Fluent Graphics

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Chapter 1

Abstract

Interactive data visualization has become a staple of modern data presentation. Yet, despite its growing popularity, there still exists many unresolved issues which make the process of producing rich interactive data visualizations difficult. Chief among these is the problem of data pipelines: how do we design a framework for turning raw data into summary statistics that can then be visualized, efficiently, on demand, and in a visually coherent way? Despite seeming like a straightforward task, there are in fact many subtle problems that arise when designing such a pipeline, and some of these may require a dramatic shift in perspective. In this thesis, I argue that, in order to design coherent generic interactive data visualization systems, we need to ground our thinking in concepts from some fairly abstract areas of mathematics including category theory and abstract algebra. By leveraging these algebraic concepts, we may be able to build more flexible and expressive interactive data visualization systems.

Chapter 2

System description

This section contains a description of the two packages developed as part of this doctoral project (plotscape and plotscaper). Since `plotscaper` provides high-level application programming interface (API) for R users, whereas `plotscape` is more concerned with more low-level JavaScript functionality, I will organize the sections accordingly, by discussing high-level API concerns alongside `plotscaper` and implementation details alongside `plotscape`. Cross-cutting concerns will be addressed towards the ends of the respective sections.

At the time of writing, the `plotscape` repository contains about ~6,400 lines of code (mainly TypeScript), whereas the `plotscaper` repository contains about ~500 lines of R code (counted using the `cloc` CLI tool).

2.1 Core requirements

The high-level system/API needs to:

- Be accessible to a wide range of users
- Provide functionality for programmatically creating interactive figures and manipulating them live
- Integrate well with popular tools within the R ecosystem, such as the RStudio IDE and RMarkdown

The low-level system needs to be able to:

- Partition the raw data into a hierarchy of parts
- Compute summary statistics on these parts
- Transform these summaries while respecting the hierarchy (e.g. stacking, normalizing by parent values)

- Map these summaries to visual encodings such as x- and y-position, width, height, or area
- Render geometric objects, axes, etc...
- Respond to user input and propagate changes reactively

2.2 Application Programming Interface (`plotscaper`)

As was discussed in Section **??**, a primary inspiration for `plotscaper`'s API was the popular R package `ggplot2`. In `ggplot2`, plots are created by chaining together a series of function calls, each of serves to compose an (immutable) plot schema:

```r
library(ggplot2)

# In ggplot, plots are created by chaining a series of function calls
ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  scale_x_continuous(limits = c(0, 10))
```

```r
# The ggplot2 call creates an immutable object defining the plot schema
plot1 <- ggplot(mtcars, aes(wt, mpg))
names(plot1)
```

```
##  [1] "data"        "layers"      "scales"      "guides"      "mapping"     "theme"
## [11] "labels"
```

```r
length(plot1$layers)
```

```
## [1] 0
```

```r
# Adding components such as geoms returns a new schema object
plot2 <- ggplot(mtcars, aes(wt, mpg)) + geom_point()
names(plot2)
```

```
##  [1] "data"        "layers"      "scales"      "guides"      "mapping"     "theme"
## [11] "labels"
```

```r
length(plot2$layers)
```

```
## [1] 1
```

While a popular choice for static graphics, the `ggplot2` API has some disadvantages when it come to interactive graphics. Specifically:

- The package is generally designed around the idea of creating individual plots. Although multi-panel figures consisting of repeats of the same plot type can be created via facetting (`facet_wrap()` and `facet_grid()`, Wickham 2016), to create multi-panel figures with a mix of different plot types, the users have to reach for external packages such as `gridExtra` (Auguie 2017) or `patchwork` (Pedersen 2024). As was discussed in Section **??**, in interactive graphics, customizing individual plots is less important however, the ability to compose and view multiple plots is key.
- The model of composing an immutable plot schema works well for static graphics, however, with interactive graphics, mutability can be highly beneficial as well. Specifically, the ability to directly modify a rendered figure through code is particularly useful. For instance, in live figure, setting the width of a histogram bin to a specific value can be effectively achieved via a simple function call, rather than by having to manipulate a widget or some other control mechanism.

- The package was developed before widespread adoption of the pipe operator in R (both `%*%` from `magrittr`, Bache and Wickham 2022; and the native `|>` pipe, R Core Team 2024) and so it used the overloaded `+` operator to implement essentially the same functionality. Hadley Wickham himself admitted that if he had discovered the pipe operator earlier, he would have never implemented `ggplot2` with `+` (Wickham, Hadley 2014).
- Many of the package's core functions make use of non-standard evaluation (e.g. `aes()` and `facet_wrap()`, Wickham 2019). While non-standard evaluation seems to be quite popular within the R community and does make some interactive code more concise, it also makes it more harder to use these functions programmatically (Wickham 2019). For example, using the default `aes()` function, we cannot plot all pairwise combinations of variables in a data set by simply looping over their names - to do this, we need to use a specialized `aes_string()` function that takes variable names as strings. Again, in interactive graphics, it is often highly desirable to be able to manipulate the figure with code, and as such, non-standard evaluation may be less useful in this context.

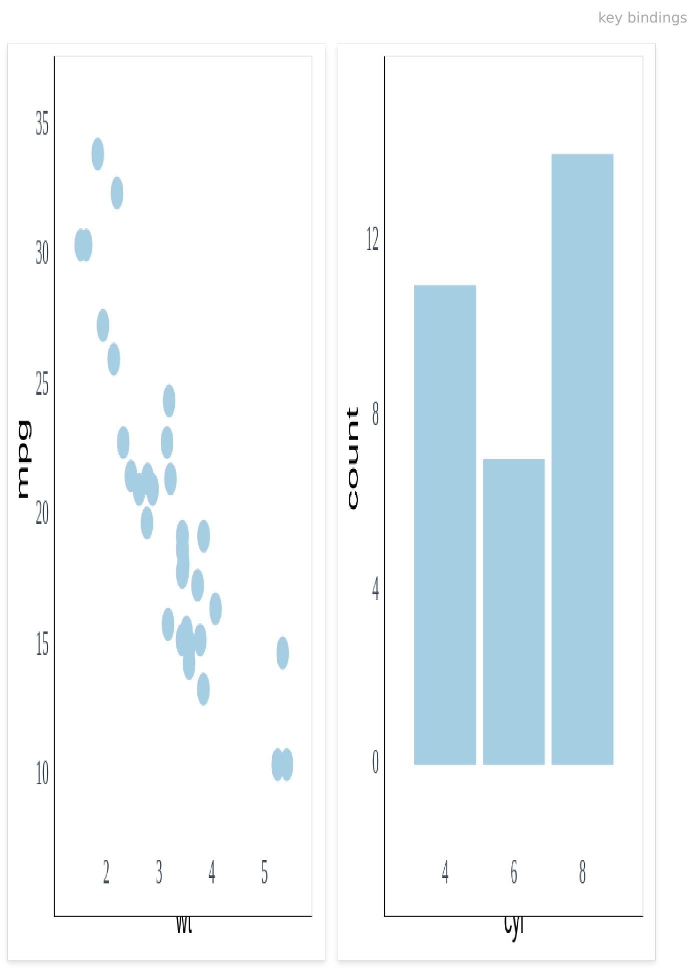
Given the reasons above, I've adopted a similar approach to `ggplot2`, giving the user the ability to create interactive figures by chaining together a series of function calls. However, unlike in `ggplot2`, the primary focus is on building figures out of multiple plots, rather than customizing individual plots. As such, the function calls typically serve to add (or remove) entire plots, although individual plots can still be modified via specialized functions which rely on selectors. Furthermore, the API supports both the creation of immutable plot schemas as well as mutable manipulation of a live figure, using largely the same set of functions. The idea is that the user can choose their preferred workflow based on their circumstances.

2.2.1 Basic example

Here's a basic example of creating an interactive figure with `plotscaper`:

```r
library(plotscaper)

create_schema(mtcars) |>
  add_scatterplot(c("wt", "mpg")) |>
  add_barplot(c("cyl")) |>
  render()
```

```
## file:////tmp/RtmpVg9u4I/file39512a8a9847/widget395165b00b64.html screenshot complet
```



We first initialize a plot schema with the `create_schema()` function that we pass data to (more on that later, in Section 2.2.2). Next, we chain together a series of function calls of the form `add_*()`, adding individual plots. Variable names are provided via character string vectors. Importantly, these string vectors do not represent direct aesthetic mapping in the same way how the `aes()` function in `ggplot2` does: in the `plotscaper` model, data variables are not directly mapped to aesthetics, but can undergo transformations and interactive remapping. Finally, the figure is rendered with the `render()` call.

2.2.2 The scene and the schema

An key part of the `plotscaper` API is the distinction between the figure schema and the live scene. In short, the schema is an immutable blueprint defining the figure, while scene scene is its live, rendered version. Both can be manipulated using largely the same set of functions. However, whereas manipulatingthe schema simply appends the corresponding function calls to an immutable ledger, manipulating the scene applies the changes directly, in a mutable way. Consequently, the scene can only be manipulated inside an interactive R session (such as, for example, inside the RStudio IDE, Posit 2024), whereas a figure schema can also be rendered statically, as part of an RMarkdown document, for example.

Here is an example of the figure schema, using the same code as above:

```r
schema <- create_schema(mtcars) |>
  add_scatterplot(c("wt", "mpg")) |>
  add_barplot(c("cyl"))

schema
```

```
## plotscaper schema:
## add-plot { type: scatter, variables: c("wt", "mpg") }
## add-plot { type: bar, variables: cyl }
```

```r
str(schema$queue)
```

```
## List of 2
##  $ :List of 2
##   ..$ type: chr "add-plot"
##   ..$ data:List of 3
##   .. ..$ type     : 'scalar' chr "scatter"
##   .. ..$ variables: chr [1:2] "wt" "mpg"
##   .. ..$ id       : 'scalar' chr "1163513f-370a-420e-bac4-1a9b4dfca4d3"
##  $ :List of 2
##   ..$ type: chr "add-plot"
##   ..$ data:List of 3
##   .. ..$ type     : 'scalar' chr "bar"
##   .. ..$ variables: chr "cyl"
##   .. ..$ id       : 'scalar' chr "f40157d8-adbc-428e-bac1-b088e8235b08"
```

As you can see, the schema is essentially just a list of messages (which are in fact stored as an R `list()` that gets converted to JSON when the figure gets rendered). The `render()` call parses these messages sequentially, applying the changes that create the figure. The main advantage of the schema is that it provides an immutable record, allowing the figure to be recreated in its exact state. Furthermore, the schema can be manipulated programmatically, by e.g. pruning or modifying some of the messages, and, since it is essentially just JSON, it can be easily transported.

Importantly, the schema does not actually encode the the figure's state directly; instead, it records the sequence of steps that generate that state. This deliberate design choice avoids duplicating the figure's state between the R client (e.g., the RStudio session) and the JavaScript "server" (the live figure). By representing the schema as a simple immutable list of messages, all figure state resides within JavaScript, eliminating the need for reconciliation or synchronization with the R side.

The scene is implicitly created via the call to `render()`. Under the hood, the call constructs a `htmlwidgets` widget (Vaidyanathan et al. 2021) which utilizes custom `plotscape` code to set up and manage the figure. When inside a live interactive R session, the render call also automatically launches an `httpuv` server (Cheng et al. 2024) for live communication with the figure. To enable this live communication, the user must first assign the scene object to a variable. Then they can call functions to modify the figure the same way as they would with a schema, however, in this case, the figure is updated live, in a mutable fashion.

```r
# NOT EVALUATED - works only inside interactive R sessions,
# not RMarkdown/bookdown documents
scene <- create_schema(mtcars) |>
  add_scatterplot(c("wt", "mpg")) |>
  add_barplot(c("cyl")) |>
  render()

# Adds a histogram, mutating the current figure
scene |> add_histogram(c("disp"))

# Selects cases by rows
scene |> select_cases(1:10)

# Query selected cases (works in interactive mode only)
scene |> selected_cases() # 1 2 3 4 5 6 7 8 9 10
```

As noted earlier, most functions work on both the schema and the scene. The one exception are state-querying functions, which include `selected_cases()`, `assigned_cases()`, and `get_scale()`. These functions retrieve the figure's state and return it as output in R (without modifying the figure in any way). For example, `selected_cases()` returns the indices of the currently selected cases as a numeric vector. These functions are designed to interactively query the figure's state, and as such it does not make sense to use them with the stateless schema.

2.2.3 HTML document embedding

Since `plotscaper` figures are just `htmlwidgets` widgets, they can be statically embedded in HTML documents such as those produced by RMarkdown (**?**) or Quarto (Allaire and Dervieux 2024). More specifically, when a `plotscaper` figure is rendered, `htmlwidgets` (Vaidyanathan et al. 2021) is used to construct a widget skeleton (consisting of HTML, CSS, and JavaScript) and injects the JavaScript corresponding to `plotscape`. The resulting widget can then be statically embedded in any kind of HTML document. This is how the `plotscaper` figures are rendered in the present thesis. As mentioned above, this means that the figure cannot be interacted live through code, however, within-figure interactive features such as linked selection and querying still work regardless (since these happen entirely on the JavaScript side).

2.3 Interactive figure platform (`plotscape`)

This section describes the actual platform used to produce and manipulate interactive figures, as implemented in `plotscape`. It contains a detailed listing of the system's components, along with descriptions of what each component does.

2.3.1 Indexable

As discussed in Section **??**, when it comes to representing data, the column-based model offer several advantages over the row-based model. In this model, data is stored in a dictionary of contiguous arrays (as in, for example, a CSV file). Thus, I chose to represent the fundamental unit of data as a column, a fixed-length array of values.

However, at times, it may be useful to have additional flexibility. Specifically, it may be useful to to extend our definition of a "column" to non-array-like things, such as derived values and values repeated across all rows. This is where `Indexable<T>` comes in.

An `Indexable<T>` represents a single "column" of data, and is just a union of three basic types:

```
Indexable<T> = T | T[] | ((index: number) => T)
```

In plain words, an `Indexable<T>` is one of three things:

- A variable of type `T`
- An array of `T`s
- A callback that takes an index and returns a `T`.

To extract a value from `Indexable<T>`, we rely on a generalized form of indexed access. The way how this indexed access works depends on the type of the indexable. First, if the indexable is an array, we subset it using the usual square bracket notation. Second, if the indexable is a non-array-like variable (but not a function), we always return it, regardless of the index (we can think of it as the value as being repeated across all rows). Third and finally, if the indexable is a callback, then we call it with the index and take the returned value. A uniform interface for this generalization of indexed access is provided by `Getter`s.

Altogether, this is similar to Leland Wilkinson's idea of a variable function (2012).

The main advantage of `Indexable<T>` is that, while the raw data will typically come in the form of arrays, there are many places further down the data visualization pipeline where constants and callbacks are useful. For example, in a typical barplot, the base of the y-axis is set to a constant value, typically zero. While we could hypothetically append an array filled with zeros to the rendering data, it is more convenient and memory efficient to instead use a constant (`0`), or a thunk (`() => 0`). As another example, often, if we have an array of several repeated values, it may be convenient to instead represent it as two arrays: a (short) underlying array of unique values or labels and an array of indices (similar to base R's `factor` class). When we need the actual values, we can use a callback to subset the array of labels.

2.3.2 Getter

A `Getter<T>` is simply a function which takes an index and returns a value of type `T`. To construct a `Getter<T>`, we take an `Indexable<T>` and dispatch on its underlying type. For illustration, here is a (slightly) simplified implementation:

```
// Getter.ts
export type Getter<T> = (index: number) => T;

export namespace Getter {
  // Constructor
  export function of<T>(x: Indexable<T>): Getter<T> {
    if (typeof x === `function`) return x;
    else if (Array.isArray(x)) return (index: number) => x[index];
    else return () => x
  }
}
```

we can then create and use `Getter`s like so:

```
import { Getter } from "./Getter"

const getter1 = Getter.of([1, 2, 3])
const getter2 = Getter.of(99);
const getter3 = Getter.of((index: number) => index - 1);

console.log(getter1(0));
console.log(getter2(0));
console.log(getter3(0));
```

```
## 1
## 99
## -1
```

Note that, by definition, every `Getter<T>` is also automatically an `Indexable<T>` (since it is a callback `(index: number) => T`). This means that we can create new getters out of other getters.

The `Getter` namespace also includes several other utility functions. One example is `Getter.constant` which takes in a value `T` and returns a thunk which always returns `T` (i.e. `() => T`). This is useful, for example, when `T` is an array and we always want to return the whole array (not just a single element):

```
import { Getter } from "./Getter"

const getter4 = Getter.constant([`A`, `B`, `C`])

console.log(getter4(0))
console.log(getter4(1))
```

```
## [ "A", "B", "C" ]
## [ "A", "B", "C" ]
```

Another utility function is `Getter.proxy`, which takes a `Getter` and an array of indices, and returns a new `Getter` which proxies the access to the original values through the array of indices:

```
import { Getter } from "./Getter"

const proxyGetter = Getter.proxy([`A`, `B`, `C`], [2, 1, 1, 0, 0, 0]);
console.log([0, 1, 2, 3, 4, 5].map(proxyGetter))
```

```
## [ "C", "B", "B", "A", "A", "A" ]
```

This function becomes particularly useful when implementing `Factor`s.

2.3.3 Dataframe

Another fundamental data structure is a `Dataframe`. A `Dataframe` is just a record of `Indexable` values:

```
interface Dataframe {
  [key: string | symbol]: Indexable
}
```

In this way, a `Dataframe` is essentially just a SoA with a bit of extra flexibility. Specifically, while in typical SoA data structures, all properties are usually arrays, in `Dataframe` they are instances of the `Indexable` type, so they may also be constants or functions. For example, the following is a valid instance of a `Dataframe`:

```
const data: Dataframe = {
  name: [`foo`, `bar`, `baz`],
  age: 99,
  canDrive: (index: number) => index < 1
}
```

The fact that the "columns" of a `Dataframe` can be constants and functions is useful, for example, when want every row to contain the same value (e.g. 0 for the base of a barplot), or when we want the value be lazily computed based on other values. This is also where the SoA representation offers a unique advantage: to achieve the same behavior in AoS layout, we would have to have a copy of the value or function pointer in every row.

`Dataframe` should always contain at least one array and all arrays in a `Dataframe` should have the same length. This is because some operations are impossible if we do not know the length of the `Dataframe` (the number of rows). For example, when rendering a scatterplot, how do we decide how many points to draw if the x- and y-positions have length 19 and 20, or if they are both constants? Thus, at least of one the dataframe's columns needs to have a fixed length (i.e. have an underlying array) and there should not be multiple different lengths.

In the current version of the system, these fixed-length constraints are not enforced via a static check (such as during a constructor call), but are instead checked dynamically during runtime, whenever the integrity of a dataframe's length becomes a key concern (using utility functions such as `Dataframe.checkLength`). This is the case, for example, when initializing a `Scene` or when rendering.

I found the dynamic fixed-length checks to be the better option, for several reasons. First, they allow us to represent data as a plain JavaScript object (POJO) rather than having to instantiate a class. Second, due to JavaScript's dynamic nature, this approach is also safer: if, during runtime, the user adds a property to a `Dataframe` which violates the fixed-length constraints, this approach will catch the error. Third, and finally, for any data sets with typical dimensionality (more rows than columns, $p << n$), the tiny performance hit that may be incurred due to having to loop through the columns to find the length dynamically will be minuscule compared with the computational cost of looping through the data set's rows and doing work such as rendering or computing statistics. For high-dimensional datasets ($p >> n$), we could always extend the system to memoize the length/number of rows on the `Dataframe` object (although then we may lose the security of the dynamic runtime checks).

2.3.4 Reactive

By definition, an interactive data visualization system needs to be able to respond to user input and propagate this information wherever it needs to go. `Reactive` is a fundamental mixin that provides this utility. It is essentially just custom implementation of the Observer/EventEmitter pattern.

Any object can be made `Reactive` by passing it into the `Reactive` constructor, and then calling it with functions from the `Reactive` namespace. Here is a simplified implementation:

```
// Reactive.ts
const LISTENERS = Symbol(`listeners`); // A symbol key to emulate private property
type Callback = (data: Record<string, unknown>) => void;

export interface Reactive {
  [LISTENERS]: Record<string, Callback[]>;
}

export namespace Reactive {
  export function of<T extends Object>(object: T): T & Reactive {
    return { ...object, [LISTENERS]: {} };
  }

  export function listen(object: Reactive, event: string, cb: Callback) {
    if (!object[LISTENERS][event]) object[LISTENERS][event] = [];
    object[LISTENERS][event].push(cb);
  }

  export function dispatch(
    object: Reactive,
    event: string,
    data: Record<string, unknown> = {}
  ) {
    if (!object[LISTENERS][event]) return;
    for (const cb of object[LISTENERS][event]) cb(data);
  }
}
```

We can use `Reactive` like so:

```
import { Reactive } from "./Reactive"

const dog = Reactive.of({ name: `Terry the Terrier` })
Reactive.listen(dog, `car goes by`, () => console.log(`Woof`))
Reactive.dispatch(dog, `car goes by`)
```

```
## Woof
```

The actual `Reactive` implementation includes more features, such as the ability to propagate events, throttle them and set their priority (determining the order in which event callbacks execute), remove listeners, and fire only once multiple events have been dispatched. However, the underlying model is the same.

2.3.5 Factors

When visualizing data, we often need to split our data into several parts. As was discussed in Introduction [ADD REFERENCE], these parts together forms a partition of the data, and there may be multiple partitions organized in a hierarchy, such that one or more parts in a child partition “add up” to a part in the parent partition.

A `Factor` provides a way to represent such data partitions and the associated metadata. In this way, it is similar to base R’s `factor` S3 class, although there are some important differences which will be discussed below.

`Factor` has the following interface:

```
interface Factor<T extends Dataframe> extends Reactive {
  cardinality: number;
  indices: number[];
  data: T
  parent?: Factor;
}
```

`cardinality` records the number of unique parts (indices) that form the partition represented by the `Factor`. For example, if the factor represents boolean partitioning of the data into two parts, the cardinality will be 2, if it represents partitioning into three parts, the cardinality will be 3, if it represents a partitionining into all countries in the world, the cardinality will be 195, and so on.

`indices` represent the actual assignment of cases (rows of the data) to the parts. For example, the array of indices `[1, 0, 1, 1, 2]` represents the following partitioning: the second case (row) is assigned to the first part, the first, third, and fourth case are assigned to the second part, and the fifth case to the third part (keeping in mind JavaScript's zero-based indexing). As was mentioned above, the number of unique values in `indices` has to match the factor's `cardinality`, and the length of `indices` has to match the number of rows of the data set that the factor partitions.

Technically, `cardinality` represents the same information as is contained in `indices` (the number of unique values). However, for some operations, it is useful to be able to access cardinality directly, in $O(1)$ time, instead of having to loop through the entire array of indices ($O(n)$ time). Such is the case, for example, when constructing product factors or when initializing arrays of summaries.

A factor may have associated metadata stored in the `data` property. The `data` property is a `Dataframe` with one row for each part (i.e. the number of rows is equal to `cardinality`). Representing metadata as a dataframe represents a departure from base R's `factor` class, which represents all metadata as a flat vector of `levels`. For instance:

```r
cut(1:10, breaks = c(0, 5, 10))
```

```
##  [1] (0,5]  (0,5]  (0,5]  (0,5]  (0,5]  (5,10] (5,10] (5,10] (5,10] (5,10]
## Levels: (0,5] (5,10]
```

With `Factor`, the same information would be represented as:

```ts
const factor: Factor = {
  cardinality: 2,
  indices: [0, 0, 0, 0, 0, 1, 1, 1, 1, 1],
  data: {
    binMin: [0, 5],
    binMax: [5, 10],
  },
};
```

There are several advantages to storing `Factor` metadata in a `Dataframe` as opposed to a flat vector/array. First, when partitioning data, we often want to associate several pieces of metadata with each part. For example, if we cut or bin some numeric variable, like in the example above, we want to store both the lower and upper bound of each part's bin. We could store both pieces of information as a single element (tuple) in an array/vector, the way that `cut` does it, however, this works well with only few pieces of metadata: once we start storing longer tuples, it becomes hard to tell what each tuple element represents. We could alleviate the problem by naming the tuple elements, but then we are essentially storing the metadata in an array of dictionaries, i.e. the AoS data structure. We can do better by storing the metadata in a table.

Second, if we store metadata in a `Dataframe`, it is easier to combine it when we take a product of two or more factors. Since taking the product of multiple factors is a fundamental operation in an interactive data visualization system, underpinning operations such as linked brushing, it makes sense to use this representation.

There are multiple types of factors which differ semantic meaning as well as the associated metadata. However, all are represented by the same underlying `Factor` data type. To construct these `Factor` subtypes, we use different constructor functions which are all exported by the `Factor` namespace. These will be discussed in the following subsections.

2.3.5.1 Bijection factors

`Factor.bijection` is the first of two trivial factor constructors. It assigns each case its individual part, such that the cardinality of the resulting factor is simply equal to the number of cases in the data. The function signature of `Factor.bijection` is as follows:

```
function bijection<T extends Dataframe>(n: number, data?: T): Factor<T>
```

Notice that, when we create a bijection factor, we need to specify the length of the data `n` (the number of cases). This is used to create `indices`. Technically speaking, explicitly specifying `n` is not necessary: we could implement `indices` as a callback which takes an index and simply returns it back (an identity function). However, since the factors are primarily used to summarize data, and we need to know how many cases to summarize, we do need to store the length of the data *somewhere*. I found it easier to simply create a dummy array of `indices`, rather than defining a separate `length` property on `Factor`. There is little computational cost associated with this, since, by definition, the partitioning represented by a bijection factor does not change[1].

`Factor.bijection` can also have associated metadata. This is just a `Dataframe` of length `n`.

[1]Unless the length of the data changes. I have not implemented data streaming for plotscape/r yet, however, it would be easy to extend bijection factor for streaming by simply pushing/popping the array of indices.

On an abstract level, a bijection factor represents a terminal object in the `Factor` category (a category of partitions with intersections as morphism). If we take the product of a bijection factor and any other factor, the result will always be another bijection.

Typical use case of `Factor.bijection` is the scatterplot. When constructing a scatterplot, we simply take two arrays of equal length (three, if representing size as well) and draw one point per each element of the arrays. Thus, the partitioning `Factor` has the same cardinality as the length of the arrays and the arrays represent the factor's metadata. Another use case is the parallel coordinates plot.

2.3.5.2 Constant factors

Constant factors, created with the `Factor.mono` constructor, are the second trivial factor subtype. They represent the dual of bijection factors, by assigning all cases of the data to a single part. Thus, the labeling function is a constant function (hence the name). The constructor signature is the same as for bijection factors:

```
function mono<T extends Dataframe>(n: number, data?: T): Factor<T>
```

The metadata associated with constant factors is, intuitively, a `Dataframe` of length 1, i.e. a dictionary of arrays with one element.

On an abstract level, `Factor.mono` represents an initial object in the `Factor` category. That is, if we take the product of a constant factor and any other factor, the result will simply be the other factor (with the constant factor's metadata repeated in all of the other factor's partitions' metadata).

The use cases for constant factors are a bit more obscure. One example is the spinogram. In a spinogram, the upper x-axis limit represents the cumulative sum (count) of all cases in the data. A convenient way to model this is by a constant factor. Another potential use case for constant factors might be plots with a single geometric object, such as a radar plot[2].

2.3.5.3 String factors

When we have array of values which can be coerced to strings (using the `.toString()` method), we can easily turn this into a factor by treating two values as the same level if their string representations match. This is the basis of string factors constructed by `Factor.from`:

[2]Not currently implemented in plotscape/r

```
type Stringable = { toString(): string };
function from(array: Stringable[]): Factor<{ labels: string[] }>
```

The metadata associated with `Factor.from` is the array of `labels`, which are simply all of the unique values produced by applying the `toString()` method to each element in `array`.

2.3.5.4 Binned factors

When we have an array of numeric values, we can turn this into a factor by assigning the values to (typically equal-sized) bins, as in a histogram. This is what `Factor.bin` is for. It has the following constructor signature:

```
function bin(
  array: number[],
  options: {
    breaks?: number[];
    nBins?: number;
    width?: number;
    anchor?: number;
  },
): Factor<{ binMin: number[]; binMax: number[] }>;
```

Notice that the constructor comes with a list of options which control how the bins are created. If `breaks` are provided, the constructor uses those as the bins directly. Otherwise it uses `nBins`, `width`, and `anchor` to determine the breaks, in decreasing order of importance.

The metadata that `Factor.bin` produces are the limits of each bin (`binMin` and `binMax`).

2.3.5.5 Product factors

A fundamental operation that we need to be able to do with factors is to take their Cartesian product. That is, when we have two factors of same length, each with its corresponding array of indices, we need to be able to take the indices, combine them element-wise, and create a new factor that will have as its cardinality the number of unique pairwise combinations of indices.

For example, take two factors represented by the following data (omitting the `data` property for conciseness):

```
{ cardinality: 2, indices: [0, 0, 1, 0, 1, 1] };
{ cardinality: 3, indices: [0, 1, 2, 0, 1, 2] };
```

If we take their product, we should end up with the following factor:

```
{ cardinality: 4, indices: [0, 1, 3, 0, 2, 3] };
```

Notice that the cardinality of the resulting factor (4) is greater than that of either of the two constituent factors (2, 3) but less than than the combined product of their cardinalities ($2 \cdot 3 = 6$). This will generally be the case: if the first factor has cardinality a and the second cardinality b, the product of the two factors will have cardinality c, such that:

- $c \geq a$ and $c \geq a$ (equality only if one or both of the factors are constant or there is only one unique element-wise index combination)
- $c \leq a \cdot b$ (equality only if all element-wise index combinations are unique)

That is, the product factor will have will be at least as many parts (but most likely more) as either of its constituent, and at most as many parts as the product of the numbers of the constituents' parts (but most likely fewer). This is a simple fact based on the logic of partitions.

2.3.5.5.1 Computing product indices A subtle challenge is how to actually compute indices of a product factor. One naive idea might be to simply sum the constituent factors' indices element-wise. However, this approach does not work: the sum of two different pairs of indices may produce the same value. For instance, in a product of two factors with cardinality 4, there are three different ways to get indices which sum to 4: $1+3$, $3+1$, and $2+2$. Additionally, this approach does not preserve order: intuitively, we would want the cases associated with lower values of the first factor's indices to come first (have lower index).

The way out of this predicament is to use the following formula (similar to one discussed in Wickham 2013) for computing product indices:

$$i_{\text{product}} = \max(a, b) \cdot i_{\text{factor 1}} + i_{\text{factor 2}}$$

We multiply the first factor's index by the greater of the two factors' cardinalities and add the index of the second factor. Intuitively then, the first factor gets assigned a greater "weight" (represented by the cardinality), and taking the maximum of the two cardinalities ensures that unique pairs of indices always produce a unique product index (since, e.g. with factors of cardinalities 2 and 3, an index pair `(0, 2)` will produce a product index `2` and index pair `(1, 0)` will produce a product index `3`).

This method works well but there are two issues with it that need to be addressed. First, computing the indices does not tell us the resulting cardinality. Second, the computed indices are not dense. For example, multiplying computing the product indices using the factors above gets us the following:

```
{ cardinality: 2, indices: [0, 0, 1, 0, 1, 1] };
{ cardinality: 3, indices: [0, 1, 2, 0, 1, 2] };

// Product
{ cardinality: ?, indices: [0, 1, 5, 0, 4, 5] }
```

Notice that the cardinality is unknown (`?`) and there are gaps in the indices (for example, we are missing indices `2` and `3`).

The issue of cardinality is unavoidable - we cannot infer the cardinality of the product factor from the cardinalities of the constituent factors alone, because we do not know how many unique combinations of indices there will be. However, what we can do is keep track of how many unique product indices we encounter while computing them (using, for example, an array or a hash set), and then use that number after we have finished looping through the indices.

The issue of the gaps in the indices is a bit more complicated. While looping through the indices, we do not know how many unique index combinations we will encounter. There are several options for dealing with this problem. First, hypothetically, we could implement the downstream parts of our system in such a way that the factor indices would only represent relative position, not absolute. I have actually tried this out but found it rather inconvenient.

Second, in a language with first-class support for pointers, another option would be to store the product indices as pointers to a shorter underlying array of "dirty" indices (with gaps), and only clean up this dirty array of indices (by removing the gaps) once we compute the product factor. Unfortunately, in JavaScript, there is no way to represent pointers to primitive types, such as numbers, strings, or booleans.

The third option, and the one I ended up going with, is to simply loop through the product indices again and clean up the gaps this way. That is, the concrete steps taken in my system are:

1. Compute product indices, keeping track of unique ones
2. Sort the unique product indices
3. Loop through product indices again, replacing them by position in the unique indices array

Steps 1. and 3. require looping through the array of same length as the data, i.e. an $O(n)$ complexity. Step 2. has hypothetically $O(n \cdot \log n)$ complexity (using the usual quicksort algorithm), however, the actual required work is likely to be much less, since, unless either of the two factors is a bijection or all of the product indices are unique (which is unlikely), the length of the array of unique indices will only be a fraction of the length of the data. Thus, the combined complexity of all three steps is likely to be $O(n)$, with $O(n \cdot \log n)$ worst case performance.

Since the operation of computing product factors represents a "hot" code path (it is required, for example, every time linked selection happens), having to loop through an array of the length of the data twice is not ideal. However, in JavaScript, there is likely no better alternative. While we could hypothetically wrap indices in objects, and store the pointers to those, the memory and data access overhead of this approach would most likely result in performance characteristic many times worse. One of the data types JavaScript engines such as V8 are best optimized to handle are packed arrays of small integers (called "smi's," V8 Core Team 2017), and so, heuristically, it makes sense to keep the indices in this format. Additionally, compared to the overhead of other operations (such as rendering), the cost of looping through an array of small integers twice is likely to be miniscule. Personally, this is what I have seen while profiling the system.

2.3.6 Reducers

2.3.6.1 Motivation

When we visualize, we draw summary statistics computed on different parts of the data. For example, when drawing a typical barplot, we split the data based on the levels of some categorical variable, count up the number of cases in each part, and then draw bars of corresponding heights.

In the preceding section, I discussed the component used to represent partitioning of the data into parts: factors. Now it is time to discuss the process of actually computing the statistical summaries representing these parts. Interestingly, while all visualizations rely on this process in one way or another, designing a generic pipeline for doing this presents some surprising challenges.

One such important challenge is displaying coherent visualization. This topic has been discussed in the introduction, in Section [ADD REFERENCE]. Briefly, in order to be a valid representation of the data, an interactive data visualization system should compute and render statistics in such a way that the resulting visualization has correct algebraic properties. As was discussed previously, monoids and groups present a framework for ensuring this, and as such should serve as the backbone of our system.

Another challenge is the hierarchical nature of graphics. In interactive data visualization, it is often desirable to be able to convert one specific plot type into a different representation. For example, a typical barplot represents counts along the y-axis. This is useful for comparing absolute counts, however, it is less useful for comparing proportions. As such, some interactive data visualization systems offer the feature of turning a barplot into a spineplot, a normalized version of the plot where the counts are instead presented along the x-axis, in a stacked order, and the y-axis represents proportion of counts, see Figure 2.1.

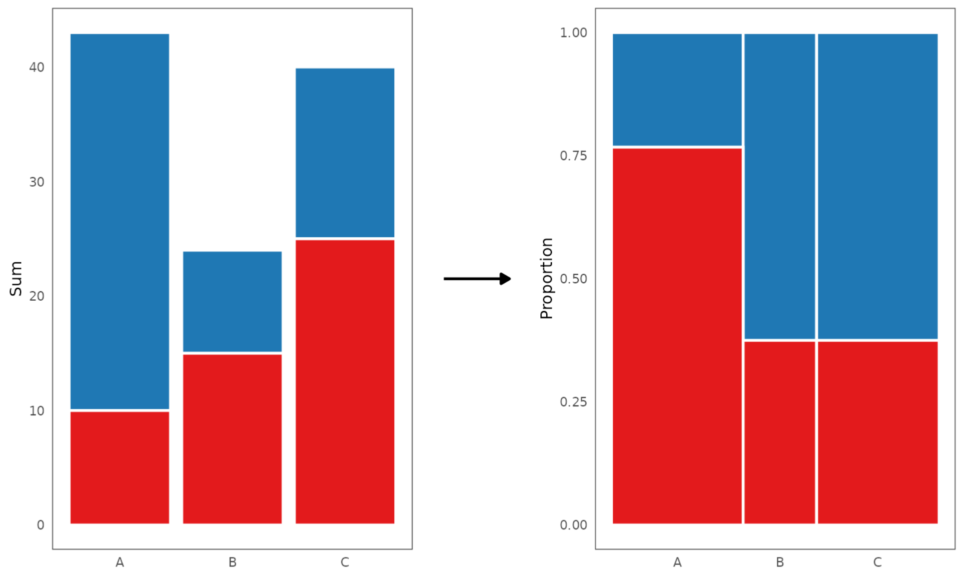


Figure 2.1: While barplot and spineplot represent the same underlying summaries, each makes it easier to see different aspects of our data. Barplot (left) makes it easier to compare absolute counts, whereas spineplot (right) makes it easier to compare proportions. Notice that the spineplot makes it much easier to see that the proportions of blue cases in categories B and C are exactly the same.

However, despite the fact that both barplots and spineplots represent the same underlying summaries (counts), turning one into the other is not always a trivial exercise. For example, in `ggplot2`, it is easy to create a barplot using simple declarative syntax, however, there is no such simple recipe for spineplots - creating the right plot in Figure 2.1 took over 10 lines of external data wrangling code (using standard `dplyr` syntax).

What is so complicated about spineplots? First of all, both the x- and y-axes represent the same variable: counts. However, the way the variable is used is different:

- Along the x-axis, we stack counts *within the levels of a single factor*
- Along the y-axis, we stack counts *within the levels of a product of two factors* and normalize them by the counts *within the levels of the parent factor*.

In other words, the spineplot forces us to confront the fact that the summaries in our plots form a hierarchy. When we compute the summaries underlying a stacked barplot or spineplot, we are not merely computing a matrix of values where the rows and the columns have no underlying meaning - instead, we are implicitly saying that objects along the x-axis (whole bars) represent a coarser level of partitioning compared with the objects (stacked segments) along the y-axis. The only difference between a barplot and spineplot is, in the barplot, we can get away with treating the two factors as if they were independent (had the same "weight"), whereas in the spineplot this is no longer possible.

This is why in declarative data visualization systems such as `ggplot2`, certain types of plots like spineplots are difficult to express. In these systems, the data is implicitly partitioned as a "flat" product of the factor variables. This representation is convenient (e.g. for defining aesthetics via a single call to `aes()`) but makes it impossible to express hierarchical structures such as the one encoded in spineplot.

Thus, ideally, our system should make it easy specify a pipeline where we compute monoidal summaries of our data within a hierarchy of partitions represented by one or more factor variables, apply some transformations to these summaries (possibly across the levels of the hierarchy), and finally map the summaries to some visual attributes.

2.3.7 Scales

To visualize data, we need to be able to translate values from the space of the data to the space of the graphical device (computer screen). In most data visualization systems, this is done by specialized components called scales or coordinate systems (see e.g. Murrell 2005; Wickham 2016; Wilkinson 2012). Scales serve as a bridge between what we have (data) and what we see (visual attributes), allowing us to cross from one domain to the other.

There exists is a fair research on the theoretical properties of scales and how they relate to the mechanisms of visual perception (see e.g. Krzywinski 2013; Michell 1986; Wilkinson 2012; Stevens 1946). However, when it comes to applying this knowledge and implementing scales in concrete data visualization systems, a lot less information is available. And, even when such information is available, it is it is often quite high-level of abstract (for some rare counter-examples, see e.g. Murrell 2005; Ziemkiewicz and Kosara 2009). Thus, the following section is based largely on how scales have been implemented in existing data visualization codebases, such as the `ggplot2` R package (Wickham 2016) or `d3-scale` module of D3 (Observable 2024; also used by Vega Satyanarayan et al. 2015), as well as on personal insights gained while implementing the package.

2.3.7.1 Overview

From a high-level perspective, a scale is just a function $s : D \to V$ which translates values of the data $d \in D$ to values of some visual attribute $v \in V$, such as the x- and y-position, length, area, radius, or color (Wilkinson 2012). This function may or may not be invertible, such that, at times, each value of the visual attribute may be identified with a unique data value (but this is not always the case).

One of the most common and typical cases is a scale where both D and V are subsets of the real numbers:

$$s : [d_{min}, d_{max}] \to [v_{min}, v_{max}] \qquad d_{min}, d_{max}, v_{min}, v_{max} \in \mathbb{R}$$

For example, suppose our data takes values in the range from 1 to 10 and we want to plot it along the x-axis, within a 800 pixels wide plotting region. Then, our scale is simply:

$$s_x : [1, 10] \to [0, 800]$$

Now, there is an infinite number of functions that fit this signature. However, one particularly nice and simple candidate is the following function:

Definition 2.1 (Simple linear mapping)**.**

$$s(d) = v_{max} + \frac{d - d_{min}}{d_{max} - d_{min}} \cdot (v_{max} - v_{min})$$

if we substitute the concrete values into the formula, this becomes:

$$s_x(d) = 0 + \frac{d - 1}{10 - 1} \cdot (800 - 0) = [(d - 1)/9] \cdot 800$$

The function acts on the data in the following way:

- $s_x(1) = (1 - 1)/9 \cdot 800 = 0$
- $s_x(10) = (10 - 1)/9 \cdot 800 = 800$
- $s_x(d) \in (0, 800)$ for any $d \in (1, 10)$

That is, the function maps the data value 1 to pixel 0 (left border of the plotting region), value 10 to to pixel 800 (right border of the plotting region), and any value in between 1 and 10 inside the interval 0 to 800, proportionally to where in the data range it is located.

It is relatively simple to translate the formula in 2.1 to code:

```
// simpleScale.ts
export function simpleScale(
  d: number,
  dmin: number,
  dmax: number,
  vmin: number,
  vmax: number,
): number {
  return vmin + ((d - dmin) / (dmax - dmin)) * (vmax - vmin);
}
```

And indeed, this function works the way we would expect:

```
import { simpleScale } from "./simpleScale.ts"

console.log(simpleScale(1, 1, 10, 0, 800))
console.log(simpleScale(5.5, 1, 10, 0, 800))
console.log(simpleScale(10, 1, 10, 0, 800))
```

```
## 0
## 400
## 800
```

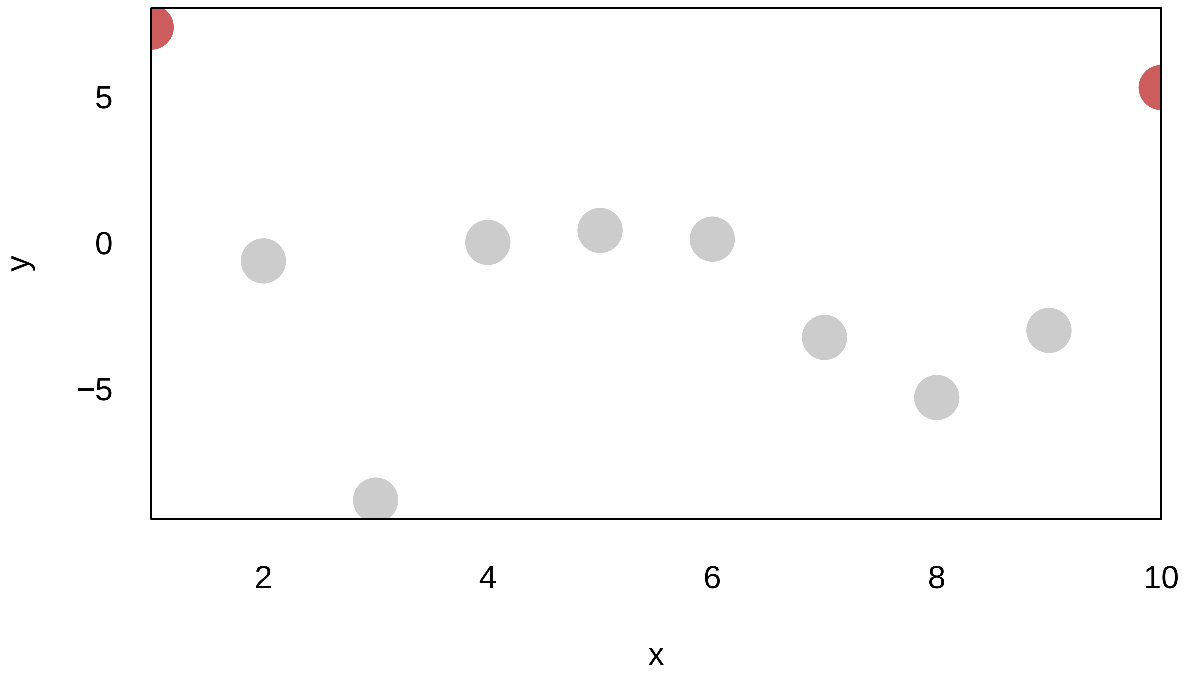
2.3.7.2 Limits of modeling scales as simple functions

Simple scale functions like the one above can work fine for basic data visualization systems. However, once we begin adding more features, this design becomes prohibitive. Consider, for example, what happens if we want to:

- Expand the scale limits
- Scale discrete data
- Apply non-linear transformations
- Pan, zoom, reverse, reorder, or otherwise modify the scale interactively

Let's take the first point as a motivating example. Consider what happens to data points at the limits of the data range under the simple linear mapping:

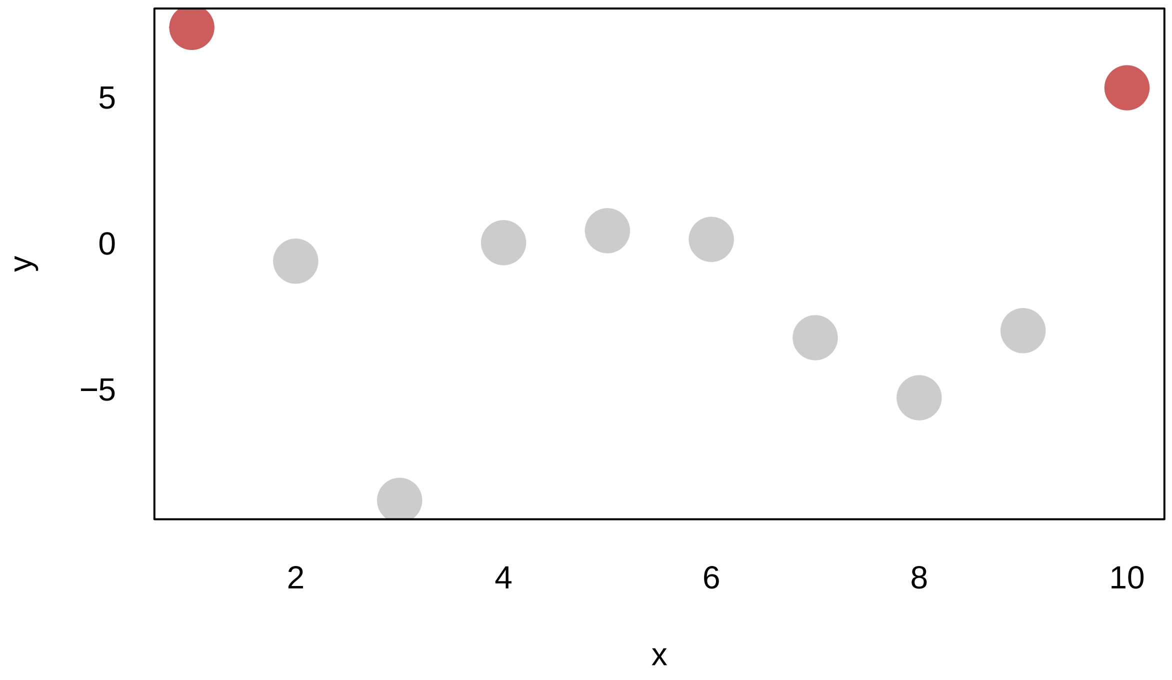
```
x <- 1:10
y <- rnorm(10, 0, 5)
col <- ifelse(1:10 %in% c(1, 10), "indianred", "grey80")

plot(x, y, col = col, cex = 3, xaxs = "i")
```



The plot above shows values scaled using the simple linear mapping along the x-axis, that is, $s : [1, 10] \rightarrow [0, 800]$ (effect of the `xaxs = "i"` argument). Notice that, since the position of the points representing the values 1 and 10 (highlighted in red) gets mapped to pixel values 0 and 800 (the left and right border of the plot), only half of each point is visible. This is quite undesirable - a fundamental principles of graphical integrity is that our graphics should not arbitrarily downplay or hide certain data points (Tufte 2001). The points at the axis limits are represented by only 1/2 of the area (or less, if at the limits of both axes), making them less salient, and this is especially pernicious since they are likely to be outliers.

To address this problem, most data visualization systems automatically expand the range of the domain by some pre-specified percentage:

```r
# By default, the plot() function automatically expands the x- and y-axis
# limits by approximately 4% on each end, see `xaxs` in ?graphics::par
plot(x, y, col = col, cex = 3)
```



We *could* achieve similar effect by modifying the simple linear mapping we have defined above and adding an additional argument:

```
// simpleScale2.ts
export function simpleScale2(
  d: number,
  dmin: number,
  dmax: number,
  vmin: number,
  vmax: number,
  exp: number, // Extra argument
): number {
  return (
    vmin + (exp / 2 + ((d - dmin) / (dmax - dmin)) * (1 - exp)) * (vmax - vmin)
  );
}
```

Now, if we set the `exp` argument to some positive value, the scaled values get mapped closer to the center of the plotting region. For example, setting `exp` to 0.2 moves each of the data limits 10% closer to the center of the plotting region:

```
import { simpleScale2 } from "./simpleScale2.ts"

console.log(simpleScale2(1, 1, 10, 0, 800, 0.2));
console.log(simpleScale2(5.5, 1, 10, 0, 800, 0.2));
console.log(simpleScale2(10, 1, 10, 0, 800, 0.2));
```

```
## 80
## 400
## 720
```

However, notice that this argument is applied symmetrically. At times, we may want to apply a different margin to each end of the scale. We could solve this by adding two arguments instead of one, e.g. `expLeft` and `expRight`, however, at this point, the function signature starts to become unwieldy. If we have to call the function in multiple places, it may become difficult to remember what each individual argument represents. Further, note that by adding arguments, the logic inside the function's body becomes denser and less readable. Finally, we may want to persist or modify some of the arguments during runtime (such as when panning or zooming). For all of these reasons, it may be a good idea to take a more structured approach and break the function down into several smaller components.

2.3.7.3 Solution: Two-component scales

The linear mapping formula in 2.1 can guide us in decomposing the scale function into smaller, more manageable parts. Let's look at it again:

$$s(d) = v_{min} + \frac{d - d_{min}}{d_{max} - d_{min}} \cdot (v_{max} - v_{min})$$

If we look closely, we may be able to see that there are two parts to the function:

That is, the linear mapping is composed of two simpler functions:

This leads us to the following definition of a scale:

Definition 2.2 (Scale as composition of two functions)**.** A scale s can be created by composing:

- A *normalize* function $n : D \to [0, 1]$, mapping data to the interval $[0, 1]$
- An *unnormalize* function $u : [0, 1] \to V$, mapping value in $[0, 1]$ to the visual attribute codomain

Such that:

$$s(d) = u(n(d))$$

Note that the terms *normalize* and *unnormalize* are arbitrary, however, I think they make for useful labels. They represent 1-D equivalent of vector normalization, mapping a value in the domain to and from a unit interval $[0, 1]$.

For the case of the linear mapping, we could rewrite this in code as follows:

```
// LinearMap.ts
export namespace LinearMap {
  export function normalize(d: number, dmin: number, dmax: number) {
    return (d - dmin) / (dmax - dmin);
  }

  export function unnormalize(p: number, vmin: number, vmax: number) {
    return vmin + p * (vmax - vmin);
  }
}
```

```
import { LinearMap } from "./LinearMap.ts"

console.log(LinearMap.normalize(5.5, 1, 10))
console.log(LinearMap.unnormalize(0.5, 0, 800))
console.log(LinearMap.unnormalize(LinearMap.normalize(5.5, 1, 10), 0, 800))
```

```
## 0.5
## 400
## 400
```

This two component system allows for a clean separation of concerns. Specifically, the normalize function only needs to know how to map the data values to $[0, 1]$. It does not need to be aware of where these normalized data values will be mapped to. Conversely, the unnormalize function only needs to understand how to translate values from $[0, 1]$ to the space of the visual attribute (such as x-axis position).

2.3.7.3.1 Beyond linear maps Another big advantage of the two-component scale system is that the functions n and u do not need to be a simple linear maps anymore. For example, suppose that our data D takes form of a set of discrete labels, such as $D = \{Prague, Vienna, Munich, Salzburg\}$. We can then replace n with a surjective function $n : D \to [0, 1]$ such that:

$$n(d) = \begin{cases} 0.2 & \text{if } d = Munich \\ 0.4 & \text{if } d = Prague \\ 0.6 & \text{if } d = Salzburg \\ 0.8 & \text{if } d = Vienna \end{cases}$$

In other words, n will place values of D at equidistant points along $[0, 1]$, ordered alphabetically. We can implement this function in code as follows:

```
// PointMap.ts
export namespace PointMap {
  export function normalize(d: string, dlabels: string[]) {
    return (dlabels.indexOf(d) + 1) / (dlabels.length + 1)
  }
}
```

Since the codomain of n is still $[0, 1]$, we can compose it with a simple linear mapping u just as easily as before:

```
import { LinearMap } from "./LinearMap.ts"
import { PointMap } from "./PointMap.ts"

const labels = ["Munich", "Prague", "Salzburg", "Vienna"];

console.log(PointMap.normalize("Munich", labels));
console.log(LinearMap.unnormalize(PointMap.normalize("Munich", labels), 0, 800));
console.log(LinearMap.unnormalize(PointMap.normalize("Prague", labels), 0, 800));
```

```
## 0.2
## 160
## 320
```

2.3.7.3.2 Inverses Additionally, another property of the two-component scale system that can be useful is that, if both n and u are invertible, then so is s. That is, we can easily obtain the inverse scale function by inverting the definition from 2.2:

Definition 2.3 (Scale inverse)**.** If a scale s is composed of invertible functions n and u, then s is invertible:

$$s^{-1}(v) = n^{-1}(u^{-1}(v))$$

This is the case for the simple linear map: the normalize and unnormalize functions are actually inverses of each other:

```
import { LinearMap } from "./LinearMap.ts"

console.log(LinearMap.unnormalize(LinearMap.normalize(300, 0, 500), 0, 500))
```

```
## 300
```

However, the inverse may not always exist. In practice, this is often the case when the domain of the data D is smaller than the codomain $[0, 1]$. Take, for example, the discrete point mapping. Since D is finite but $[0, 1]$ has infinitely many values, there will always be some values in $[0, 1]$ that no $d \in D$ maps to. For example, if $D = \{Munich, Prague, Salzburg, Vienna\}$ and $Munich$ maps to 0.2, $Prague$ maps to 0.4, and $Salzburg$ maps to 0.8, then there are no cities which map to 0.9, 0.444, or 0.123456789. Conversely, if we get given those numeric values, then there is no obvious way to map them back to the cities.

One thing we can do is to replace the inverse/unnormalize function with a weaker form of inverse, called retraction (Lawvere and Schanuel 2009). Specifically, if we have a normalize function $n : D \to [0, 1]$, then an unnormalize retraction u^* will have the property that:

$$u^*(n(d)) = d \qquad \forall d \in D$$

However, the converse doesn't necessarily hold:

$$\neg \big[n(u^*(v)) = v \qquad \forall v \in V \big]$$

For example, for the discrete point mapping, a retraction may map a value in $[0, 1]$ to the closest data value $d \in D$:

```
// PointMap.ts
export namespace PointMap {
  export function normalize(d: string, dlabels: string[]) {
    return (dlabels.indexOf(d) + 1) / (dlabels.length + 1)
  }

  // Retraction - find the closest label
  export function unnormalize(p: number, dlabels: string[]) {
    const k = Math.round(p * (dlabels.length + 1) - 1)
    return dlabels[k]
  }
}

const labels = ["Munich", "Prague", "Salzburg", "Vienna"];
const [prague, munich] = ["Prague", "Munich"].map(x => PointMap.normalize(x, labels))
const midpoint = (prague + munich) / 2

// Helper function for stripping away floating point error
const strip = (x: number) => parseFloat(x.toPrecision(12))

console.log(`Midpoint between Munich and Prague: `, strip(midpoint))
console.log(`unnormalize(0.2999): `, PointMap.unnormalize(0.2999, labels))
console.log(`unnormalize(3): `, PointMap.unnormalize(0.3, labels))
```

```
## Midpoint between Munich and Prague:  0.3
## unnormalize(0.2999):  Munich
## unnormalize(3):  Prague
```

While inverses are always unique (Lawvere and Schanuel 2009; Fong and Spivak 2019), we may be able to come up with many different retractions for any given function. For example, with the discrete point map above, we could use the floor function instead of rounding and assign label to a value in $[0, 1]$ if it is less than the value of the normalized label (but more than the preceding labels).

The non-uniqueness of retractions presents a bit of a dilemma. How do we decide which retraction to use? And, if a certain retractive implementation of `unnormalize` returns a value, how do we decide if it is the "correct one"?

However, in practice, this is not much of a problem. While developing the package, I found that I've only ever had to use the `unnormalize` function with continuous data (`LinearMap`), and so the inverse was always well-defined. This is probably also why packages like `ggplot2` and `D3` can get by without this functionality. However, I still find it helpful to include the `unnormalize` function as a first class citizen (instead of it being relegated to some special case), both in terms of the mental model and also for debugging.

2.3.7.3.3 Some other remarks about the two-component scale system It is worth noting that there is nothing inherently special about the interval $[0, 1]$ as the intermediate domain: any finite subset of $\mathbb{R}$ would do. However, the interval $[0, 1]$ is convenient, both in terms of interpretation as well as for implementation, as we will see later.

Finally, so far I have discussed scales as *functions*: the scale function, the normalize function, and unnormalize function. Framing scales as composition of functions leads to a nice correspondence between the mathematical definition and the code. However, in practice, it may be more convenient to implement the domain and codomain as *objects* or *classes*, as we will also see in the following section. The important point is that, no matter how the two components are represented, each is responsible for translating values from/to its domain and the interval $[0, 1]$.

2.3.7.4 Past implementations of scales

Two-component scale systems such as the one sketched out above are fairly standard across data visualization libraries. For example, in D3 (Bostock, Ogievetsky, and Heer 2011), scales are implemented in a functional style, such that the data domain and the visual attribute codomain are passed as tuples or arrays of values to a higher-order `scale*` function (such as `scaleLinear`, `scalePoint`, or `scaleBand`), which then returns a new function that can be used for scaling. The domain and codomain can also be changed at a later point, by using the `scale*.domain` and `scale*.range` methods respectively (JavaScript functions are objects and can have other functions/methods attached to them).

For illustration, here is an example from the official documentation (Observable 2024):

```
const x = d3.scaleLinear([10, 130], [0, 960]);
x(20); // 80
const color = d3.scaleLinear([10, 100], ["brown", "steelblue"]);
color(20); // "rgb(154, 52, 57)"
// The domain and codomain can be changed after initialization
const y = d3.scaleLinear().domain([10, 130]);
```

Internally, the `scale*` functions rely on other specialized functions to translate from its domain to the codomain (such as the `normalize()` and `scale()` functions for continuous and discrete/ordinal domains, respectively, and various `interpolate()` functions for codomains).

Similarly, in `ggplot2` (Wickham 2016), scales are built upon the `Scale` class, with each subtype implementing `limits` and `palette` properties. The `limits` property is a vector which corresponds to the data domain and the `palette` property is a function which corresponds roughly to the visual codomain (the x- and y-position behave slightly differently, due to being transformed via coordinate systems). Internally, the package uses the `rescale` function from the `scales` package (Wickham, Pedersen, and Seidel 2023) to map data values to $[0, 1]$ and then the `palette` function is responsible for mapping these normalized values to the visual attribute. For illustration, here's the full definition of the `map` method on the `ScaleContinuous` class (I've added comments for clarity):

```
map = function(self, x, limits = self$get_limits()) {
  # Limits are just a tuple, rescale maps x to [0, 1]
  x <- self$rescale(self$oob(x, range = limits), limits)

  uniq <- unique0(x)
  # Palette is a function which returns a vector of attribute values
  pal <- self$palette(uniq)
  scaled <- pal[match(x, uniq)]
  ifelse(!is.na(scaled), scaled, self$na.value)
}
```

2.3.7.5 Proposed model of scales

One feature that the models of scales that `D3` and `ggplot2` rely on is that they both treat the data domain and the visual attribute codomain as different types. In `D3`, fundamentally different functions are used to translate from $D \to [0, 1]$ and from $[0, 1] \to V$, and in `ggplot2`, `limits` is a simple vector/tuple whereas `palette` is a function. While these approaches may have some benefits, such as perhaps offering greater flexibility, they also add additional complexity. Specifically, we have to use two different mental models: one when considering the domain and another when considering the codomain. Further, these models of scales only work in one direction: mapping values $D \to V$. For going the the other way, i.e. mapping $V \to D$, other specialized functions have to be used.

I propose a model of scales which implements both the domain and the codomain as components of the same type: `Expanse`. Fundamentally, this makes it so that the only difference between the data domain and the visual attribute codomain is which property of the scale they are assigned to.

Here is a (slightly) simplified version of the `Scale` interface:

```
interface Scale<D extends Expanse, V extends Expanse> {
  domain: D
  codomain: V
}
```

`D` and `V` represent the data domain and the visual attribute codomain, respectively.

The two fundamental functions connected to `Scale` are:

```
function pushforward<D, V>(scale: Scale<D, V>, value: ValueOf<D>): ValueOf<V>
function pullback<D, V>(scale: Scale<D, V>, value: ValueOf<V>): ValueOf<D>
```

The `pushforward` function *pushes values forward* through the scale, first through its domain and then its codomain, and the `pullback` function *pulls values back*, first through its codomain and then through its domain. The `ValueOf` type helper just identifies the type associated with the expanse's data (e.g. `number` for a continuous `Expanse`, `string` for a discrete `Expanse`, etc...). I've omitted the generic type parameter constraint (`<D extends Expanse, V extends Expanse>`) for brevity.

Here is a simplified implementation of the two functions:

```
namespace Scale {
  function pushforward<D, V>(scale: Scale<D, V>, value: ValueOf<D>): ValueOf<V> {
    const { domain, codomain } = scale;
    return Expanse.unnormalize(codomain, Expanse.normalize(domain, value));
  }

  function pullback<D, V>(scale: Scale<D, V>, value: ValueOf<V>): ValueOf<D> {
    const { domain, codomain } = scale;
    return Expanse.unnormalize(domain, Expanse.normalize(codomain, value))
  }
}
```

We can see that most of the work is done by the two `Expanse` components: we use `domain` to translates $D \to [0, 1]$ and codomain to translate $[0, 1] \to V$. `Scale` only serves as plumbing, connecting the two together.

I argue that this model provides several benefits. First of all, it makes the code easier to reason about. Since both the `domain` and `codomain` are of the same type, we only need to keep a single mental model in mind. Second, if `domain` and `codomain` provide inverse functions (`unnormalize`), we get the inverse scale function $V \to D$ for free (this is just the `pullback` function).

However, before we discuss `Expanse`, there are also some important functionalities that we may want to implement on `Scale` directly. There are two main reasons for this. First, we may want these functionalities to apply generally, across the various `Expanse` subtypes. Second, by implementing them on `Scale`, we can keep the `Expanse` interface cleaner. These general functionalities will be the subject of the next few sections.

2.3.7.5.1 Zero and one Recall how in Section 2.3.7.2, we discussed the problem of expanding axis limits to display margins. Clearly, this is something that we also want to be able to do with our two-component scales. However, since we are designing an interactive data visualization system, we also want to be able to do more with axis limits: we want to be able to manipulate them dynamically during runtime, to implement features such as zooming and panning.

In Section 2.3.7.2, we solved the problem of expanding axis limits by adding an additional argument to the `simpleScale` function. However, as was discussed previously, this approach does not scale well for more featureful implementations of scales. So how should we go about implementing dynamic axis limits in the context of the two-component scale system?

Suppose we want to add margins to a scale where both the domain or codomain are continuous, such as the x-axis in a typical scatterplot. To implement margins, we could either expand the range of the data (the domain) or shrink the range of the visual attribute (the codomain). However, expanding the domain seems like a bad idea - this only works if the domain is continuous, and, clearly, we may want to add margins to discrete scales too, such the the x-axis of a barplot. Shrinking the range of the codomain could work (most visual attributes are continuous), however, we would need to implement some custom logic for when the plot gets resized. Also, by treating codomain differently than the codomain, we would be breaking away from our intention of representing both with the same generic `Expanse` type.

So what can we do? As was foreshadowed at end of the previous section, we can put the functionality for expanding axis limits directly onto `Scale`. Specifically, notice that any values passing through a scale are first converted to the interval $[0, 1]$ and then back to the space of either the domain or codomain:

$$D \to [0, 1] \to V$$

If we re-normalize these normalized values in $[0, 1]$, we effectively expand or shrink axis limits without having to touch either the domain or codomain. To give a metaphor, if we imagine `Scale` as a pipe connecting the `domain` and `codomain`, we can manipulate axis limits by stretching or squeezing this pipe, allowing more or less water to flow through.

To actually implement this, we can add two additional parameters to `Scale`, `zero` and `one`:

```
interface Scale<D extends Expanse, V extends Expanse> {
  domain: D
  codomain: V
  props: { // A dictionary of properties
    zero: number
    one: number
  }
}
```

Now, we can use these two parameters to implement a new version of the `pushforward` function:

```
function pushforward<D, V>(scale: Scale<D, V>, value: D): V {
  const { domain, codomain, props } = scale;
  const { zero, one } = props
  let normalized = Expanse.normalize(domain, value)
  normalized = zero + normalized * (one - zero) // Re-normalize
  return Expanse.unnormalize(codomain, normalized)
}
```

The new function's body is a bit more dense, however, the only real change is in the line with the comment. When we re-normalize, we scale the normalized value by the `(zero - one)` range and increment it by `zero`. In other words, `zero` tells us the proportion of the codomain range that the minimum data value gets mapped to, and `one` tells us the proportion of the codomain range that the maximum data value gets mapped to.

For example, suppose we set `zero` to 0.1 and `one` to 0.9. Then we have effectively implemented 10% margins on either side of the scale. If our scale has a $[1, 10]$ domain and $[0, 800]$ codomain, this will result in the following mapping:

- The "minimum" data value (1) gets mapped to 10% of the codomain range (80)
  - Because `zero + 0 * (one - zero) = zero = 0.1`
- The "maximum" data value (10) gets mapped to 90% of the codomain range (720)
  - Because `zero + 1 * (one - zero) = one = 0.9`

Note the quotation marks around the words "minimum" and "maximum" - there is no requirement for the data to be continuous. For example, if the domain is a discrete `Expanse` which maps the string value `"A"` to zero, then the `pushforward` function will map `"A"` to 10% of the codomain range, just as it did in the case of the continuous domain. Likewise, the codomain could also be discrete - we could use this to implement scales for binned versions of visual attributes such as color or size.

Thus, we can use `zero` and `one` to implement margins. However, there is much more we can do with these parameters. First, despite the names, `zero` and `one` can both take values *less* than zero and *more* than one. For example, suppose we increment both `zero` and `one` by the same amount, e.g. we set `zero` to 0.1 and `one` to 1.1. Then, the minimum data value will get mapped to the 10% of the codomain range, and the maximum data value will get mapped to 110% of the codomain range (which may lie outside the space representable by the graphic device). If the codomain represents the x-axis position, then we have shifted all of the geometric objects 10% to the right. We have effectively implemented *panning*:

```
function move(scale: Scale, amount: number) {
  scale.props.zero += amount;
  scale.props.one += amount;
}
```

That's it. We have implemented a functionality for panning which will work no matter if `domain` translates numbers, strings, or some other more complex data types.

We can also stretch or shrink `zero` and `one` in opposite directions. For example, by setting `zero` to -0.5 and `one` to 1.5, then the minimum and maximum data values will get mapped 50% below and 50% above the limits of the codomain range, respectively, and the 25 and 75 data percentiles will get mapped to the minimum and maximum of the codomain range. If we apply this to the x- or y-axes, we've just implemented *zooming*.

To be perfectly honest, there's a bit more ceremony involved with zooming. Specifically, if we don't start from `zero = 0` and `one = 1` (e.g. if our plot already has margins or if we're zooming in multiple levels deep), then we need to re-normalize within these values. This took me a bit of time to nail down, however, it's just (highschool) algebra:

```
function rangeInverse(min: number, max: number) {
  return 1 / (max - min);
}

function invertRange(min: number, max: number) {
  const ri = rangeInverse(min, max);
  return [-min * ri, ri - min * ri];
}

namespace Scale {
  export function expand(
    scale: { props: { zero: number; one: number } },
    zero: number,
    one: number
  ) {
    const { zero: currentZero, one: currentOne } = scale.props;
    const currentRange = currentOne - currentZero;

    // Re-normalize within current values
    zero = (zero - currentZero) / currentRange;
    one = (one - currentZero) / currentRange;

    // Invert
    [zero, one] = invertRange(zero, one);

    scale.props.zero = zero;
    scale.props.one = one;
  }
}

const scale1 = { props: { zero: 0, one: 1 } }; // Mock of default scale
const scale2 = { props: { zero: 0.1, one: 0.9 } }; // Mock of scale with margins

// Zoom into the middle 50% of either scale
Scale.expand(scale1, 0.25, 0.75);
Scale.expand(scale2, 0.25, 0.75);

console.log(`Zoomed in scale with no margins`, scale1.props);
console.log(`Zoomed in scale with 10% margins`, scale2.props);
```

```
## Zoomed in scale with no margins {
##   zero: -0.5,
##   one: 1.5,
## }
## Zoomed in scale with 10% margins {
##   zero: -0.3,
##   one: 1.3,
## }
```

As you can see, zooming into the middle 50% of a scale that already includes margins has a smaller effect on `zero` and `one`, since the margins have effectively expand the space we're zooming into (i.e., a scale with margins is already *zoomed out*, in a way).

2.3.7.5.2 Direction

In the same way we can think about expanding/shrinking axis limits in a way that is not coupled to any particular data representation or visual attribute, it may also be helpful to make direction a property of `Scale` rather than either of the `Expanse` components.

We *could* do this by manipulating the `zero` and `one` properties. For example, by setting `zero` to 1 and `one` to 0, we could effectively reverse the direction of the scale. However, in practice, this would complicate our logic and make it harder for someone to interpret the `Scale` properties. It is a better idea to add an explicit `direction` parameter instead:

```
interface Scale<D extends Expanse, V extends Expanse> {
  domain: D
  codomain: V
  props: {
    zero: number
    one: number
    direction: 1 | -1 // Extra parameter
  }
}
```

Like with `zero` and `one`, `direction` acts on the normalized values in $[0, 1]$. This means that we need to apply it in any transformations that use these values. For example, here's an updated version of the `move` function:

```
export function move(scale: Scale, amount: number) {
  let { direction, zero, one } = scale.props;
  zero += direction * amount;
  one += direction * amount;
}
```

Likewise, the `pushforward`, `pullback`, and `expand` functions also need to take `direction` into account. Either way, with this functionality in place, it becomes trivial to flip or reverse a scale:

```
export function flip(scale: Scale) {
  scale.props.direction -= 1;
}
```

2.3.7.5.3 Multipliers Finally, it may also be helpful to have the ability to shrink/expand the normalized values by some constant without having to modify properties of either the `domain` or `codomain`. Again, this could be done by using the `zero` and `one` properties, however, it's better to define separate properties instead. Specifically, we can add *two* additional parameters:

```
interface Scale<D extends Expanse, V extends Expanse> {
  domain: D
  codomain: V
  props: {
    zero: number
    one: number
    direction: 1 | -1
    scale: number // Extra parameter
    mult: number // And another one
  }
}
```

The reason it is better to have two multiplier parameters instead of just one is that there are different reasons for why we may want to multiply values by a constant. First, we may want to multiply the values by some constant that remains fairly static throughout the lifetime of the program/visualization. That is the job of the `scale` parameter. Conversely, we may want to also dynamically manipulate the constant by which the values are multiplied. That is what `mult` is for. Having two multipliers makes it easier to reason about the scale's behavior, as well as to apply changes such as restoring to defaults.

A good example of this is the barplot. In a typical barplot, all bars share the same width, which is some fraction of the width of the entire plotting region. Clearly, this fraction needs to depend on the number of bars in the plot, such that, with k categories/bars, the bar width will be proportional to k. However, we may also want to be able to make the bars wider/narrower interactively, e.g. by pressing the `+\-` keys. Thus, the width of the bars is proportional to $c \cdot k$ where k is the static part of the constant (`scale`) and c is the dynamic part of the constant (`mult`).

We apply the constant to the normalized value each time we push/pull a value through a scale:

```
// This will be included in the body of pushforward(); see below for full example
let normalized = Expanse.normalize(domain, value)
normalized = normalized * scale * mult
```

Finally, we could hypothetically extend this idea to an entire array of different multipliers, that we could reduce into a single constant each time we push a value through a scale. This could be useful in some circumstances, however, in my application, I found that having two parameters was enough to solve all of my scaling problems. Additionally, having an array of multipliers might make the scaling functions slightly less performant, if we have to reduce the array each time we `pushforward/pullback`, or it might make keeping track of the state of the `Scale` object slightly more complicated, if we roll these multipliers into one constant each time we update the array. We would also lose the semantic distinction that we have with `scale` and `mult`. This might be a perfectly fine trade-off if our scales require more multipliers, however, I did not find this to be the case in my implementation.

2.3.7.5.4 The Full Monty With all of the pieces in place, we can put together the full implementation of the `pushforward` function.

It may be helpful to define two helper function for applying the `Scale` properties to a normalized value. First, the `applyDirection` function simply applies the `direction` property, such that `applyDirection(x, 1)` is simply the identity whereas `applyDirection(x, -1)` returns `1 - x` (i.e. moving from `one` down):

```
function applyDirection(x: number, direction: 1 | -1) {
  return 0.5 * (1 - direction) + direction * x;
}

console.log(applyDirection(0.75, 1))
console.log(applyDirection(0.75, -1))
console.log(applyDirection(1.25, -1))
```

```
## 0.75
## 0.25
## -0.25
```

Second, we can define the `applyPropsForward` function which takes a normalized value and applies all of the `Scale` properties to it:

```
type Props = {
  zero: number;
  one: number;
  direction: -1 | 1;
  scale: number;
  mult: number;
};

function applyPropsForward(x: number, props: Props) {
  const { zero, one, direction, scale, mult } = props;
  x = x * scale * mult;
  x = zero + x * (one - zero);
  return applyDirection(x, direction);
}
```

Now we ready to define the full `pushforward` function. As one final note, we should probably be able to handle the case where the `domain` and `codomain` work on arrays of values rather than scalars (this can be helpful, for example, in the case of a parallel coordinates plot). As such, we can add an `if` block to check where the normalized value is an array and handle appropriately. In total:

```
function pushforward<T extends Expanse, U extends Expanse>(
  scale: Scale<T, U>,
  value: Expanse.Value<T>,
): Expanse.Value<U> {
  const { domain, codomain, props } = scale;
  let normalized = Expanse.normalize(domain, value);

  if (Array.isArray(normalized)) {
    normalized = normalized.map((x) => applyPropsForward(x, props));
  } else {
    normalized = applyPropsForward(normalized, props);
  }

  return Expanse.unnormalize(codomain, normalized);
}
```

This is the full definition of the `pushforward` function in `plotscape` as of 2025-02-20. The implementation for `pullback` function is very similar, with the only differences being that the order of the `domain` and `codomain` arguments reversed, and it uses the `applyPropsBackward` function, which is not too difficult to derive.

2.3.8 Expanses

So far, we have discussed scales, and described them as a sort of bridge between two properties of type `Expanse` - the domain and the codomain. However, we have left the precise nature of the `Expanse` type vague. Now it is finally time to discuss `Expanse` and its various subtypes concretely.

As mentioned previously, the job of the `Expanse<T>` is to translate values of type `T` (its domain) to and from the interval $[0, 1]^n$. This makes `Expanse` similar to the maps discussed in Section 2.3.7.3. The reason why the normalized interval is identified as $[0, 1]^n$ instead of the one-dimensional interval $[0, 1]$ is because, sometimes, we may want to map multi-dimensional values. For example, in the parallel-coordinates plot, we want to map values of several different variables to the y-axis. Typically, the dimensionality of the normalized values will be the same as that of `T`, however, we could imagine a situation where it might not be so, for example, we could imagine mapping 3-dimensional vectors to their (normalized) length.

Most of the functionality is implemented by the specific subtypes of `Expanse`, however, there is also some shared behavior. The simplified interface of `Expanse` is:

```
interface Expanse<T> {
  value: T;
  normalized: number | number[]
}
```

Here, the `value` and `normalized` properties are opaque types (used on type-level only), which simply indicate the domain type `T` and the dimensionality of the normalized values (`number | number[]`).

Each namespace corresponding to a subtype of `Expanse<T>` exports two important functions:

- A *normalize* function $n : T \rightarrow [0, 1]^n$, mapping values from T to $[0, 1]^n$
- An *unnormalize* function $u : [0, 1]^n \rightarrow T$, mapping values from $[0, 1]^n$ to T

There are two other important methods that each `Expanse` subtype must export: `train` and `breaks`. The `train` function allows the expanse to train on new data (for example, after a histogram binwidth has been changed). The `breaks` function simply returns an array of breaks of type `T`. Thus, each subtype of `Expanse` implements the following polymorphic methods:

```
interface ExpanseMethods<T> {
  normalize(expanse: Expanse<T>, value: T): number | number[];
  unnormalize(expanse: Expanse<T>, value: number | number[]): T;
  train(expanse: Expanse<T>, values: T[], options?: Record<string, any>): void;
  breaks(expanse: Expanse<T>, zero?: number, one?: number): T[] | number[];
}
```

2.3.8.1 Continuous expanses

A continuous expanse is a generalization of the linear mapping discussed in Section 2.3.7.3. That is, it translates values to and from a continuous interval given (roughly) by $[\min, \max]$. Here is a simplified interface:

```
interface ExpanseContinuous {
  min: number;
  max: number;
  offset: number;
  trans: (x: number) => number;
  inv: (x: number) => number;
  ratio: boolean;
}
```

The `min` and `max` properties are fairly self-explanatory - they denote the minimum and maximum of the data. The `offset` property allows us to move values by some constant, either before they have been normalized or after they have been unnormalized. This is useful, for example, when we want to ensure that the width of a spineplot bar is exactly 1 pixel less than the available space. The `trans` and `inv` properties allow us to perform non-linear transformations (they should, intuitively, be inverses of each other). By default, they are both set to the identity function (`(x) => x`). Finally, the `ratio` property is a simple boolean flag which indicates whether the expanse is part of a ratio scale. If this flag is set to `true`, then the `min` value of the expanse must always be zero and we cannot change it by, for example, training on new data.

The normalize and unnormalize functions in the `ExpanseContinuous` namespace are generalizations of the linear map:

```
// ExpanseContinuous.ts
export namespace ExpanseContinuous {
    export function normalize(expanse: ExpanseContinuous, value: number) {
    const { min, max, offset, trans } = expanse;
    return (trans(value - offset) - trans(min)) / (trans(max) - trans(min));
  }

  export function unnormalize(expanse: ExpanseContinuous, value: number) {
    const { min, max, offset, trans, inv } = expanse;
    return inv(trans(min) + value * (trans(max) - trans(min))) + offset;
  }
}
```

And these work as we would expect:

```
import { ExpanseContinuous } from "./ExpanseContinuous"

const identity = (x) => x;
// I could have defined a proper constructor above but opted not to to save lines
const exp = { min: 1, max: 16, offset: 0, trans: identity, inv: identity };

console.log(ExpanseContinuous.normalize(exp, 4));
exp.trans = Math.sqrt; // Technically, we should also set inverse to square
console.log(ExpanseContinuous.normalize(exp, 4));
```

```
## 0.2
## 0.3333333333333333
```

Finally, the `ExpanseContinuous` namespace also export a `train` function, which goes through an array values and updates the min and max properties (max only if `ratio` is set to `true`), and a `breaks` function which returns a list of breaks, using an algorithm inspired by base R's `pretty` function.

2.3.8.2 Point expanses

A point expanse is the simplest type of discrete expanse. It simply places values at equidistant points along the $[0, 1]$ interval, based on an ordered array of labels. Here is a simplified interface:

```
interface ExpansePoint {
    labels: string[];
    order: number[];
}
```

The `labels` array contains the all of the unique values that data take (strings). The `order` array is a simple array of indices which represent the order in which the labels get assigned to points in the $[0, 1]$ interval.

The normalize and unnormalize functions in the `ExpansePoint` namespace simply use a label to find the corresponding point in $[0, 1]$ or the use a point to find the closest label, while respecting the `order`:

```
// ExpansePoint.ts
export namespace ExpansePoint {
  export function normalize(expanse: ExpansePoint, value: string) {
    const { labels, order } = expanse;
    const index = order[labels.indexOf(value)];
    if (index === -1) return index;
    return index / (labels.length - 1);
  }

  export function unnormalize(expanse: ExpansePoint, index: number) {
    const { labels, order } = expanse;
    index = Math.round(index * (labels.length - 1));
    return labels[order[index]];
  }
}
```

Again, these functions work as we would expect:

```
import { ExpansePoint } from "./ExpansePoint"

const cities = ["Berlin", "Prague", "Vienna"]

const exp = {
  labels: cities,
  order: [0, 1, 2],
};

console.log(cities.map(city => ExpansePoint.normalize(exp, city)));
exp.order[0] = 1; // Swap the order of the first two values
exp.order[1] = 0;
console.log(cities.map(city => ExpansePoint.normalize(exp, city)));
```

```
## [ 0, 0.5, 1 ]
## [ 0.5, 0, 1 ]
```

Like `ExpanseContinuous`, the `ExpansePoint` namespace also contains a `train` function, which loops through an array of labels and finds all of the unique values, as well as a `breaks` function, which simply returns ordered `labels`. Further, the namespace also contains a `reorder` function which mutates the `order` property based on an array of indices.

2.3.8.3 Band expanses

While `ExpansePoint` places values at equidistant points along $[0, 1]$, `ExpanseBand` places values at the midpoints of corresponding bins or bands. These bands can have variable widths, which is useful, for example, when specifying the x-axis position in a barplot. The simplified interface of `ExpanseBand` is the following:

```
export interface ExpanseBand {
  labels: string[];
  order: number[];
  weights: number[];
  cumulativeWeights: number[];
}
```

Like `ExpansePoint`, `ExpanseBand` has the `labels` and `order` properties, which work exactly the same way as before. However, additionally, it also has the `weights` and `cumulativeWeights` properties, which are numeric arrays that define the width of each band. `weights` record the width of each band, and `cumulativeWeights` record the cumulative sums of the weights, which are used in the `normalize` and `unnormalize` functions. Thus, each time we update `weights`, we need to also update `cumulativeWeights` as well.

The normalize and unnormalize functions in the `ExpanseBand` namespace map labels to and from the midpoint of their corresponding bands:

```
export namespace ExpanseBand {
  export function normalize(expanse: ExpanseBand, value: string) {
    const { labels } = expanse;
    const index = labels.indexOf(value);
    return getMidpoint(expanse, index);
  }

  export function unnormalize(expanse: ExpanseBand, value: number) {
    const { labels, order, cumulativeWeights } = expanse;

    const weight = value * last(cumulativeWeights);
    let index = 0;

    while (index < cumulativeWeights.length - 1) {
      if (cumulativeWeights[index] >= weight) break;
      index++;
    }

    return labels[order[index]];
  }

  function getMidpoint(expanse: ExpanseBand, index: number) {
    const { order, cumulativeWeights } = expanse.props;
    index = order[index];
    const lower = cumulativeWeights[index - 1] ?? 0;
    const upper = cumulativeWeights[index];
    const max = last(cumulativeWeights);

    return (lower + upper) / 2 / max;
  }
}
```

Notice that, because of the cumulative nature of the bands, the logic in the functions' bodies is a bit more complicated. First, to `normalize` a label, we need to first find the index of the label and then return the corresponding midpoint of the band, taking `weights` and `order` into account. Second, to `unnormalize`, we actually have to loop through the array of `cumulativeWeights` - there is no way to determine which bin a normalized value belongs to in $O(1)$ time (as far as I am aware). This is not much of a problem since the `ExpanseBand.unnormalize` is not used anywhere in the system (all scales implemented thus far use only `ExpanseBand.normalize`), however, it is important to be mindful of this.

Chapter 3

Applied example

> Please note that the data set used in this section is fairly large (~70,000 rows) and so the figures take some time to load (please allow ~30 seconds).

This section demonstrates a typical interactive workflow with `plotscaper`. The goal is to showcase the package's key features and capabilities by exploring a large, real-world data set, pertaining to a pressing issue: mental health.

Mental health is a global concern. In developed nations, mental health disorders are primary contributor to years lived with disability, significantly impacting both the well-being of individuals and the economic productivity of entire countries (Organization 2022). This issue, however, extends beyond developed nations. The global burden of mental health disorders has been steadily rising over the recent decades, a trend which is particularly concerning in low-income countries where access to mental health services is even more limited (Patel et al. 2018).

Having had personal experience with friends and relatives impacted by mental health issues, as well as having majored in psychology during my undergraduate studies, I have had a long-standing interest in the topic. It is clear to me that mental health is a key challenge that the world is facing today, and the first step towards solving it will require clearly identifying key trends and patterns. For this reason, I chose to dedicate this section to an exploration of a large longitudinal mental health data set.

3.0.1 About the data set

The Institute of Health Information and Statistics of the Czech Republic (IHIS, ÚZIS in Czech) is a government agency established by the Czech Ministry of

Health. Its primary responsibility is the collection, processing, and reporting of medical data within the country of Czechia (ÚZIS 2024). Of interest, the institute provides high-quality, open-access medical data, including information about the use and manufacture of pharmaceutics, fiscal and employment records from healthcare facilities, and various epidemiological data sets.

The Long-term Care data set (Soukupová et al. 2023) contains longitudinal information about long-term psychiatric care in Czechia. More specifically, it contains aggregated data on individuals released from psychiatric care facilities between 2010 and 2022. It includes information such the region of the treatment facility, the sex of the patients, age category, diagnosis based on the international ICD-10 classification (World Health Organization 2024a, 2024b), the number of hospitalizations, and the total number of days spent in care by the given subset of patients.

Here's the data set at a quick glance:

```r
df <- read.csv("./data/longterm_care.csv")
dplyr::glimpse(df)
```

The data contains over 68,000 rows, totaling over 410,000 individual-patient hospitalizations. Each row records the number patients with a particular set of of characteristics released from a treatment facility during a given year, and the number of days the patients spent in treatment in total.

In the original version of the data set, the column names as well as the labels of the categorical variables are in Czech. To make the analysis more easily accessible to non-Czech speakers, I took the liberty of translating most of these to English (excluding the `region` variable). The translation script is available in the thesis repository. Additionally, the data set website contains a JSON schema with a text description of each of the variables (Soukupová et al. 2023). I translated these descriptions as well and provide them below, in Table **??**:

Before we go on to explore the data set with interactive figures, there are a couple of things to note about the data set. The first is that the data has been pre-aggregated, such that each row represents the combined number of releases within a given subgroup of patients. For example, the first row indicates that, in the year 2019, 13 women aged 40-49 were released from treatment facilities in Olomoucký kraj (region), after receiving short-term care for F10 ICD-10 diagnosis (mental and behavioural disorders due to alcohol use, World Health Organization 2024a) for a sum total of 196 days:

```r
df[1, ]
```

The reason for this aggregation is likely to anonymize the data and reduce the risk of identifying individual patients (see e.g. Pina et al. 2024). However, when creating visualizations, we need to take the fact that each row represents a group of patients into account. For instance, when drawing a barplot, simply plotting row counts would not be appropriate, since that would ignore the size of the patient groups. Instead, to represent the data properly, we should aggregate (sum) either `cases` or `days`, depending on the question of interest. The same applies to all other aggregation plots, such as histograms (i.e. weighted histograms, see e.g. Unwin, Theus, and Härdle 2008) and fluctuation diagrams.

Fortunately, as we will see, `plotscaper` makes it easy to create these weighted types visualizations. And further, while the information this aggregated data provides inherently less granular information than patient-level records, we will see that it still preserves a large amount of structure.

3.0.2 Interactive exploration

3.0.2.1 The relationship between cases and days

We start by exploring the relationship between the two primary continuous variables of interest: `cases` (the number of patients in a given subgroup released from care) and `days` (the total number of days the given subgroup of patients spent in care). Intuitively, we would expect a positive, linear relationship between these variables, such that a larger patient groups should spend more days in care. We can use `plotscaper` to visualize this relationship via a scatterplot:

```r
library(plotscaper) # Load in the package

df |>
  create_schema() |> # Create a declarative schema for the figure
  add_scatterplot(c("cases", "days")) |> # Add a scatterplot
  render() # Render the schema into an interactive figure
```

Interestingly, the points did not show a simple linear trend. Instead, they seemed to cluster in three distinct "leaflets", each exhibiting a roughly linear trend. This suggests the presence of a pooling effect, such that the overall trend is the result of combining three distinct groups. Closer inspection of the data reveals that the `stay_category` variable has three levels: short-term (< 3 months), medium-term (3-6 months), and long-term (6+ months) care. Color-coding the cases indeed confirms that the three levels of `stay_category` correspond to the leaflets:

```r
df |>
  create_schema() |>
  add_scatterplot(c("cases", "days")) |>
  add_barplot(c("stay_category", "cases")) |> # y-axis is weighted by cases
  assign_cases(which(df$stay_category == "short"), 1) |> # Mark short-term green
```

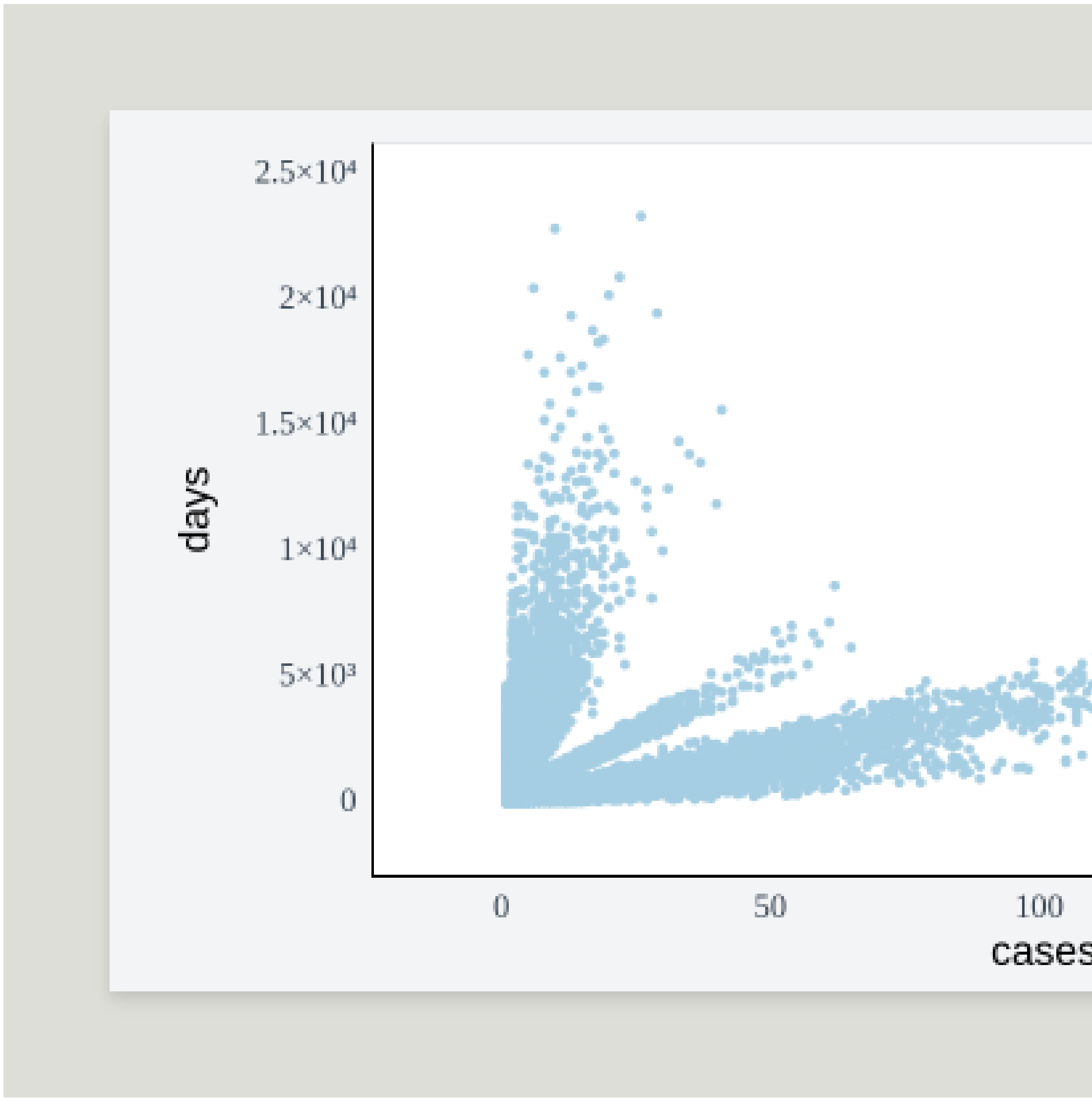


Figure 3.1: Relationship between the number of cases in a patient subgroup and the total number of days spent in care.

```
  assign_cases(which(df$stay_category == "long"), 2) |> # Mark long-term red
  render()
```

> Click on the barplot bars to confirm there is a fairly minimal overlap between points belonging to the three categories (selected points will be brought to the foreground). To remove all selection, double-click the figure.

However, the pooling effect does not itself explain the absence of points between the three leaflets. If the distribution of cases and days within each of the three `stay_category` levels were uniform, we should expect to see more points in the gaps between the leaflets. This additionally suggests a potential selection process, where patients are less likely to be discharged at durations near the category boundaries. We can confirm this by plotting the average number of days spent in care:

```
# Compute the average number of days spent in treatment
df$avg_days <- df$days / df$cases

df |>
  create_schema() |>
  add_scatterplot(c("cases", "avg_days")) |>
  add_barplot(c("stay_category", "cases")) |>
  assign_cases(which(df$stay_category == "short-term"), 1) |>
  assign_cases(which(df$stay_category == "long-term"), 2) |>
  set_scale("scatterplot1", "y", # Log-transform the y-axis
            transformation = "log10", default = TRUE) |>
  render()
```

Now we can clearly see the gaps between the three different distributions along the y-axis.

> Try querying the points near the y-axis gaps by pressing the `Q` key and hovering over them. You should observe that the gaps roughly span the 60-90 day and 150-210 day ranges, corresponding to 2-3 months and 5-7 months, respectively.

The trend we see in the scatterplot above strong indication of a selection process is at work. Specifically, it seems that patients who stay in treatment for more than two months are likely to be transferred to medium-term care and kept around for longer, and, likewise, those who stay in treatment for more than five months are likely to be moved to long-term care. There are likely administrative of health-insurance related reasons for this trend, nevertheless, it is still an interesting pattern to take note of.

3.0.2.2 Number of cases over time

A key question is how have the numbers of patients in treatment evolved over time. We can investigate this by plotting the same scatterplot as we did in the section above, as well as two barplots showing the total number of cases and the total number days in treatment, within each year. We can also include a histogram of the number of days, for a good measure:

```
schema <- df |>
  create_schema() |>
  add_scatterplot(c("cases", "days")) |>
  add_barplot(c("year", "cases")) |>
  add_barplot(c("year", "days")) |>
  add_histogram(c("days", "days")) |> # Again, make sure to weigh the y-axis
  set_parameters("histogram1", width = 20) # Set histogram binwidth to 20 days

schema |> render()
```

From the barplots, we can immediately see an interesting pattern: while the numbers of cases seem to have declined over time, the number of days patients spent in care seem to seems to have remained fairly constant. This suggest that while there are fewer patients over all, they are being hospitalized for longer.

We can confirm this interactively. Click on the bars corresponding to the year 2010 and 2022, in either of the two barplots (feel free to mark either of the bars by holding down the `1` or `2` keys and clicking them). You should see that, compared to 2010, there were more patients in long term care in 2022, and the relationship between the number of cases and the number of days in care was steeper.

On its own, the declining number of cases over time might appear as a positive development; however, the constant number days in treatment suggests a more worrying trend. Specifically, treatment facility placements are limited resource (Organization 2022), and the fact that days in treatment have stayed constant while cases have declined may indicate that the Czech healthcare system is becoming burdened by patients in long-term care, reducing its capacity to serve new clients.

Another way we can scrutinize the trend more closely by zooming into the histogram:

```
schema |>
  assign_cases(which(df$year == 2010), 1) |>
  assign_cases(which(df$year == 2022), 2) |>
  zoom("histogram1", c(-100, 0, 3e03, 1e05), units = "data") |>
  render()
```

> You can zoom into a plot in two ways: programmatically using the `zoom` function (as shown above), or manually by clicking and dragging to select a rectangular region and pressing the `Z` key. You can chain multiple zooms to magnify small regions of the plot. To undo zooming, press either the `X` to revert back one level of zoom, or `R` to reset the figure to its default state (including the default zoom level).

By clicking on the two bars, you should be able to see that, compared to 2010, the 2022 distribution of days spent in treatment had a fatter tail, suggesting that there were more patients who spent very long time in care.

3.0.2.3 Age and child and adolescent mental health

The global mental health decline affects adults and children alike, however, childhood mental health disorders are particularly concerning. If these disorders manifest during critical developmental periods, they can have serious, often lifelong consequences, causing irreversible changes in brain physiology even with successful treatment (see e.g. Keeley 2021). Children also have less agency than adults in managing their mental health, relying heavily on caregivers and schools for support. For these reasons and more, monitoring the mental health of children and adolescents is critical.

Fortunately, the overall proportion of children and adolescents in the data set was fairly low, amounting to <9% of all cases and <6% of the total number of days spent in treatment:

```r
aggregate(cbind(cases, days) ~ care_category, sum, data = df) |>
  lapply(function(x) { if (is.numeric(x)) return(x / sum(x)) else x }) |>
  data.frame()
```

To investigate how these numbers evolved over time, we can make use of the following figure:

```r
# Create a figure layout with two small plots in the left
# column, and one tall plot in the right column
layout <- matrix(c(
  1, 3,
  2, 3
), nrow = 2, byrow = TRUE)

df |>
  create_schema() |>
  add_barplot(c("year", "cases")) |>
  add_barplot(c("year", "days")) |>
  add_barplot(c("care_category", "cases")) |>
  set_layout(layout) |> # Set the layout
  render()
```

So far, we have been using a fairly simple interactive workflow that could be easily recreated via code, taking only one or two interactive actions at a time. However, now it is time to see the full potential of interactivity by chaining several interactive actions together. To explore how the proportion of child and adolescent patients evolved over time, try taking the following steps:

1. Mark the cases corresponding to children: click on the corresponding bar in the right barplot while holding down the `1` key.
2. Normalize the two leftmost barplots: click each of on the plots to activate it and press the `N` key while the plot is active (you can revert back to absolute counts by pressing the `N` key again).
3. Zoom into the regions of the leftmost barplots containing selected cases: click-and-drag to select a rectangular region and pressing the `Z` key.

By following these steps, you should end up with a figure similar to the one below:

```
df |>
  create_schema() |>
  add_barplot(c("year", "cases")) |>
  add_barplot(c("year", "days")) |>
  add_barplot(c("care_category", "cases")) |>
  assign_cases(which(df$care_category == "child")) |>
  plotscaper::normalize("barplot1") |>
  plotscaper::normalize("barplot2") |>
  zoom("barplot1", c(0, 0, 1, 0.15)) |>
  zoom("barplot2", c(0, 0, 1, 0.15)) |>
  set_layout(layout) |>
  render()
```

Interestingly, the two barplots show the opposite trend. While the proportion of the treatment days used by children and adolescents has declined over time, the proportion of total cases they make up has increased. The relative increase in cases appears to be driven by an overall decline in patient numbers: in absolute counts, the number of child and adolescent patients has remained fairly constant between 2010 to 2022, while the total patient count has decreased.

We can also get a more granular breakdown by plotting the age category variable:

```r
df |>
  create_schema() |>
  add_barplot(c("age_category", "cases")) |>
  add_barplot(c("year", "cases")) |>
  add_barplot(c("age_category", "days")) |>
  add_barplot(c("year", "days")) |>
  render()
```

Again, if we interrogate the figure by employing interactive actions such as selection, zooming, and normalization, we can discover that one age category in which there has been steady growth in both the proportion of cases and days spend in treatment are 70-79 year olds. This aligns with the limited placement availability hypothesis: while these patients account for a relatively small fraction of the total cases, they represent a disproportionately large and increasing proportion of days in treatment. Later, we will also see evidence that many of these patients suffer from neurodegenerative diseases, which require intensive long-term care. It may be the case that, with increasing life-expectancy, the healthcare system is not able to handle the influx of older patients, limiting the availability of placements.

3.0.2.4 Prevalence of diagnoses

Another important information we can glean from the data set is the prevalence of different diagnoses and their demographic characteristics. The data set identifies mental disorders according to ICD-10, an internationally recognized disease classification system published by the World Health organization which organizes various diseases into categories based on aetiology (World Health Organization 2024a).

It is first necessary to discuss the coding scheme of the diagnoses. The codes were directly translated from the Czech version of the data set (Soukupová et al. 2023). The vast majority diagnoses come from the F category, which represents mental and behavioral disorders, although there are also few references to the G category, which classifies diseases of the nervous system. Further, note that while some levels of the `diagnosis` variable represent a singular ICD-10 diagnosis (e.g. `f10`), others represent a range of diagnoses (e.g. `f11-f19`), a union (e.g. `f0 and g30`), or an exclusive difference (e.g. `f4 without f42`).

Importantly, some of the codes also represent a range of diagnoses *implicitly*. For instance, whereas `f10` code refers to the F10 diagnosis (alcohol-use disorders), the part `f4` in `f4 without f42` does *not* refer to the F04 diagnosis (organic amnesic syndrome, not induced by alcohol and other psychoactive substances) but instead to the F40-F48 range of diagnoses (neurotic, stress-related and somatoform disorders, World Health Organization 2024a). Likewise, `f2` represents F20-F29 (schizophrenia, schizotypal and delusional disorders), `f7` represents F70-F79 (mental retardation), and `f5` represents F50-F59 (behavioural syndromes associated with physiological disturbances and physical factors). I have confirmed this via personal communication with the data set's authors (Melicharová 2025).

Table **??** lists codes used in the data, in order of their prevalence (the number of all cases across all time), along with a short description based on the ICD-10 (World Health Organization 2024a), and some clarifying notes in parentheses that I myself have added:

To explore the prevalence of the various diagnoses as well as their demographic characteristics, we create another interactive figure. For this figure, I decided to plot the following variables: `diagnosis`, `age_category`, `sex`, and `reason_for_termination`. These seemed like the most interesting demographic variables. The `region` variable could also be an interesting choice, however, initial exploration did not reveal any interesting trends so I decided to omit it.

From now on, I will describe interesting features of the data in text rather than through individual figures. You are encouraged to verify these findings by interacting with the figures and using the techniques discussed so far.

```r
# Create ordering for barplots based on frequency
order_df <- aggregate(cases ~ diagnosis, sum, data = df)
order_df <- order_df[order(order_df$cases), ]

order_df2 <- aggregate(cases ~ reason_for_termination, sum, data = df)
order_df2 <- order_df2[order(order_df2$cases), ]

df |>
  create_schema() |>
  add_barplot(c("diagnosis", "cases")) |>
  add_barplot(c("age_category", "cases")) |>
  add_barplot(c("sex", "cases")) |>
  add_barplot(c("reason_for_termination", "cases")) |>
  # Sort the bars by prevalence (can also do interactively by pressing `O` key)
  set_scale("barplot1", "x", breaks = order_df$diagnosis) |>
  set_scale("barplot4", "x", breaks = order_df2$reason_for_termination) |>
  render()
```

The barplot in the top left panel of the Figure **??** shows that the five most common disorders accounted for the majority of patient cases. Each of these disorders affected over 40,000 patients between 2010 and 2022, representing over 75% of all cases (319,557 out of 414,242).

> Press the `Q` key and hover over the bars in the top left panel of Figure **??** to see what diagnosis each represents.

In order of prevalence, the top five disorders were, were: alcohol-use disorders, schizophrenia, Alzheimer's disease, neurotic and stress-related disorders, and disorders caused by psychoactive substances (excluding alcohol). Overall, the high prevalence of these disorders is fairly, given that their high socio-economic impact is well-known to psychiatrists. Nevertheless, it may be illustrative to take a closer look at this data and examine demographic trends.

First, alcohol use disorders were the most common diagnosis. This is not surprising, since, globally, alcohol use disorders rank among the most common disorders and are associated with high mortality due to chronic health conditions and injury (Carvalho et al. 2019). In the data set, this diagnosis was about twice as common in men and showed a fairly symmetric, normal-shaped age distribution, occurring the most frequently in 40-49 and 50-59 year-olds (this can be seen by selecting the corresponding bar in the top-left panel of figure Figure **??** and normalizing the age-category barplot).

The second most prevalent category of diagnoses were schizophrenia, schizotypal, and delusional disorders. While the individual lifetime prevalence of schizophrenia is not as high as some other disorders on this list, the reason for its high representation in the data set is likely its chronic and serious nature. Among those with mental illness, people with schizophrenia have one of the lowest life expectancies (see e.g. Chang et al. 2011), and often require multi-year or even life-long hospitalization (Messias, Chen, and Eaton 2007). This debilitating nature of schizophrenia has prompted some experts to describe it as "arguably one of the most severe health conditions affecting mankind" (see e.g. Messias, Chen, and Eaton 2007; Tandon et al. 2024). In the data set at hand, schizophrenic disorders had a fairly balanced sex ratio and a fairly flat age distribution.

Third most prevalent disorder categories was Alzheimer's disease. The high prevalence of this disorder is unfortunately also to be expected, as, in developed countries, Alzheimer's disease tends the leading cause of long-term psychiatric care in old age (see e.g. Cao et al. 2020; Langa et al. 2017). It also tends to be more prevalent in women. These patterns could be seen fairly well in the data set: the age distribution of Alzheimer's disease was strongly skewed, occurring much more frequently in older patients (and, in fact, making up the majority of >70 year-old patients), and the diagnosis was about ~40% more prevalent in women than in men. We can also see that Alzheimer's patient made up the vast majority of patients who had died in care, further reinforcing its status as a disease of old age.

The fourth most prevalent category of disorders were neurotic, stress-related, and somatoform disorders (excluding the obsessive-compulsive disorder, F42) which was classified as its own category in the data set. This category includes disorders such as specific phobias, generalized anxiety disorder, and the post-traumatic stress disorder (World Health Organization 2024a). These disorders are known to be relatively common, occur roughly twice as often in women as in men, and have a generally even age distribution, with decline in prevalence in older age (Bandelow and Michaelis 2015). This pattern could be seen well in the data set, with women making up the majority of the cases and the age distribution being fairly uniform, until a drop-off starting at about 60-69 years of age. In fact, these disorders were the most common diagnosis for women under 40:

```r
df$age_category_n <- as.numeric(factor(df$age_category, ordered = TRUE))
under_40 <- unique(df$age_category_n[df$age_category == "30-39"])

subset(df, sex == "female" & age_category_n <= under_40) |>
  (\(x) aggregate(cases ~ diagnosis, sum, data = x))() |>
  (\(x) x[order(-x$cases), ])() |>
  head(5) |> knitr::kable(align = "ll", row.names = FALSE)
```

The fifth and final of the top five diagnoses were disorders due to use of psychoactive substances. This finding is also not particularly surprising, since, among European countries, Czechia ranks moderately high in consumption psychoactive substances, particularly ecstasy and cannabis (Mounteney et al. 2016). By contrast to some of the earlier categories, this diagnosis was significantly more common in males and in young people, showing a skewed age distribution with peak in the 20-29 category. Interestingly, the patients in this category also made up a fairly high proportion of those who had their care terminated early. It is hard to say what this means exactly (a more detailed coding schema for this variable is not available), however, other disorders with high proportion of early terminations included personality disorders (F60-F61 and F62-F69), suggesting that perhaps some patients may be released from care early because of serious behavioral problems.

Overall, the high prevalence of the top five diagnoses seemed to stem from their broad scope which encompassed a wide range of disorders. For instance, alcohol and other psychoactive substance use disorders can manifest in diverse symptoms, including dependence, psychosis, and amnesic syndrome (World Health Organization 2024a). Similarly, as was mentioned above, the stress-related diagnosis covers a broad spectrum of conditions. Alzheimer's disease was one notable exception, representing a fairly specific diagnosis with well-established physiological markers such as the presence of amyloid plaques and neurofibrillary tangles (see e.g. DeTure and Dickson 2019). It could be the case that, under a different classification scheme, Alzheimer's disease would be the most prevalent disorder.

Regardless, the diagnoses which followed the top five tended to be more specific, generally encompassing only one or two ICD-10 codes. Such was the case, for example, for depressive episode and recurrent depressive disorder (F32-F33), specific and mixed personality disorders (F60-F61), and so on. While it could be the case that these disorders would rank higher if some of the top five diagnoses were more granular as well, it is also possible that these disorders require less long-term care due to being more amenable to outpatient treatment methods (see e.g. Roiser, Elliott, and Sahakian 2012).

3.0.2.5 Prevalence of diagnoses over time

We can also scrutinize the prevalence of different mental disorders over time. Again, we need to distinguish between the number of cases versus the number of days patients spent in care. We can use the following figure:

```r
df |>
  create_schema() |>
  add_barplot(c("diagnosis", "cases")) |>
  add_barplot(c("year", "cases")) |>
  add_barplot(c("year", "days")) |>
  set_layout(matrix(c(1, 1, 2, 3), nrow = 2, byrow = TRUE)) |>
  set_scale("barplot1", "x", breaks = order_df$diagnosis) |>
  render()
```

Overall, over time, the proportion of both cases and days in treatment the various diagnoses made up seemed to remain fairly constant, with perhaps a slight general decreasing trend in the number of cases. Of the top five diagnoses, the one which seemed to buck this trend was schizophrenia (F20-F29), which had a fairly marked increasing trend in the proportion of days. Furthermore, the number of cases related to psychoactive substance use disorders (excluding alcohol) seemed to also be rising slightly.

Of the rarer disorders, the one in which there seemed to be a significant relative rise in both the proportion of cases and days in treatment were mental and behavioral disorders associated with physiological disturbances and physical factors (F50-F59). This category includes disorders such as anorexia, bulimia, sleep disorders, and sexual dysfunction disorders. Given that this category was more prevalent in women and young people (as can be seen by interrogating Figure **??**), the likely explanation for this trend is rise in the number of cases of anorexia and bulimia. There also seemed to be slight of a decrease in the number of days spent in treatment by patients with stress-related disorders (F40-F49 without F42) and depression disorders (F32 and F33).

We can quickly verify these findings by fitting simple linear regressions for each diagnosis. First, we can model the number of cases by year:

As we can see in Table **??**, for most diagnoses, there seemed to be a decreasing trend in the number of cases over time. The only diagnosis for which the number of cases was significantly *increasing* over time was F50-F59, confirming the observations made in the interactive figure.

We can do the same for the number of days by year:

Here, the situation was a bit more varied. For most diagnoses, the number of days patients spent in care seemed to increase, with particularly large increases being observed for schizophrenia (F20-F29), Alzheimer's disease (F02 and G30), mental retardation (F70-F79), and personality disorders (F62-F69). The two diagnosis for which the number of days in treatment actually decreased were, interestingly, stress-related disorders (F40-F49 without F42) and depression disorders (F32 and F33).

3.0.2.6 Characteristics of patient cohorts over time

One final things we are going to investigate are characteristics of patient cohorts. Specifically, given that each row of data represents one patient cohort within a given year, of a given sex, diagnosis, and so on, we can investigate whether there were any interesting patterns within the patient cohorts over time. One way we can do this is via the following figure:

```r
df |>
  create_schema() |>
  add_barplot(c("diagnosis", "cases")) |>
  add_barplot(c("year", "cases"), list(reducer = "max")) |>
  add_barplot(c("year", "days"), list(reducer = "max")) |>
  set_scale("barplot1", "x", breaks = order_df$diagnosis) |>
  set_layout(matrix(c(1, 1, 2, 3), nrow = 2)) |>
  render()
```

In Figure **??**, I show plots of diagnoses, as well as a summary of days and cases over time. However, note that, whereas all barplots of days and cases over time shown before had sum (of cases and days) as the y-axis summary statistic, the two barplots in the lower half of figure Figure **??** show maximum, not sum. These plots effectively tell us the size and the number of days in treatment for the largest/longest hospitalized patient cohort within a given year. Based on theory in Section **??**, we know that these plots will behave well under linked selection (with one selection group).

By investigating the diagnoses, we can discover some interesting trends in the patient cohorts. Specifically, by comparing the schizophrenia (F20-F29) and the Alzheimer's disease diagnoses (F0 and G30), we can see that they show a complementary trend in the maximum number of days hospitalized. Specifically, whereas Alzheimer's disease generally accounted for the longest-hospitalized patient cohorts up until 2016, schizophrenia accounted for the longest-hospitalized patient cohorts for five of the six years following 2016 (excluding 2020, where Alzheimer's disease narrowly beat it out). This occurred despite schizophrenia patient cohorts shrinking in size over time and the fact that Alzheimer's disease was more restricted in terms of age-range, so we would naturally expect larger cohorts (due to "lumping"). On that note, developmental disorders (F80-F99), despite the making up only a small proportion of the total number cases, made up many of the largest patients cohorts year over year. This is understandable given that these patients came almost exclusively from the youngest age group and were otherwise relatively homogeneous.

3.1 Summary

I have used the Long-term Care data set (Soukupová et al. 2023) to demonstrate the typical data analytic workflow using `plotscaper`. By creating interactive figures and leveraging a suite of interactive features such as linked selection, representation switching, querying, and zooming and panning, we were able to quickly discover many interesting features about the data set, highlighting the usefulness of the package and interactive data visualization in general.

Some key take-away points were:

- Since 2010, the number of cases has generally decreased, while the number of treatment days has remained constant, suggesting that fewer individuals are receiving long-term psychiatric care, but for longer durations. This suggests a limited placement availability hypothesis, where the healthcare system may be struggling to accommodate new patients due to existing patient load.
- The trend of decreasing number of cases and increasing number of days was reversed for children, who represented a growing proportion of patients but a smaller proportion of treatment days over time.
- The proportion of treatment days represented by older patients (60-69 and 70-79 year olds) has increased over time, further supporting the limited placement hypothesis, since these patients often require longer care.
- There were few patients staying in care for periods of between 2-3 months and 5-7 months, suggesting that there may be potential selection mechanisms influencing hospitalization duration (e.g. administrative reasons).
- The five most common diagnoses were, in order: alcohol use disorders, schizophrenia, Alzheimer's disease, stress-related disorders, and psychoactive substance use disorders. Patient demographics for these disorders showed some very strong trends which largely aligned with the existing literature.
- One diagnostic category which actually shown a significant increase in the number of cases over time were behavioural syndromes associated with physiological disturbances and physical factors. Given that this category includes disorders like anorexia and bulimia, and that the majority of cases were young women, this suggests that, while rare, eating disorders may be on the rise, and should be given attention.
- While initially, the longest hospitalized patient cohorts tended to be Alzheimer's patients, over time, schizophrenia patients became the longest hospitalized patient cohorts

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