Data Frames

We have to be able to filter the data to remove rare connections. This function builds and rebuilds the data set. I'm going to forego error checking here and keep this as simple as possible...

```r
assemble_frames <- function(.dat, .left, .right,
                            right_name = 'right') {
  # .data is the RAW data with left-right string pairs (in two variables) that
  #  show a link between source (.left) and target (.right).

  grouped <- .dat %>%
    group_by({{ .left}}, {{.right}}) %>%
    summarize(weight = n(),
              .groups = 'drop')

  # browser()
  # there is probably a more efficient way to extract labels, that avoids
  # building an unnecessary data frame, but this works, and lets me use
  # tidyverse indirection....

  labs <- grouped %>%
    mutate(left = factor({{ .left}}),
           right = factor({{.right}}))

  #I can ignore order here because the Sankey function does....
  # By calling `factor()` here, it re-levels and drops empty categories.
  left = levels(factor(labs$left))
  right = levels(factor(labs$right))
  rm(labs)

  nodes <- tibble(node_name = c(left, right),
                  groups = c(left,
                             rep(right_name, length(right))))
  links <- grouped %>%
    mutate(link_group = as.character({{.left}}),
           "{{.left}}" := match({{.left}}, nodes$node_name) - 1,
           "{{.right}}":= match({{.right}}, nodes$node_name) - 1)

  return(list(Nodes = as.data.frame(nodes), Links = as.data.frame(links)))
}
```

```r
test <- tmp %>%
  assemble_frames(User_Category, Data_Group, 'bicycle')
```

```r
test$Nodes[10:20,]
#>          node_name          groups
#> 10 Marine Business Marine Business
#> 11      Recreation      Recreation
#> 12          Energy          Energy
#> 13       Transport         bicycle
#> 14      Inundation         bicycle
#> 15         Erosion         bicycle
#> 16           Waves         bicycle
#> 17        Sediment         bicycle
#> 18     Water Level         bicycle
#> 19  Water Movement         bicycle
#> 20     Temperature         bicycle
```

```
head(test$Links,5)
#>   User_Category Data_Group weight    link_group
#> 1             0         13      1 Harbor Design
#> 2             0         14      5 Harbor Design
#> 3             0         15      5 Harbor Design
#> 4             0         16      6 Harbor Design
#> 5             0         18      3 Harbor Design
```

Draw Sankey Plot

This encapsulates data frame preparation, color assignment and my selected plot characteristics.

```
my_sankey <- function(.dat, .left, .right,
                      final_color = NULL, drop_below = NULL) {

  right_name <- 'right'
  left_str <- as.character(ensym(.left))
  right_str <- as.character(ensym(.right))

  if (! is.null(drop_below)) {
    .dat <- .dat %>%
      group_by({{.left}}, {{.right}}) %>%
      mutate(links = n()) %>%
      filter(links >= drop_below)%>%
      select(-links)
  }

  my_data <- assemble_frames(.dat, {{.left}}, {{.right}},
                             right_name = right_name)

  left <- my_data$Links %>%
    mutate(left = as.character(link_group)) %>%
    pull(left)
  left <- unique(as.character(left))

  the_colors <- d3_colors(left, right_name = right_name,
                          final_color = final_color)
  #browser()
  the_graphic <- sankeyNetwork(Links = my_data$Links,
              Source = left_str,
              Target = right_str,
              Value = "weight",
              LinkGroup = "link_group",
              NodeGroup = "groups",
              Nodes = my_data$Nodes,
              NodeID = "node_name",
              colourScale = the_colors,
              nodeWidth = 20,
              nodePadding = 10,
              height = 700,
              fontSize = 28,
              fontFamily = 'Montserrat ExtraBold',
```

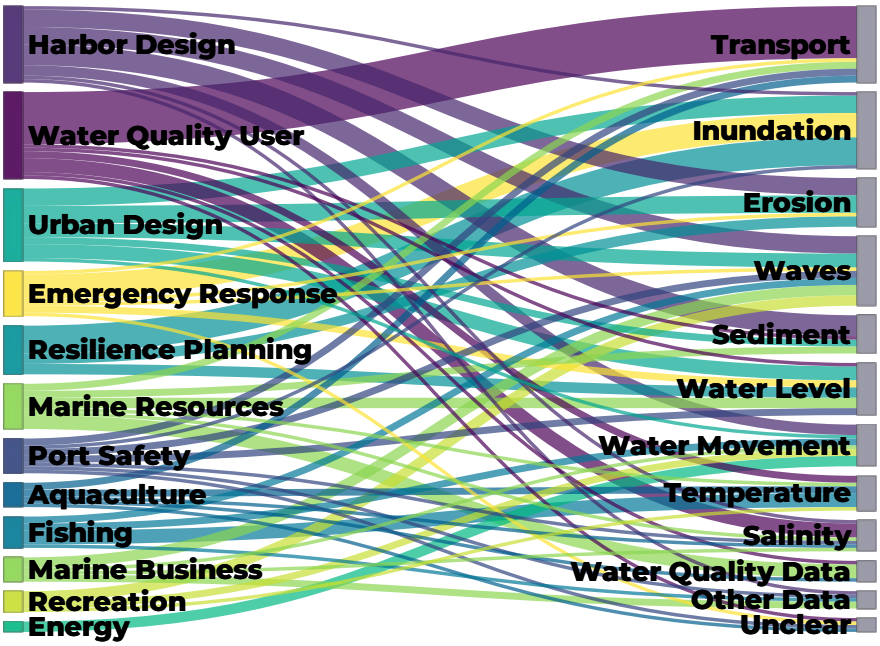
```
              iterations = 0)

 return(the_graphic)
}
```

From User to Data Types

Full Data

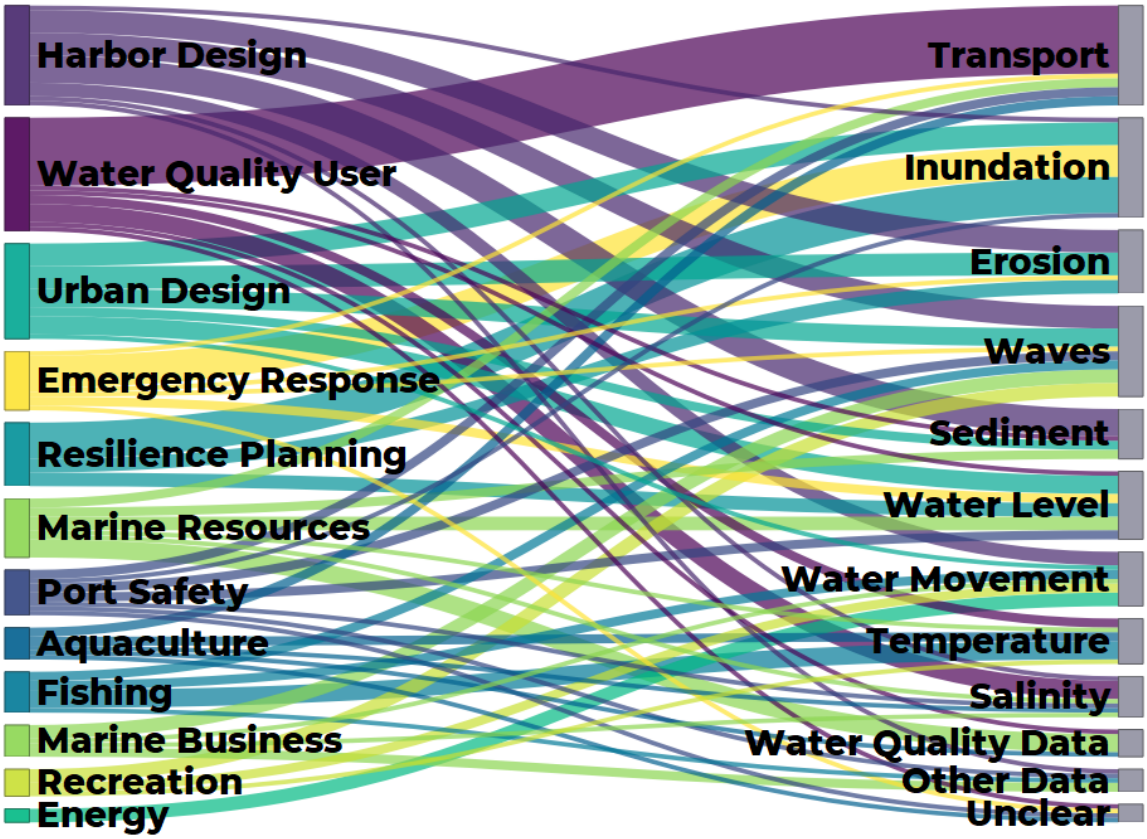
Based on data organized previously.

```
plt <- tmp %>%
  my_sankey(User_Category, Data_Group, final_color ="#9090a0")
plt
```



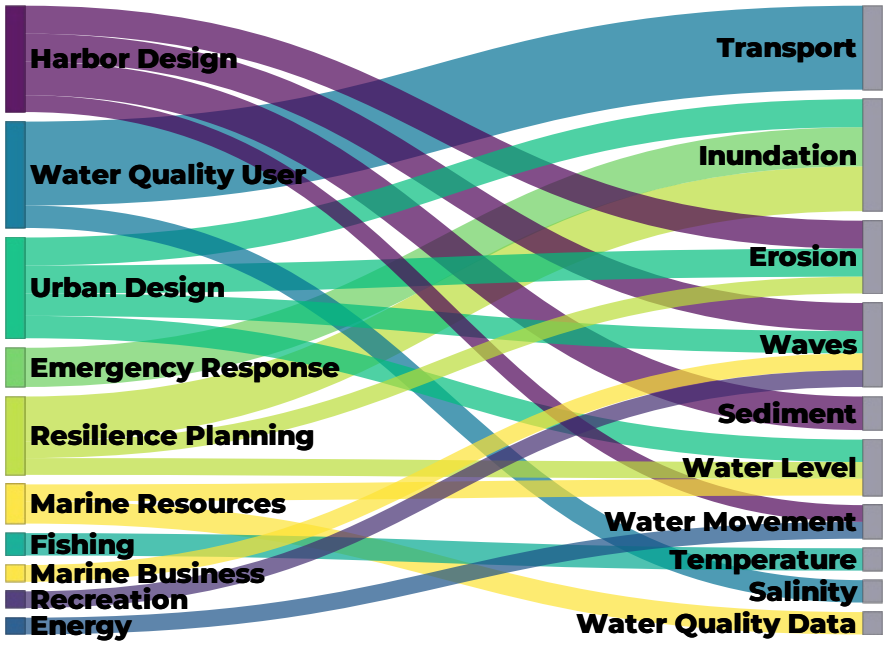

```
saveNetwork(plt, file = 'figures/users and data.html', selfcontained = TRUE)
webshot::webshot('figures/users and data.html', 'figures/users and data.png')
```

¶¶¶



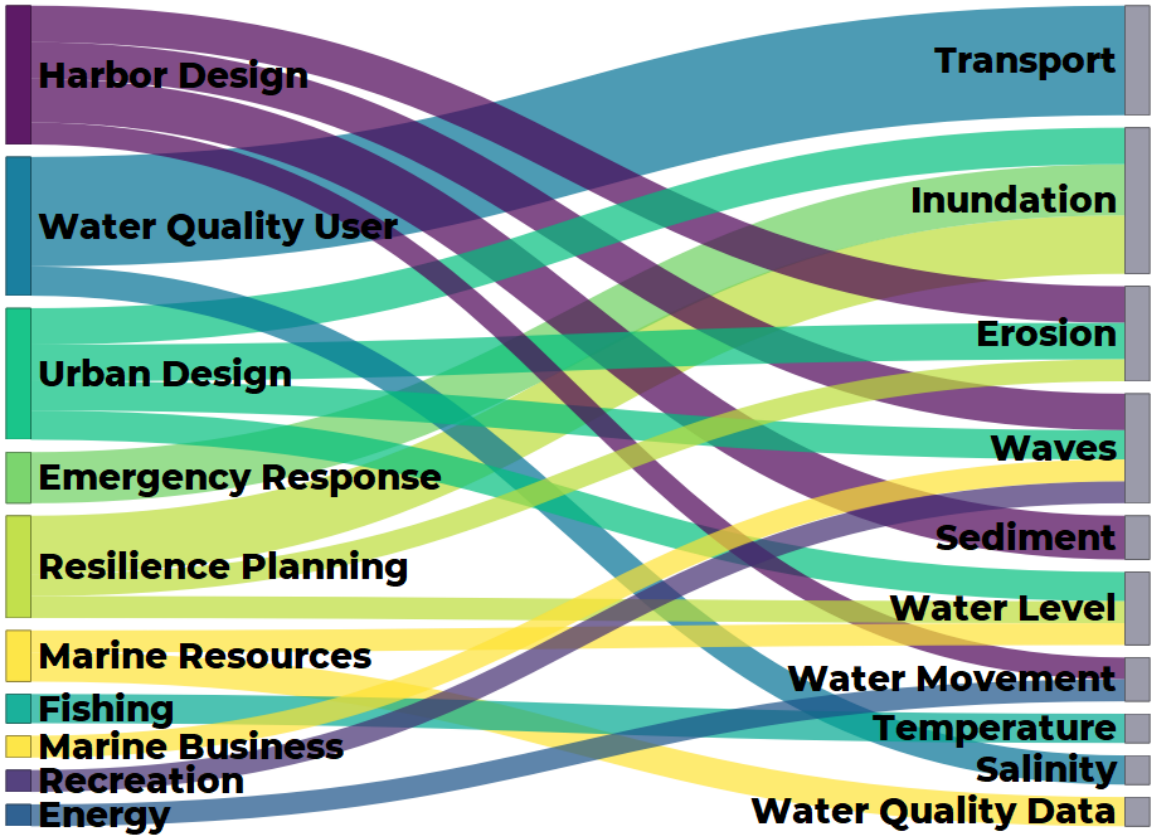
Simplified Plot

```
plt <- tmp %>%
  my_sankey(User_Category, Data_Group, final_color ="#9090a0", drop_below = 3)
plt
```




```
saveNetwork(plt, file = 'figures/users and data simple.html',
            selfcontained = TRUE)
webshot::webshot('figures/users and data simple.html',
                 'figures/users and data simple.png')
```

¶¶¶

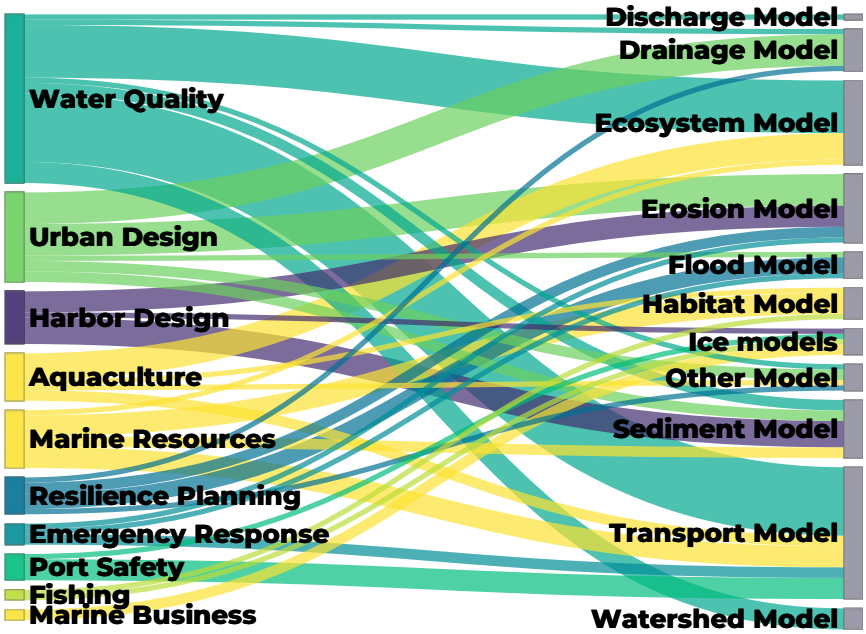


From User to Model Extensions

Full Data

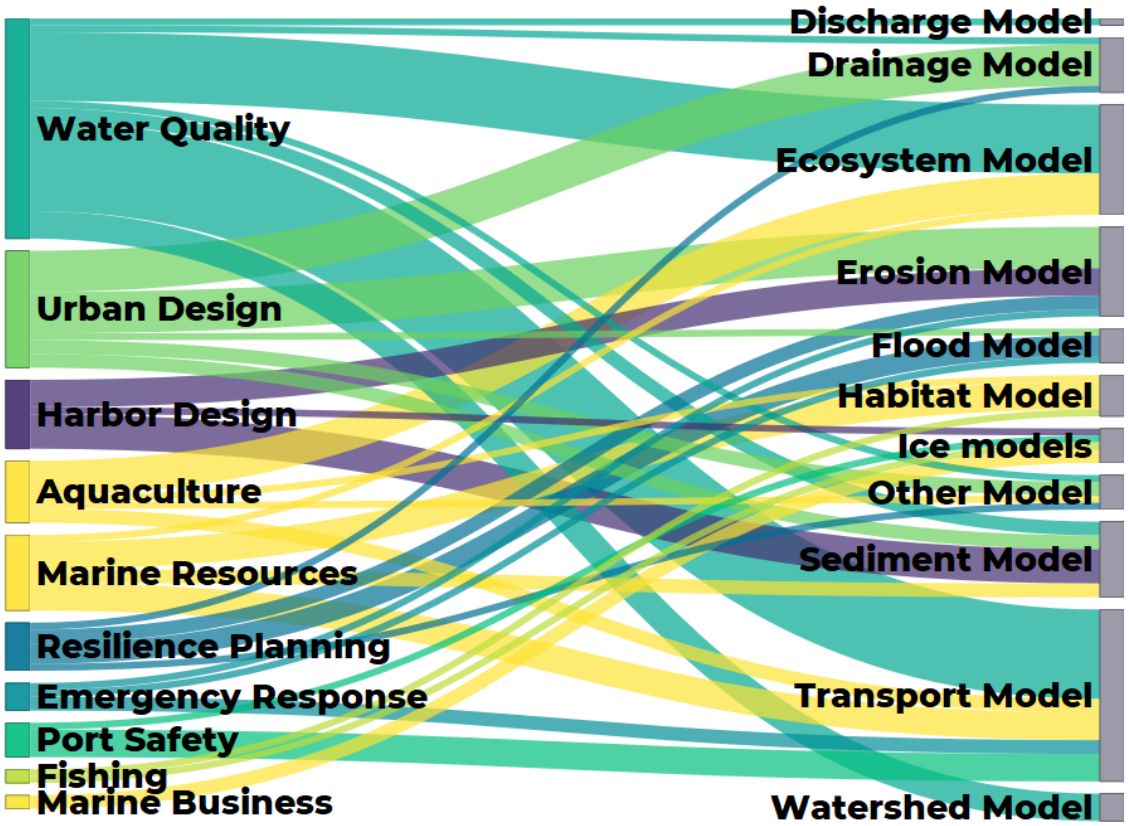
```
tmp <- the_data %>%
  select(ID, User_Category, Extension_Category) %>%
  filter(! is.na(User_Category)) %>%
  filter(! is.na(Extension_Category)) %>%
  mutate(User_Category = if_else(User_Category == 'Other',
                                 'Other User', User_Category),
         Extension_Category = if_else(Extension_Category == 'Other',
                                 'Other Model',Extension_Category)) %>%
  mutate(User_Category = fct_infreq(User_Category),
         Data_Group = fct_infreq(Extension_Category)) %>%
  unique()
```

```
plt <- tmp %>%
  my_sankey(User_Category, Extension_Category, final_color ="#9090a0")
plt
```



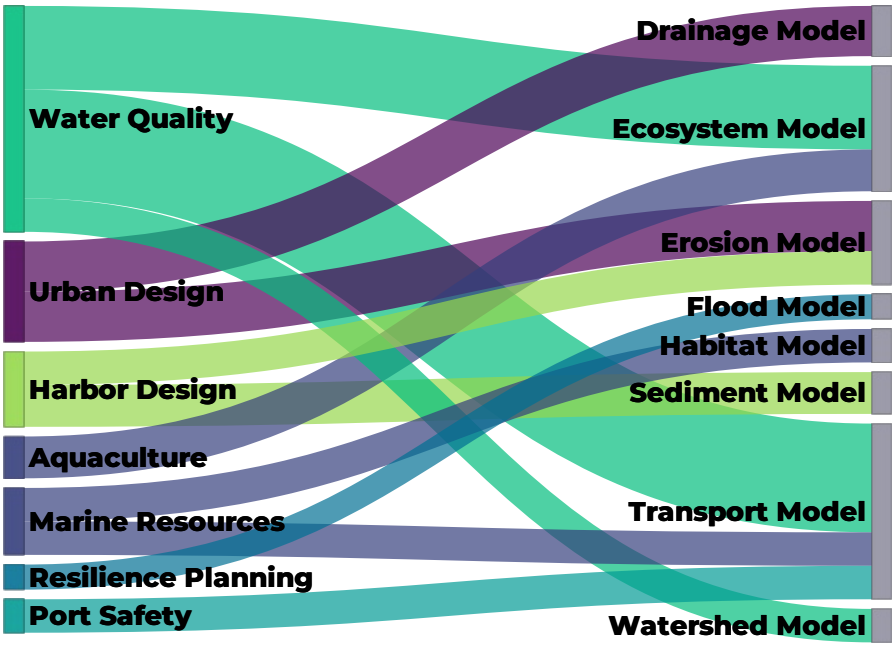

```
saveNetwork(plt, file = 'figures/users and models.html', selfcontained = TRUE)
webshot::webshot('figures/users and models.html',
                 'figures/users and models.png')
```

¶¶¶



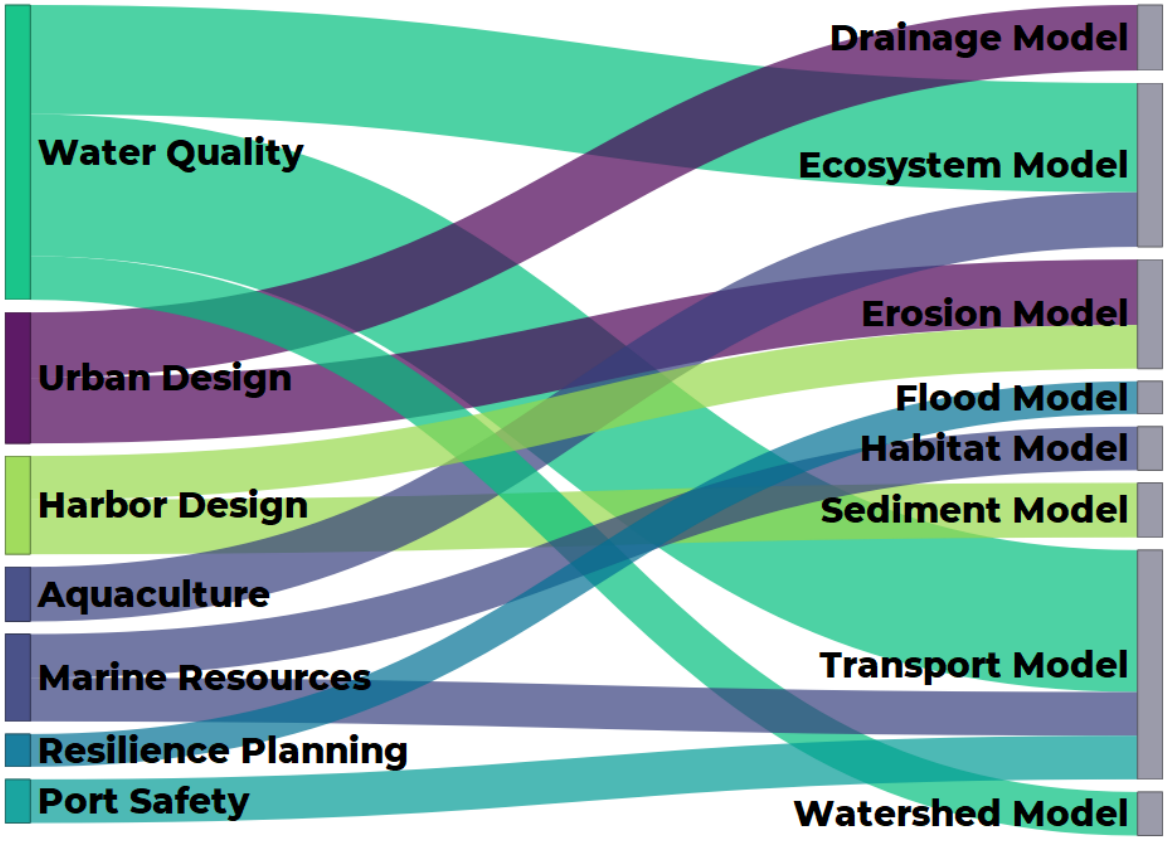
Simplified Plot

```
plt <- tmp %>%
  my_sankey(User_Category, Extension_Category, final_color ="#9090a0",
            drop_below = 3)

plt
```




```
saveNetwork(plt, file = 'figures/users and models simple.html',
            selfcontained = TRUE)
webshot::webshot('figures/users and models simple.html',
                 'figures/users and models simple.png')
```

¶¶¶

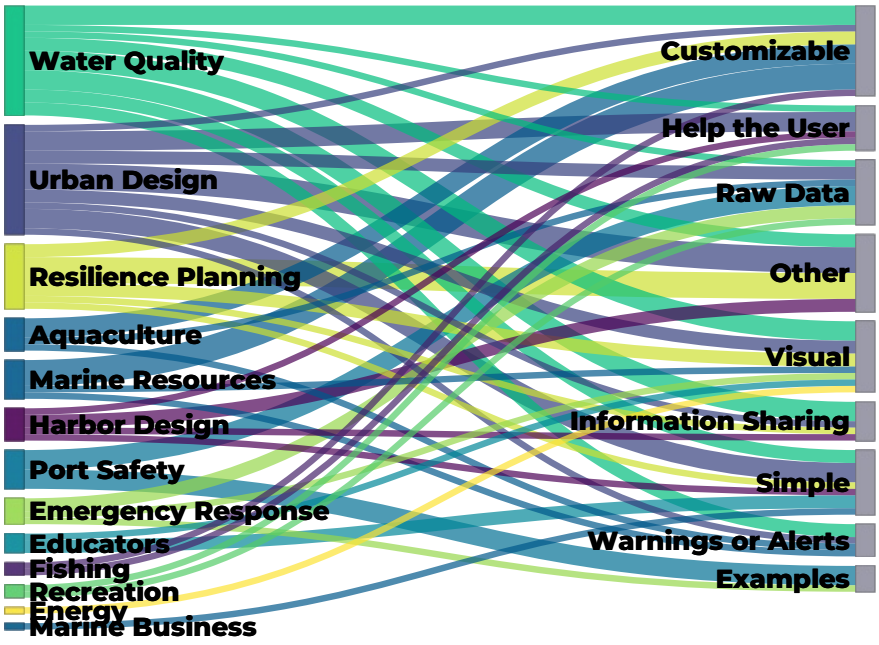


From User to User Interface Ideas

Full Data

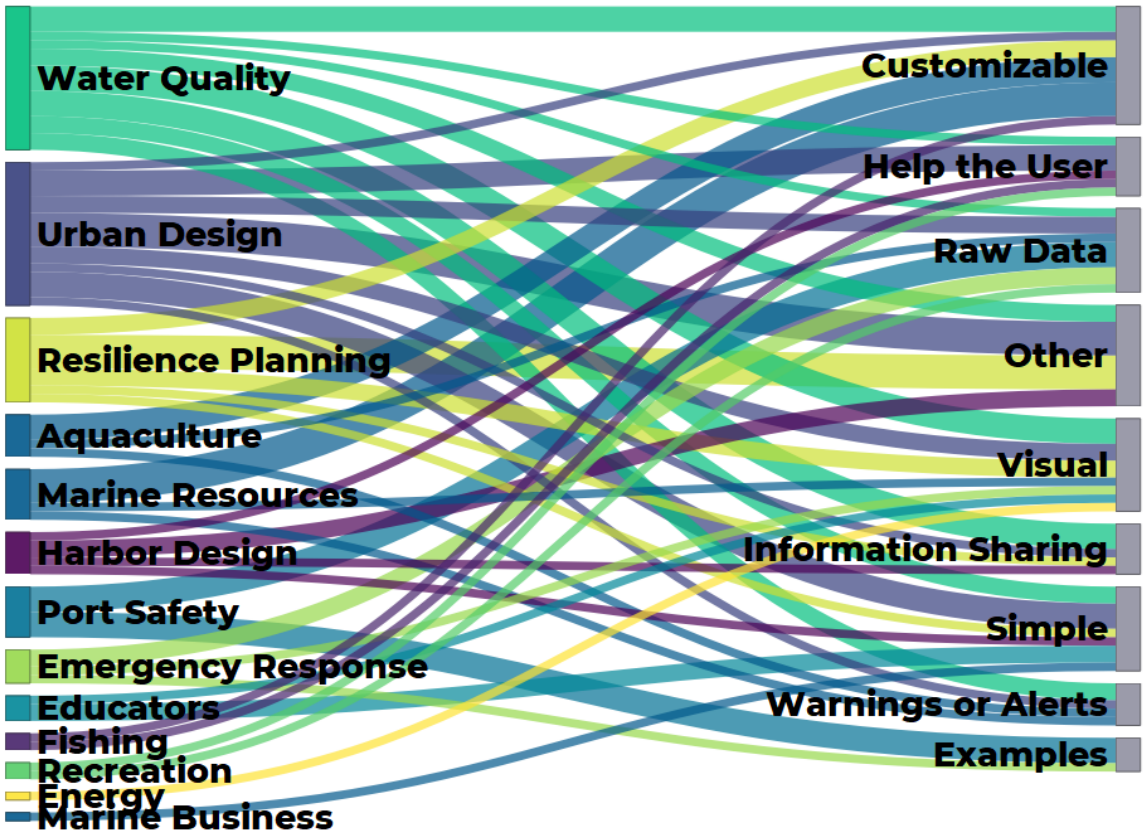
```
tmp <- the_data %>%
  select(ID, User_Category, Interface_Category) %>%
  filter(! is.na(User_Category)) %>%
  filter(! is.na(Interface_Category)) %>%
  mutate(User_Category = if_else(User_Category == 'Other',
                                 'Other User', User_Category)) %>%
  mutate(User_Category = fct_infreq(User_Category),
         Interface_Category = fct_infreq(Interface_Category)) %>%
  unique()
```

```
plt <- tmp %>%
  my_sankey(User_Category, Interface_Category, final_color ="#9090a0")
plt
```



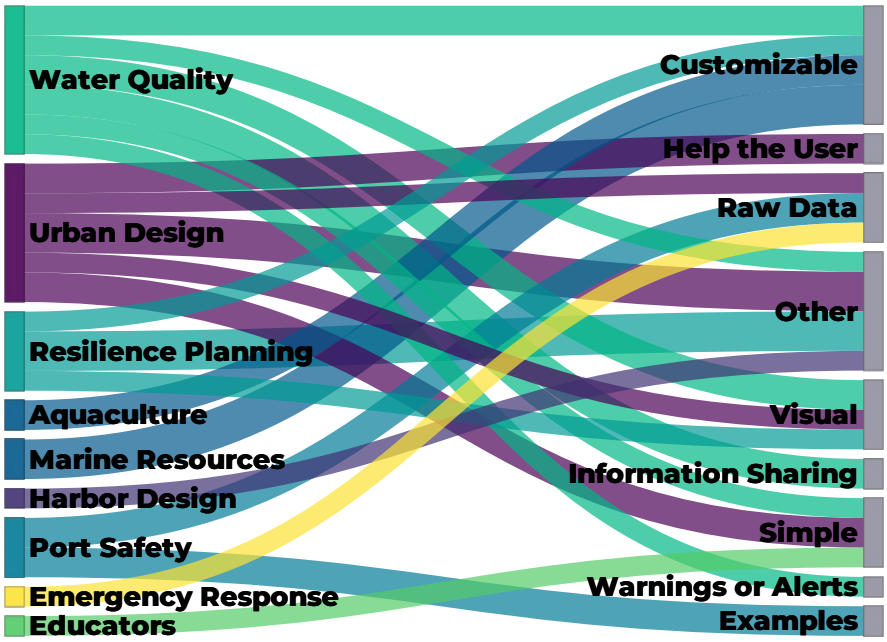

```
saveNetwork(plt, file = 'figures/users and interfaces.html',
            selfcontained = TRUE)
webshot::webshot('figures/users and interfaces.html',
                 'figures/users and interfaces.png')
```

¶¶¶



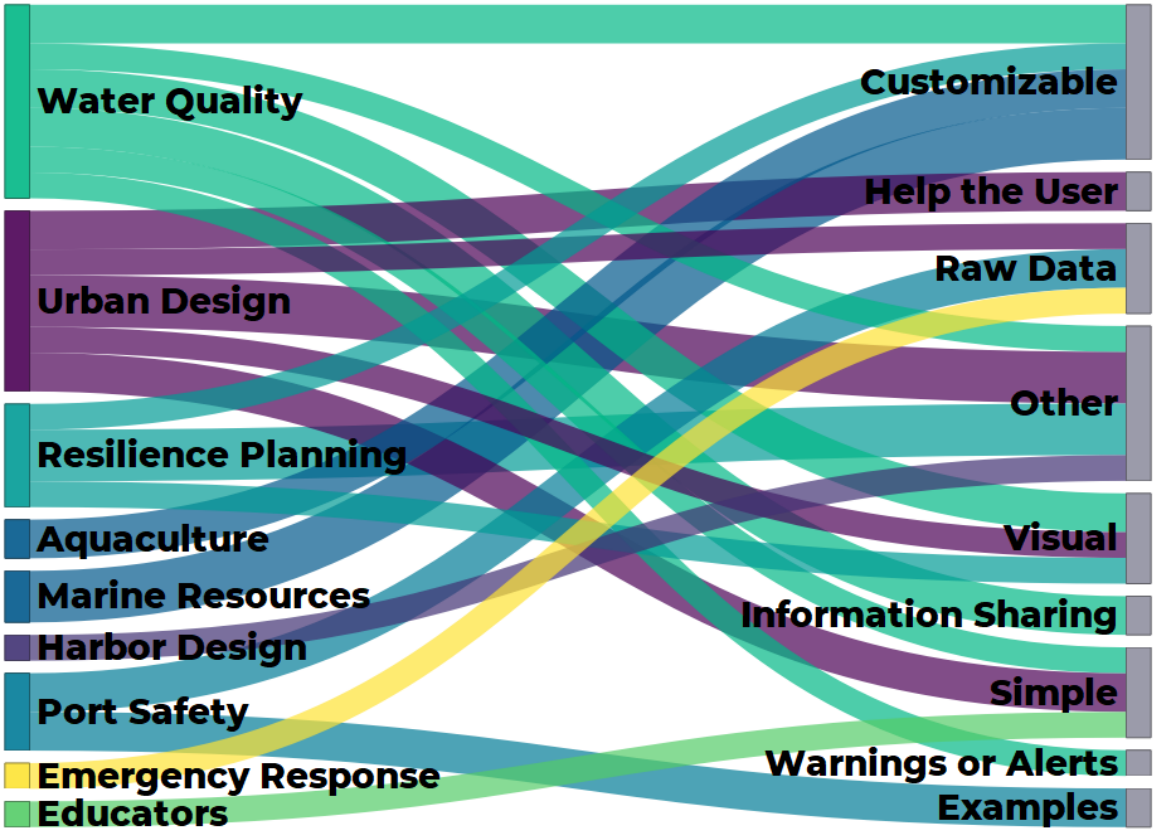
Simplified Plot

```
plt <- tmp %>%
  my_sankey(User_Category, Interface_Category, final_color ="#9090a0",
            drop_below = 2)

plt
```




```
saveNetwork(plt, file = 'figures/users and interfaces simple.html',
            selfcontained = TRUE)
webshot::webshot('figures/users and interfaces simple.html',
                 'figures/users and interfaces simple.png')
```

¶¶¶



Not very useful. . . .

From Data Requests to Time Domain

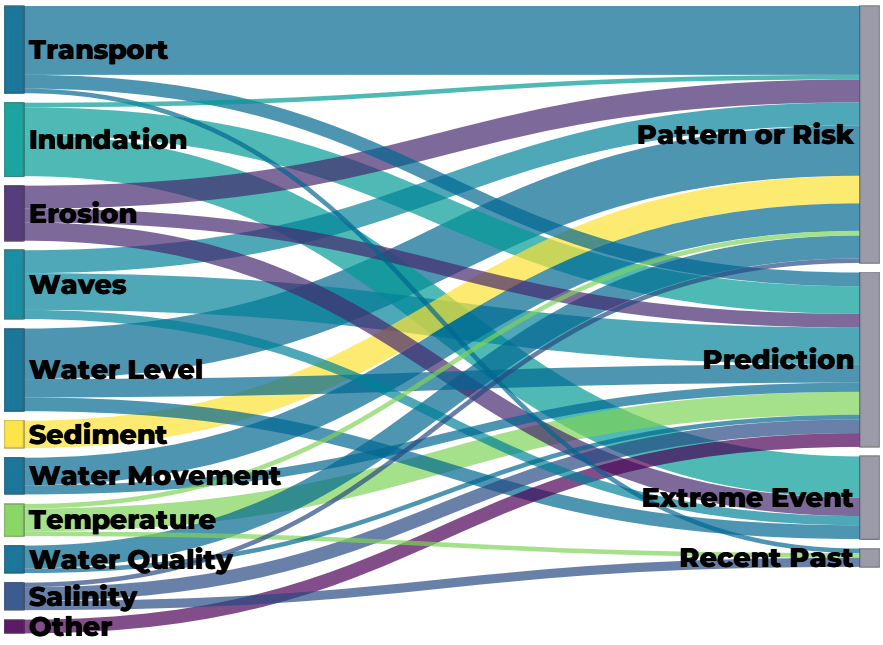
Full Data

Note that data preparation requires avoiding category conflicts between the "source" and "target" note lists here. Specifically, "Unclear" appears in both lists here. We need to rename or delete at least one of them. We chose to delete the "Unclear" categories entirely, since they are not informative in this context.

```
unique(the_data$Data_Group)
#>  [1] NA               "Waves"          "Inundation"     "Water Level"
#>  [5] "Transport"      "Water Movement" "Temperature"    "Erosion"
#>  [9] "Sediment"       "Water Quality"  "Salinity"       "Unclear"
#> [13] "Other"
cat("\n")
unique(the_data$Data_Timing)
#> [1] NA               "Extreme Event"   "Pattern or Risk" "Unclear"
#> [5] "Prediction"     "Recent Past"
```

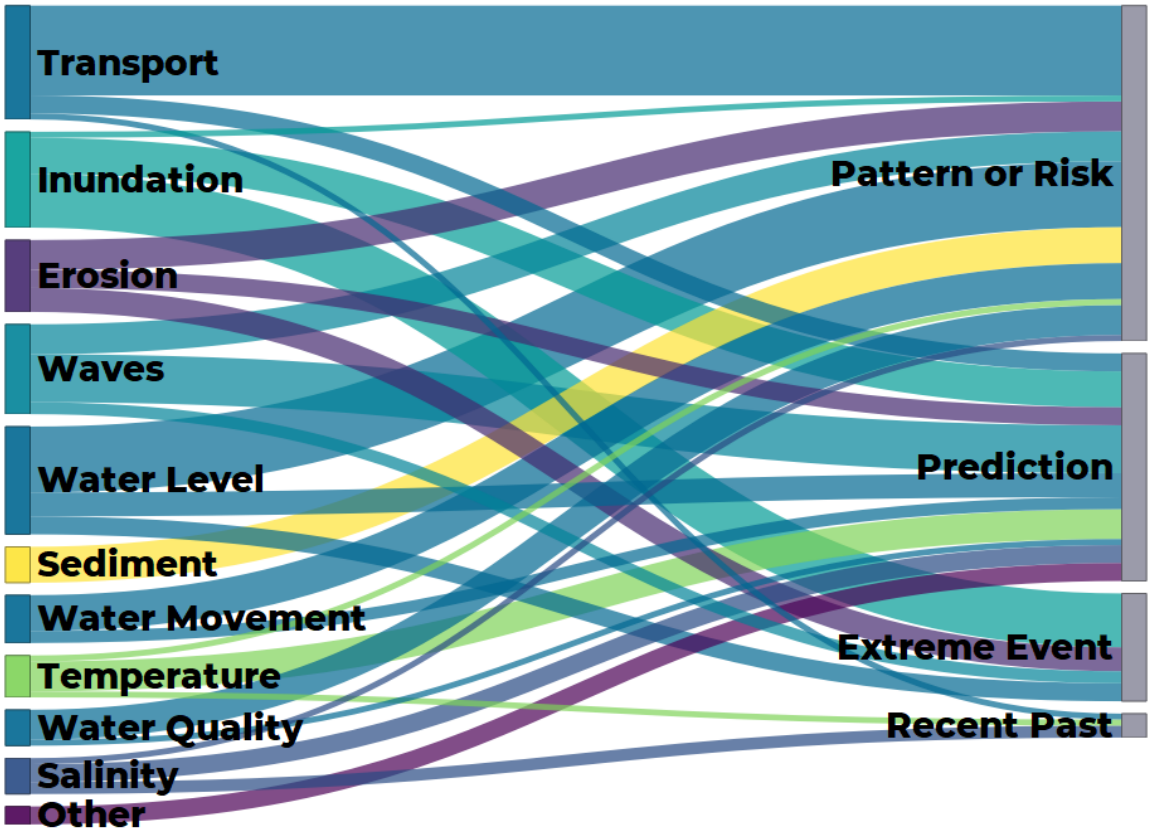
```
tmp <- the_data %>%
  select(ID, Data_Group, Data_Timing) %>%
  filter(Data_Timing != "Unclear",
         Data_Group != "Unclear") %>%
  filter(! is.na(Data_Group),
         ! is.na(Data_Timing)) %>%
  mutate(Data_Timing = fct_infreq(Data_Timing),
         Data_Group = fct_infreq(Data_Group)) %>%
  unique()
```

```
plt <- tmp %>%
  my_sankey(Data_Group, Data_Timing, final_color ="#9090a0")
plt
```



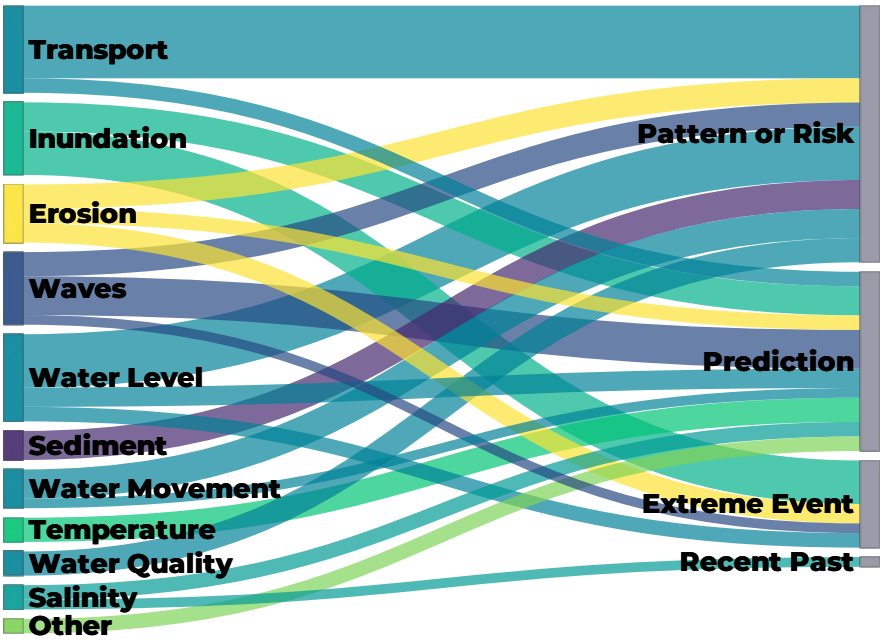

```
saveNetwork(plt, file = 'figures/data to timing.html', selfcontained = TRUE)

webshot::webshot('figures/data to timing.html', 'figures/data to timing.png')
```

¶¶¶



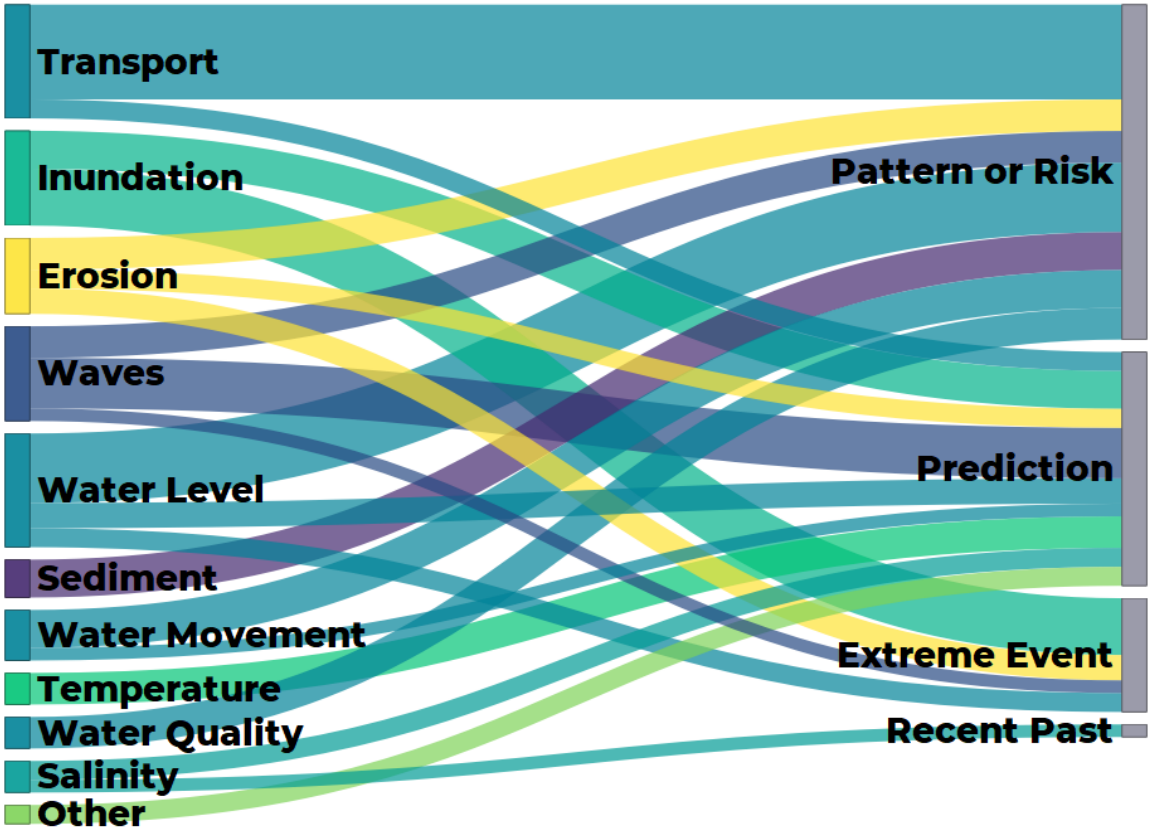
Simplified Plot

```
plt <- tmp %>%
  my_sankey(Data_Group, Data_Timing, final_color ="#9090a0", drop_below = 2)
plt
```




```
saveNetwork(plt, file = 'figures/data to timing simple.html',
            selfcontained = TRUE)

webshot::webshot('figures/data to timing simple.html',
                 'figures/data to timing simple.png')
```

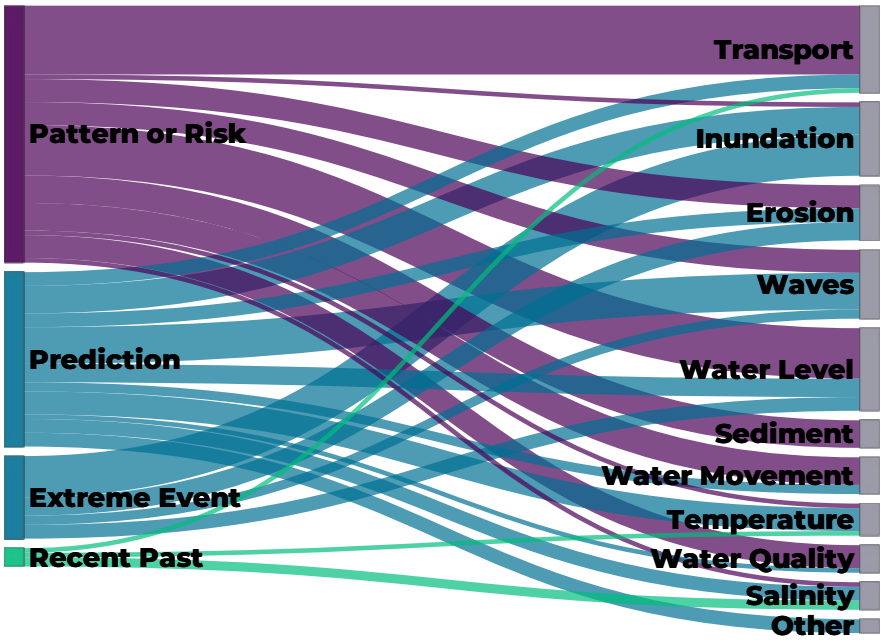
¶¶¶



From Time Domain to Data Requests

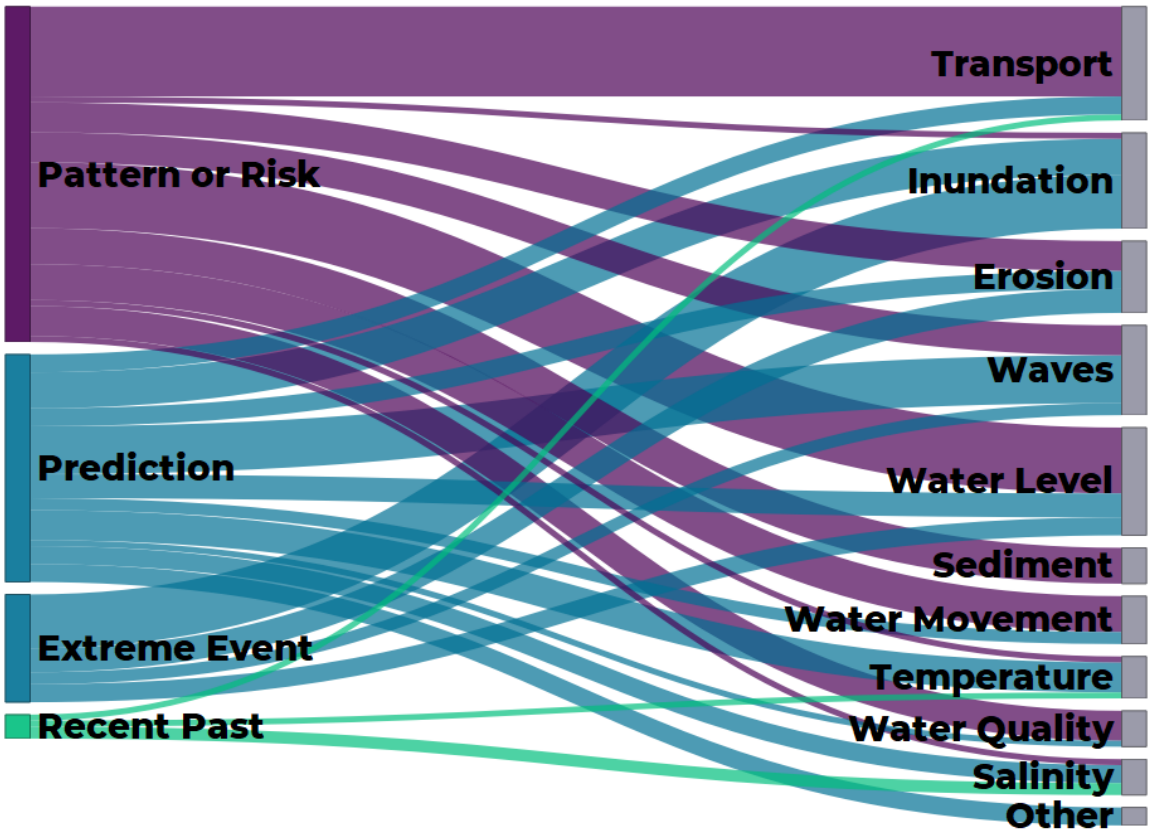
Full Data

```
plt <- tmp %>%
  my_sankey(Data_Timing, Data_Group, final_color ="#9090a0")
plt
```



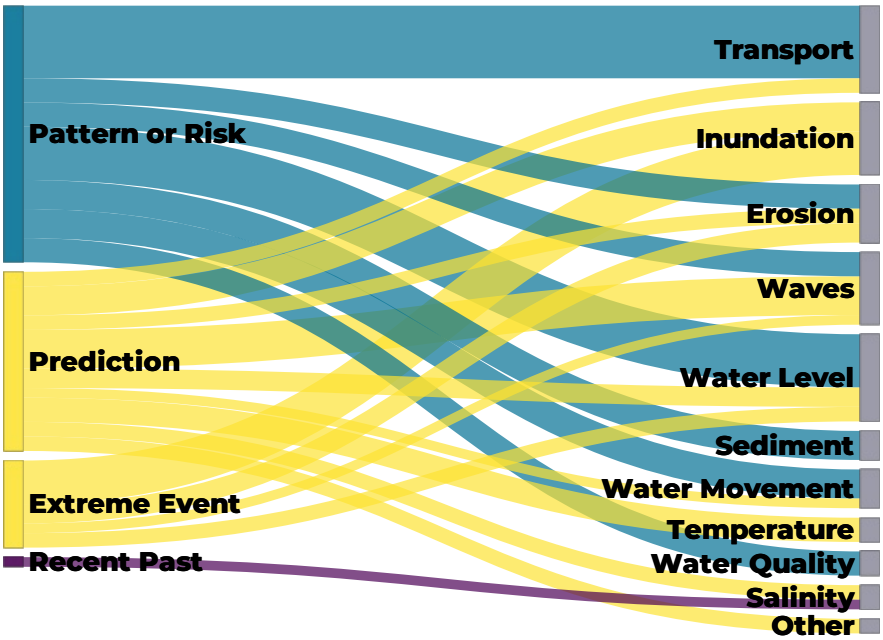

```
saveNetwork(plt, file = 'figures/timing to data.html', selfcontained = TRUE)

webshot::webshot('figures/timing to data.html', 'figures/timing to data.png')
```

¶¶¶



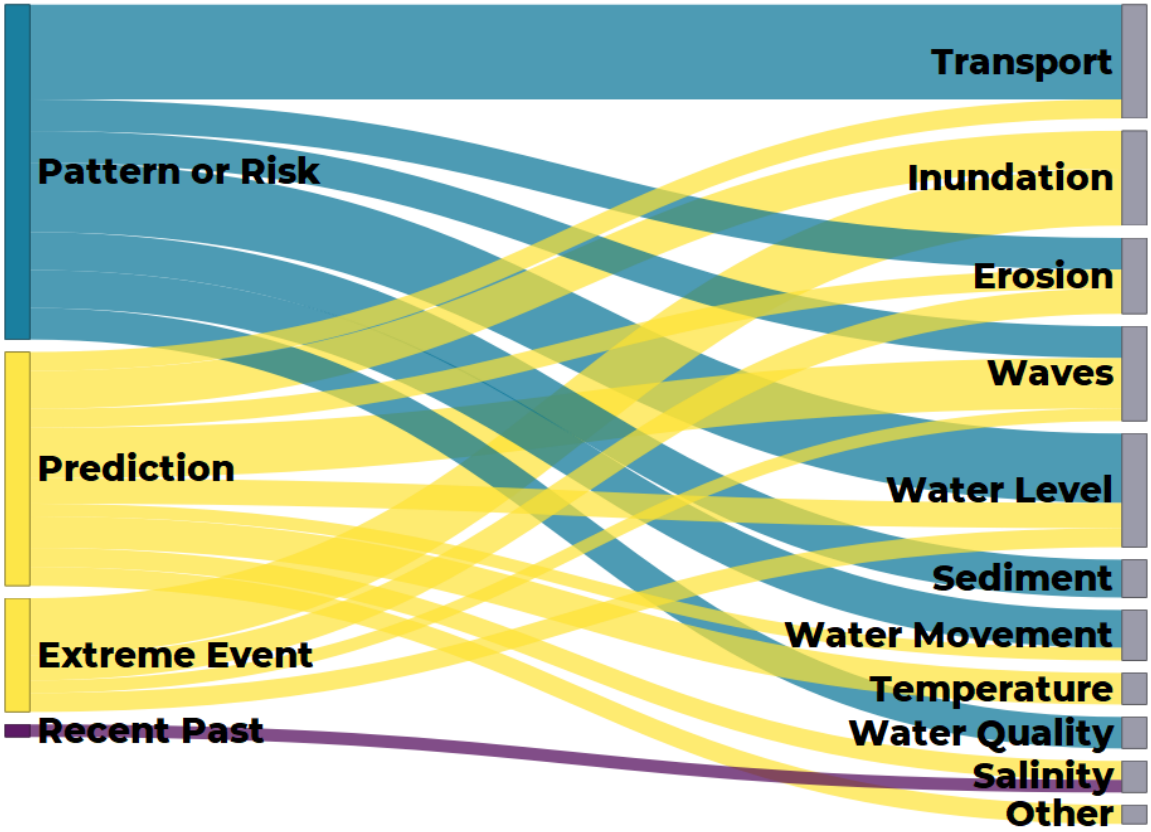
Simplified Plot

```
plt <- tmp %>%
  my_sankey(Data_Timing, Data_Group, final_color ="#9090a0", drop_below = 2)
plt
```




```
saveNetwork(plt, file = 'figures/timing to data simple.html',
            selfcontained = TRUE)

webshot::webshot('figures/timing to data simple.html',
                 'figures/timing to data simple.png')
```

¶¶¶


Pattern or Risk
Prediction
Extreme Event
Recent Past
Transport
Inundation
Erosion
Waves
Water Level
Sediment
Water Movement
Temperature
Water Quality
Salinity
Other