## 02 Small Worlds and Large Worlds

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```
i listening
```

In the analogy, models are "Small", self-contained worlds.

Within the small world, all possibilities are nominated.

## Garden of forking paths.

I was thinking of working out the probabilities by doing random sampling...

```
library(tidyverse)
library(gt)
library(patchwork)
library(here)
source(here("_defaults.R"))
```

Generating the marble dataframe

```
tibble(
  blue_marbs = 0:4,
  white_marbs = 4 - blue_marbs
) |>
  rowwise() |>
  mutate(
    marbles = list(c(rep("blue", blue_marbs), rep("white", white_marbs)))
  ) ->
  marbles
```

```
marbles |>
  gt()
```

Table 1: The marble sampling distributions

blue_marbs	white_marbs	marbles
0	4	white, white, white
1	3	blue, white, white, white
2	2	blue, blue, white, white
3	1	blue, blue, blue, white
4	0	blue, blue, blue, blue

In retrospect, I'm glad I did this, because I thought we were sampling without replacement.

Here's a function that will repeatedly sample from a set of marbles, and compare the result to a reference group.

- (1) I'll capture everything within a tibble.
- (2) Rowwise, sample from marbles with replacement.
- (3) Return T or F if the sequence matches the pattern exactly.
- (4) The mean() of the T, F column to get the proportion that match.

```
sampling_df(
    marbles = marbles$marbles[[4]],
    n = 5000
)

# A tibble: 1 x 1
    prop_match
```

```
<dbl>
1
      0.133
  marbles |>
   ungroup() |>
   mutate(
      prob = map(marbles, ~sampling_df(.x, n = 10000))
    unnest(prob) |>
    mutate(norm_probs = prop_match/sum(prop_match))->
    marble_probs
  marble_probs |>
    ggplot(aes(blue_marbs, norm_probs))+
      geom_col(fill = "steelblue4")+
      labs(
        title = "blue, white, blue",
        x = "# of blue marbles",
        y = "probability"
      ) +
    ylim(0,1)->probs1
  probs1
```

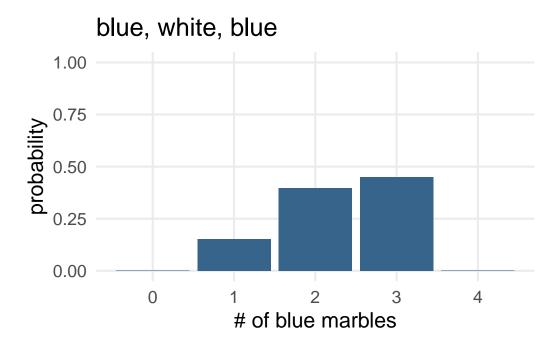


Figure 1: Probability of each composition of marbles

## **Updating probabilities**

What if we draw one more blue

## probs2 probs1 | probs2

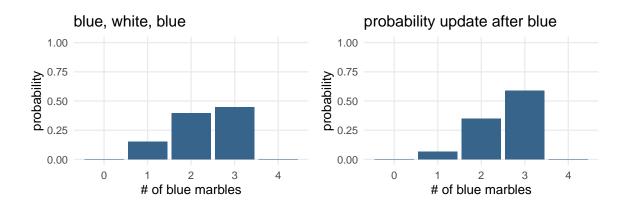


Figure 2: Bayesian update