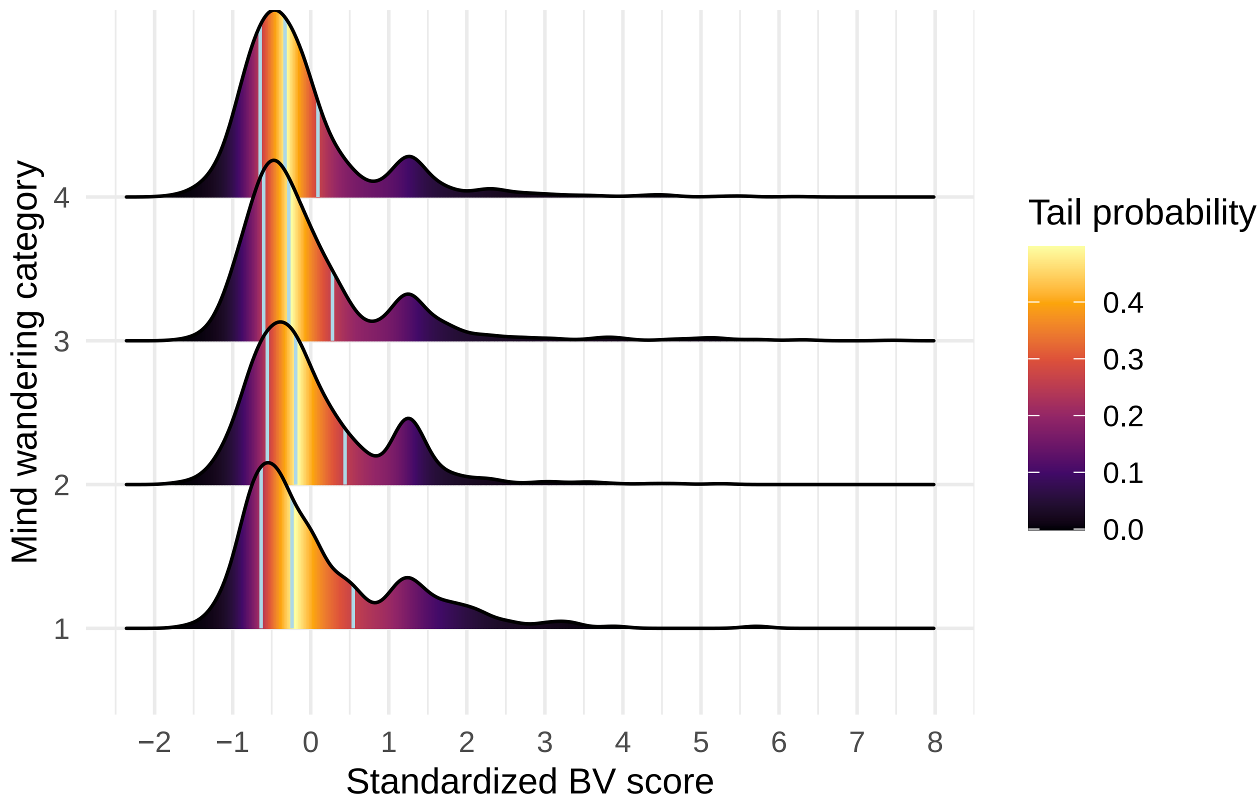
Multivariate visualization: categorical-continuous variable



For this exercise, I will visualize distributions over a categorical variable. More specifically, I would like to visualize the distribution of AE over different cognitive states (such as mind wandering and mind blanking). As noted in the previous report, visualizing over categories can be more informative if we expect that one state should result in a different outcome. In our case, we might expect that when people report being focused on the task that their randomness generation is improved, as compared to the other cognitive states.

Firstly, I load the libraries and transform the data.

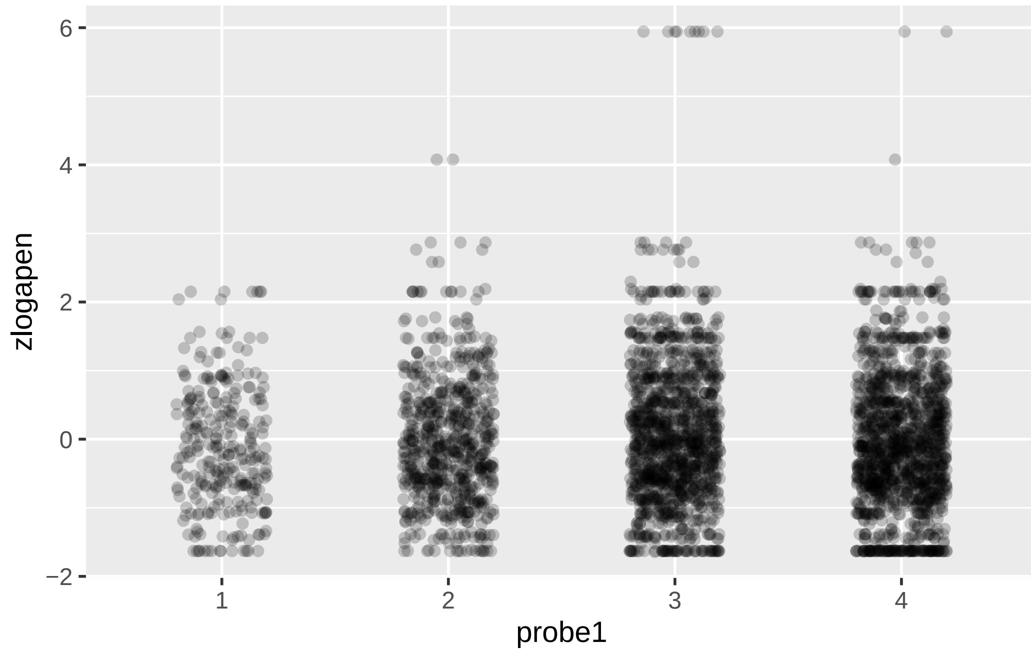
```
library(tidyverse)
library(ggridges)
read_csv("../../ex3/data/raw_mwtms_data.csv") -> all_mw_data
source("../../ex3/src/transformation.R") # AE calculation
```

```
all_mw_data |>
  dplyr::select(-region.y) |>
  filter(stimulation == "sham") -> mw_data
da_pro(mw_data, nback = 25) -> trans_mw
```

```
# A tibble: 3,509 x 14
   subj  session block proberound probe1 probe2 probe3      apen     bv stim
   <chr> <chr>   <chr>      <dbl> <ord>  <ord>  <ord>      <dbl>  <dbl> <chr>
 1 AG001 S2      B0             1 4      4      2        0.458    0.0923 sham
 2 AG001 S2      B0             2 4      4      2        0.444    0.0527 sham
 3 AG001 S2      B0             3 3      2      3        0.120    0.0574 sham
 4 AG001 S2      B0             4 3      3      4        0.535    0.0832 sham
 5 AG001 S2      B0             5 2      4      2        0.151    0.0877 sham
 6 AG001 S2      B0             6 2      2      4        0.117    0.180  sham
 7 AG001 S2      B0             7 2      4      4        0.247    0.165  sham
 8 AG001 S2      B0             8 2      4      2        0.295    0.0488 sham
 9 AG001 S2      B0             9 2      4      3       -0.000945 0.0439 sham
10 AG001 S2      B0            10 3      4      2        0.189    0.178  sham
# i 3,499 more rows
# i 4 more variables: logapen <dbl>, logbv <dbl>, zlogapen <dbl>, zlogbv <dbl>
```

Then we can start by visualizing the distribution of the different cognitive states. I will start with a simple point plot

```
trans_mw |>
  ggplot(aes(x=probe1, y=zlogapen))+
  geom_point(alpha = .2, position = position_jitter(.2))
```



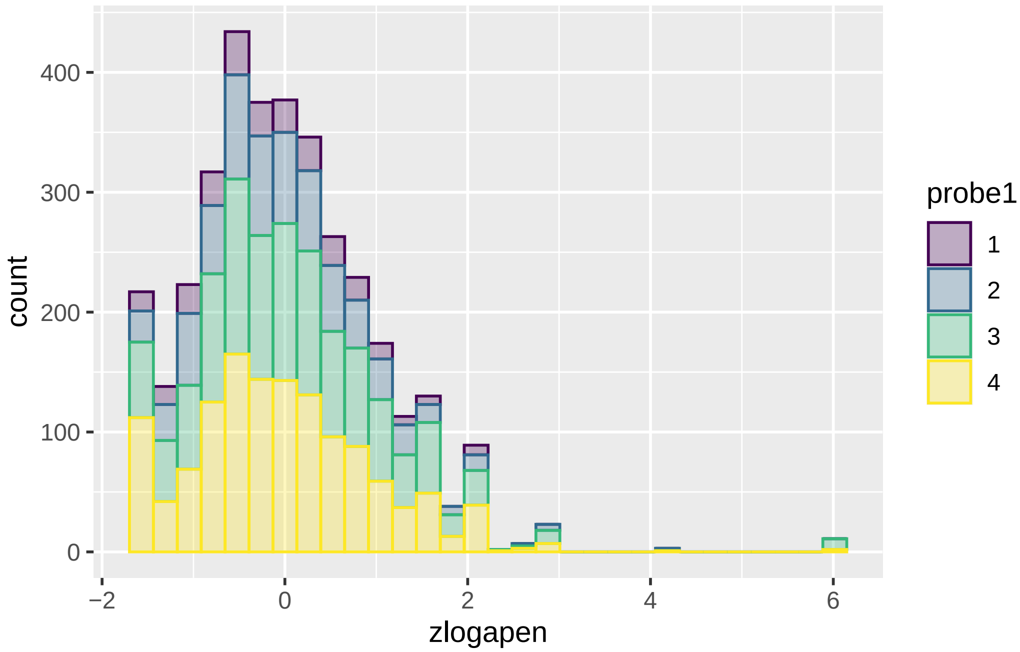
(Lower values indicate more mind wandering.)

Visualizing data in this way makes it hard to understand the distribution within each category. Although we can clearly see that 3 and 4 have more responses than 1 and 2. That is, the difference between the conditions categories are evident, even though it is not entirely clear whether it is normally distributed.

To investigate this, we can use a histogram and colour them according to the categorical response.

```
trans_mw |>
  ggplot(aes(x=zlogapen, group=probe1, col=probe1,fill=probe1))+
  geom_histogram(alpha=.3)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



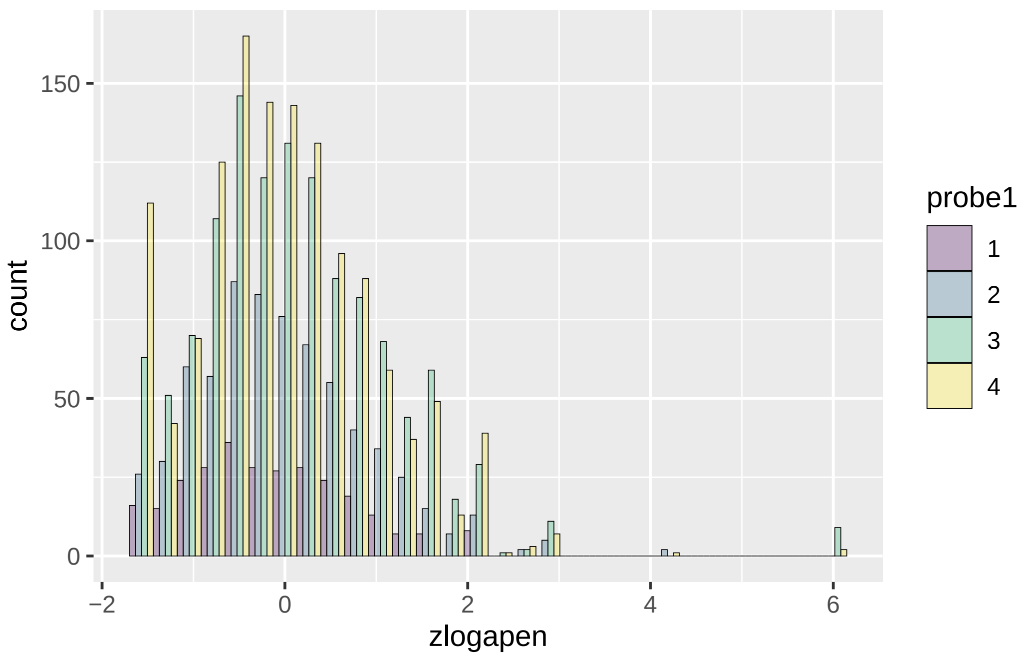
In this plot, the bars are stacked on top of each other, which can make it problematic to see whether the data is distributed normally, especially for the lower probe responses (higher stacked bars). To fix this, we can position the bars beside each other.

```
trans_mw |>
  ggplot(aes(x=zlogapen, group=probe1, fill=probe1))+
  geom_histogram(alpha=.3, position = position_dodge(), col="black", size=.15
                 ) -> p_hist
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

```
p_hist
```

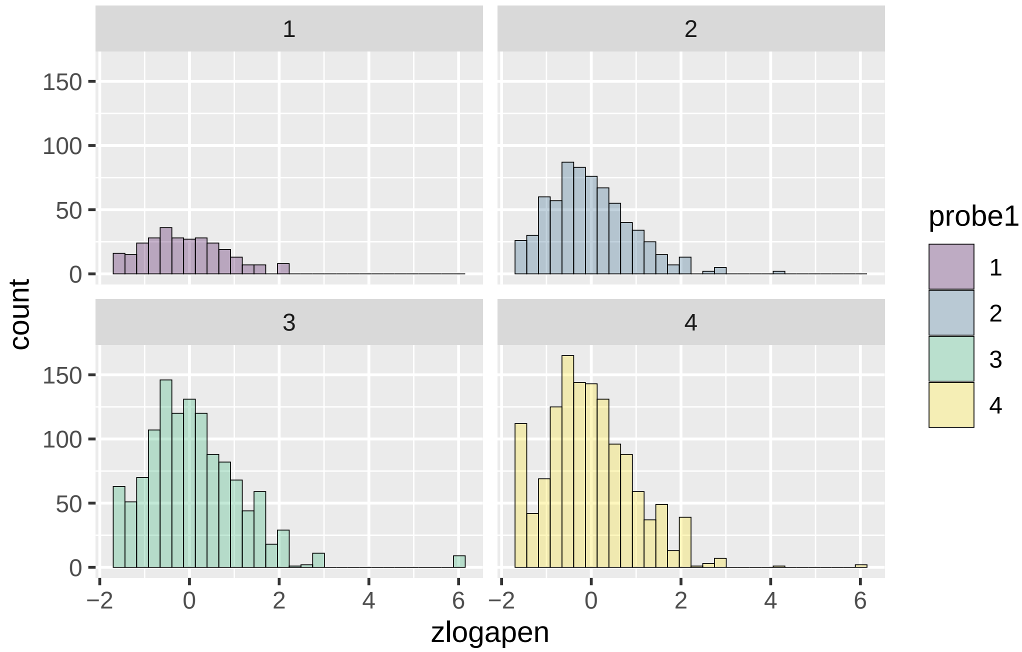
```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



With this plot, the distribution within each categorical response is more evident, but regardless, still difficult to read. This can be fixed by splitting the distribution, which can be done by using facets.

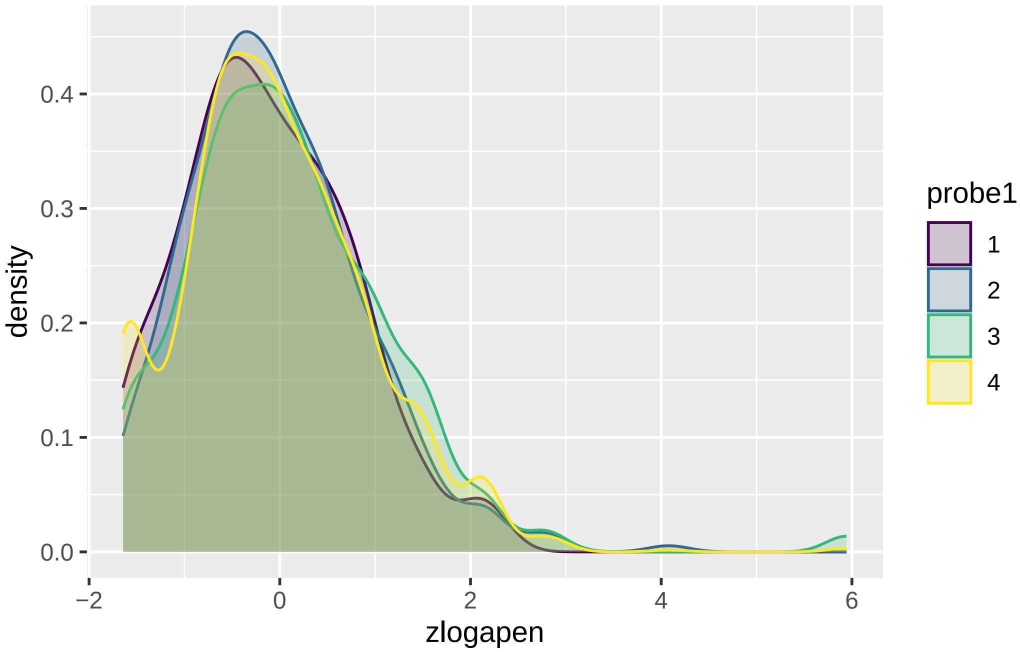
```
p_hist +
  facet_wrap(~probe1)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



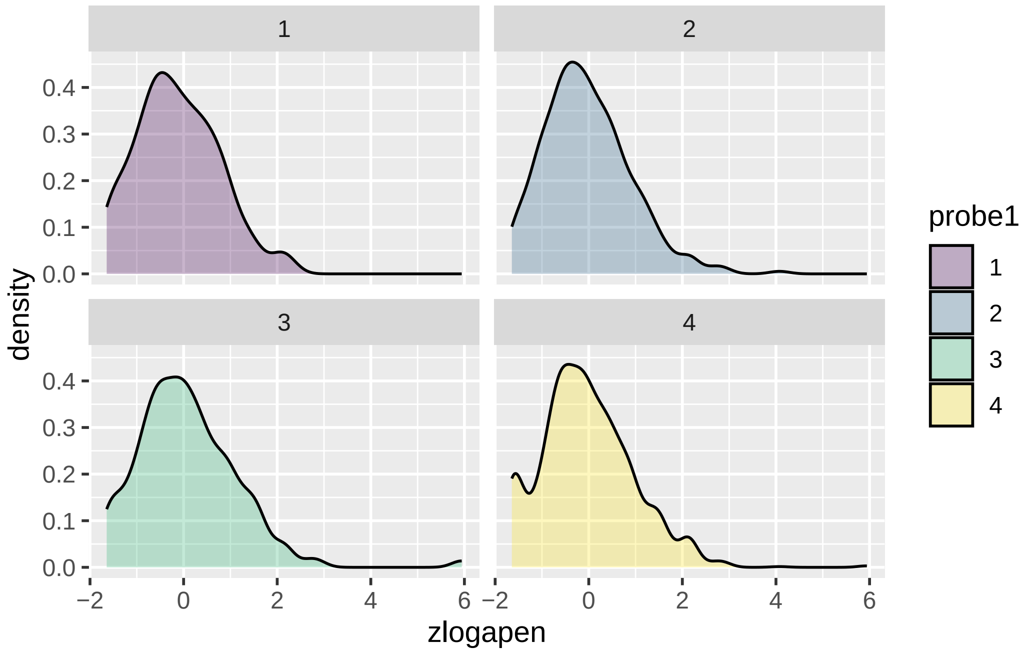
In this graph, the distribution within each response is clearly evident and easy to read. Moreover, it appears as though the distribution within the first categorical response is flat, at least compared to the other distributions. To further investigate this, we can easily change the distribution to a density distribution. A kernel density estimation creates a smooth and continuous representation of the distribution.

```
trans_mw |>
  ggplot(aes(x=zlogapen, group=probe1, fill=probe1, col=probe1))+
  geom_density(alpha=.2)
```



As we can see from the plot, all the distributions over each category are surprisingly similar, at least compared to the histogram representation. We can further split the difference between the distributions by using *facets*.

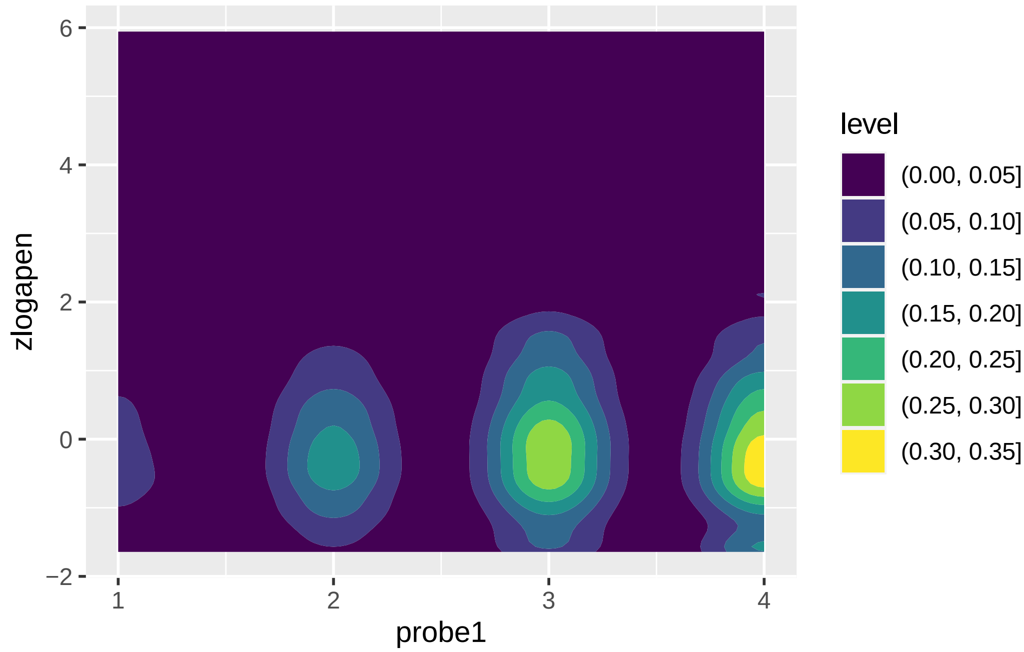
```
trans_mw |>
  ggplot(aes(x=zlogapen, group=probe1, fill=probe1))+
  geom_density(alpha=.3)+
  facet_wrap(~probe1)
```



With this plot, we can see more nuances in each distribution. However, they appear to be more similar than dissimilar.

Similarly to exercise 3, we can also visualize the distribution using a 2d density visualization.

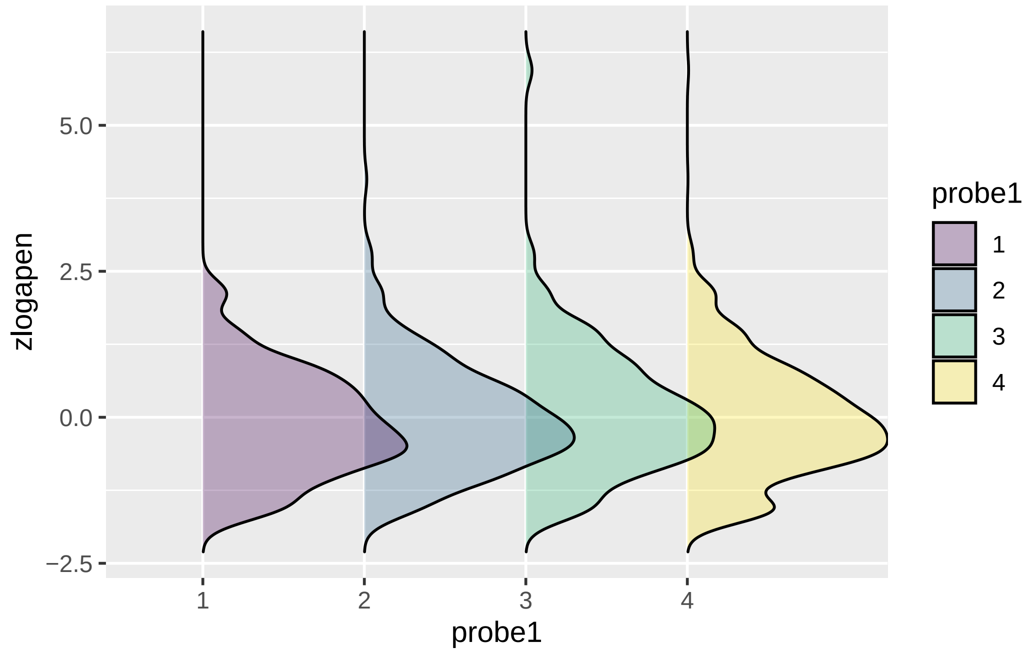
```
trans_mw |>
  mutate(probe1=as.numeric(probe1)) |>
  ggplot(aes(x=probe1, y=zlogapen))+
  geom_density2d_filled()
```



We can clearly see that the fourth response received more responses than the first. However, since the density is spread over plus and minus values, it appears as though responses are spread around the categorical response. It is important to point out that it remains a bit ambiguous how to interpret the distribution. Readers are aided to think of the distribution as happening in two dimensions when it only really happens in one dimension. That is to say, the data distribution within one categorical response only happens according to the cluster of data points of AE values - not at the same time a distribution around the probe response. It is suggested that the data distributes around each response (e.g., 2.9 to 3.1), even though they are perfectly symmetrical and one side could safely be removed. With such a choice, it would be more evident that we are talking about only a one dimensional distribution over different categories. One way of achieving this is to use the *ggridges* library, which makes it easy to visualize data distributions over categories.

```
trans_mw |>
  ggplot(aes(x=zlogapen, y=probe1, fill=probe1))+
  geom_density_ridges(scale = 1.3, alpha=.3)+
  coord_flip()
```

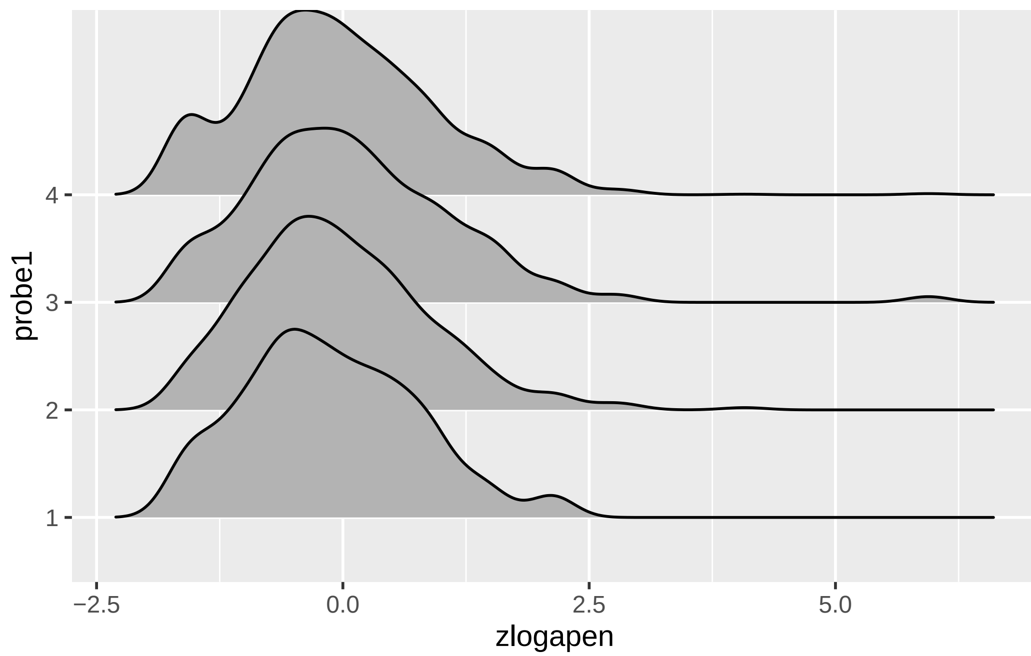
```
Picking joint bandwidth of 0.221
```



With this plot, we can more easily understand that we are talking about a distribution over one categorical response. Moreover, it is easier to comprehend the distribution over each categorical response than the (above) 2D distribution. The *ggridges* library is clearly superior in many regards, as it overlays the distributions without disrupting the distribution behind it, but still making comparisons easily. For instance, the first cases used histograms, which makes it hard to compare the distribution because it uses count summary. While using density made comparison of the distribution easier, it was hard to see the individual distributions when they were overlapped, but difficult to compare when they were split by facets. Thus, *ggridges* makes it a better compromise between these two options, making it easier to both see the individual distribution, but also compare the distribution over each response.

```
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
  geom_density_ridges()
```

```
Picking joint bandwidth of 0.221
```

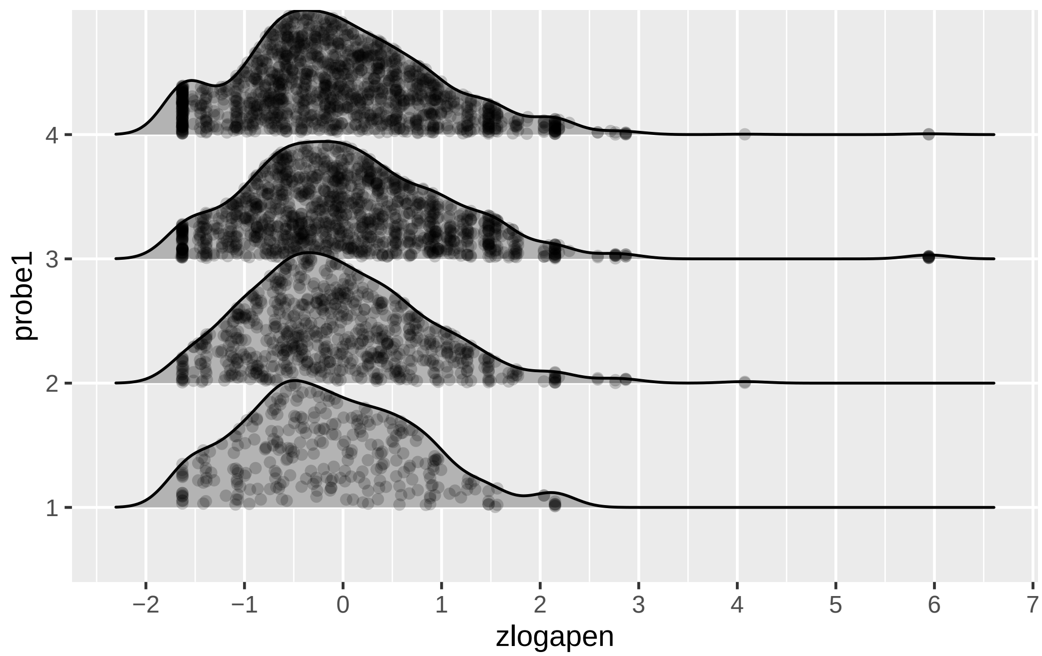


This leads to a more neat presentation of the distribution over each of the categorical responses. Moreover, it is now a bit easier to read the distributions. It seems like the 3 and 4 response have slightly longer distributions, suggesting that higher AE might be associated with more on task reporting. Although, this is by no means obvious, but a mere suggestion based on the distributions.

With this, there are a couple of aesthetic changes we can do. For instance, we could draw all individual points:

```
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
  geom_density_ridges(jittered_points = T, # Add jittering points
                      point_alpha = .2,
                      scale = 1.05)+
  scale_x_continuous(breaks = seq(-8,8,1))
```

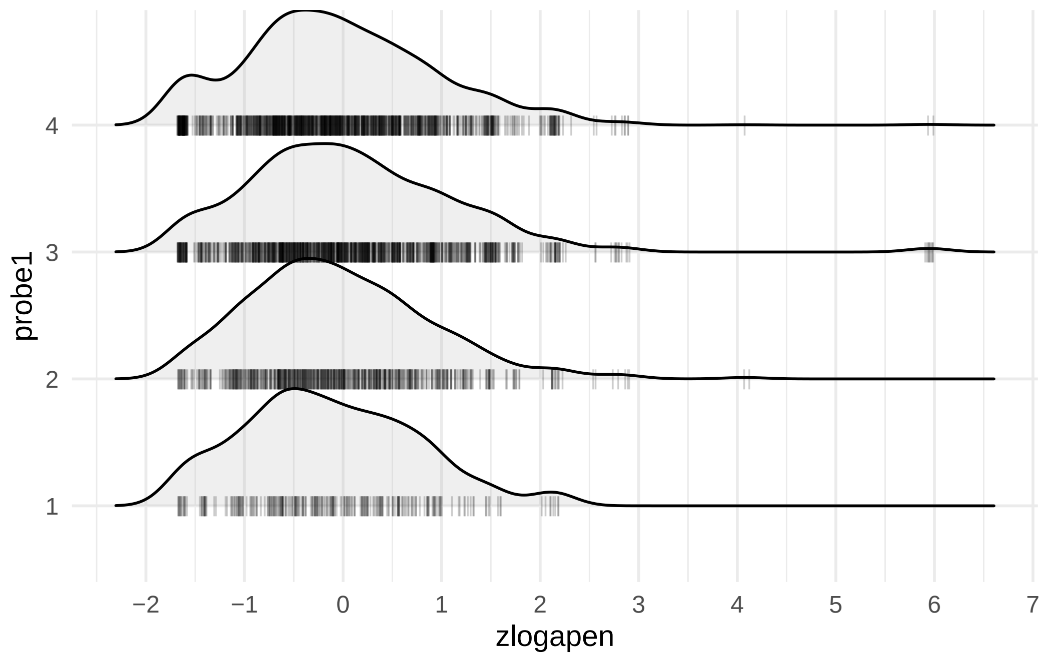
```
Picking joint bandwidth of 0.221
```



However, the resulting plot can be more difficult to interpret, granted a large data set. Indeed, for massive data sets, it is possible that there will be nothing other than a black graph - of points.

```
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
   geom_density_ridges(
     jittered_points = T, scale = .95,
     position = position_points_jitter(width = 0.05, height = 0),
       # Creates a rug position of the "points"
     alpha = .2,
       # This sets the transparency of the Density distribution (the points
       # ("|") are drawn behind the distribution).
     # Point changes:
     point_shape = '|',  # Shape of the point
     point_size = 2.5,
     point_alpha = .2 )+
  scale_x_continuous(breaks=seq(-8,8,1))+
  theme_minimal()
```

```
Picking joint bandwidth of 0.221
```

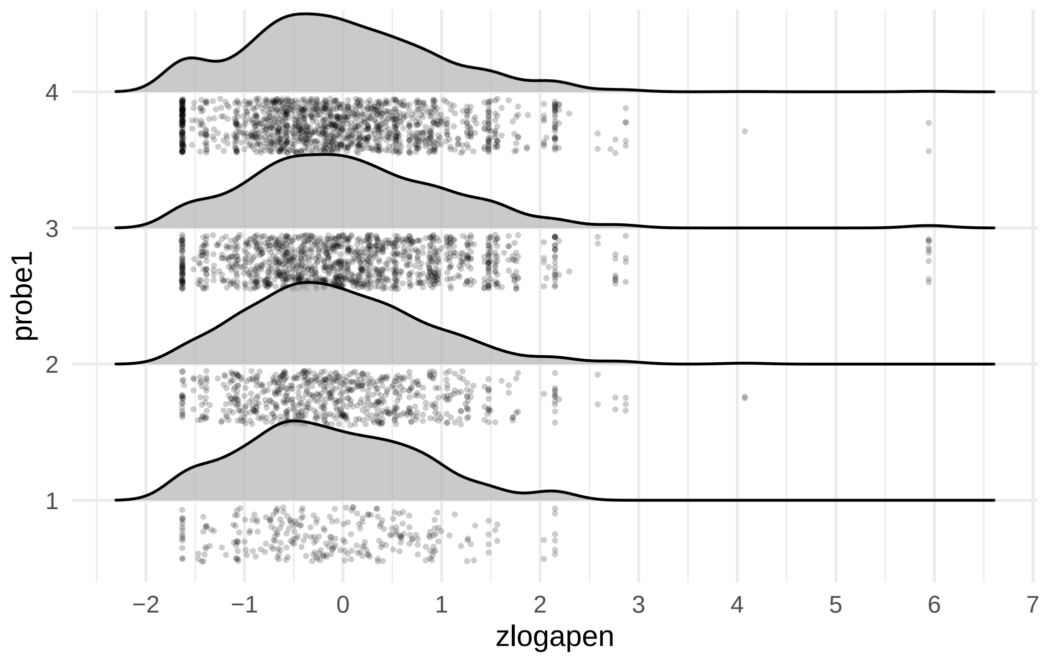


This plot is more intelligible than the former point plot. Here, we can see how certain areas contain more data points. More specifically, how points gather around -1.75 for the 3 and 4 response categories, as well as a tendency for the other categories. As noted earlier, it is also suggested that there are, in fact, slightly more points for higher AE for the 3 and 4 category. Although, this might merely be because these categories have more overall responses, as the same pattern can be found for the first and second category.

Another way of plotting is using a "raincloud":

```
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
   geom_density_ridges(
     jittered_points = T, scale = 0.6, alpha = 0.7,
     position = position_raincloud(),
     point_size = 0.4, point_alpha = .2)+
  scale_x_continuous(breaks=seq(-8,8,1))+
  theme_minimal()
```

```
Picking joint bandwidth of 0.221
```

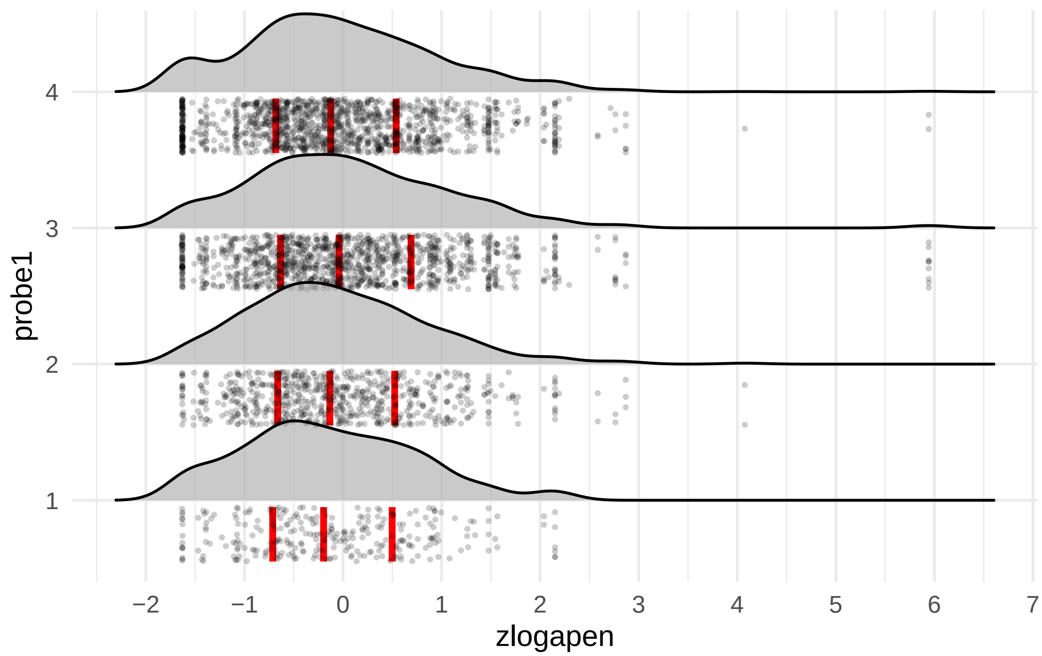


In this plot, each of the individual data points "rain down" from the distribution. With this plot, it is easier to see which distribution contains the most observations (4), and the least (1). Moreover, we can see how many observations cluster around certain values (e.g., -1.6 and 2.2).

With this package, it is also possible to easily add quantile lines:

```r
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
   geom_density_ridges(
     jittered_points = T, scale = 0.6, alpha = 0.7,
     position = position_raincloud(adjust_vlines = T),
     point_size = 0.4, point_alpha = .2,
     quantile_lines = T,
     vline_size = 1.2, vline_color = "red")+
  scale_x_continuous(breaks=seq(-8,8,1))+
  theme_minimal()
```

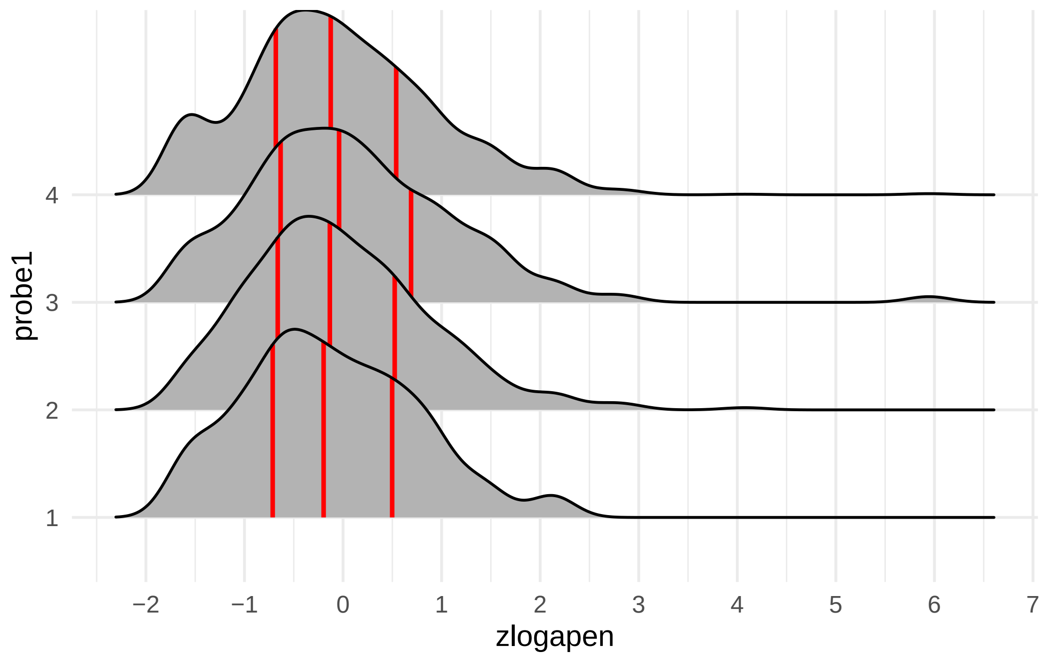
```
Picking joint bandwidth of 0.221
```



In this plot, the red lines indicate the quantiles, in which an equal number of data observations are found. With the above plot, the quantiles are displayed over the "raincloud" of data points. If we remove the "jittered_points" (FALSE) then we get the quantiles over the distribution itself:

```
trans_mw |>
  ggplot(aes(x = zlogapen, y = probe1))+
   geom_density_ridges(
     quantile_lines = T,
     vline_size = .8, vline_color = "red")+
  scale_x_continuous(breaks=seq(-8,8,1))+
  theme_minimal()
```

```
Picking joint bandwidth of 0.221
```

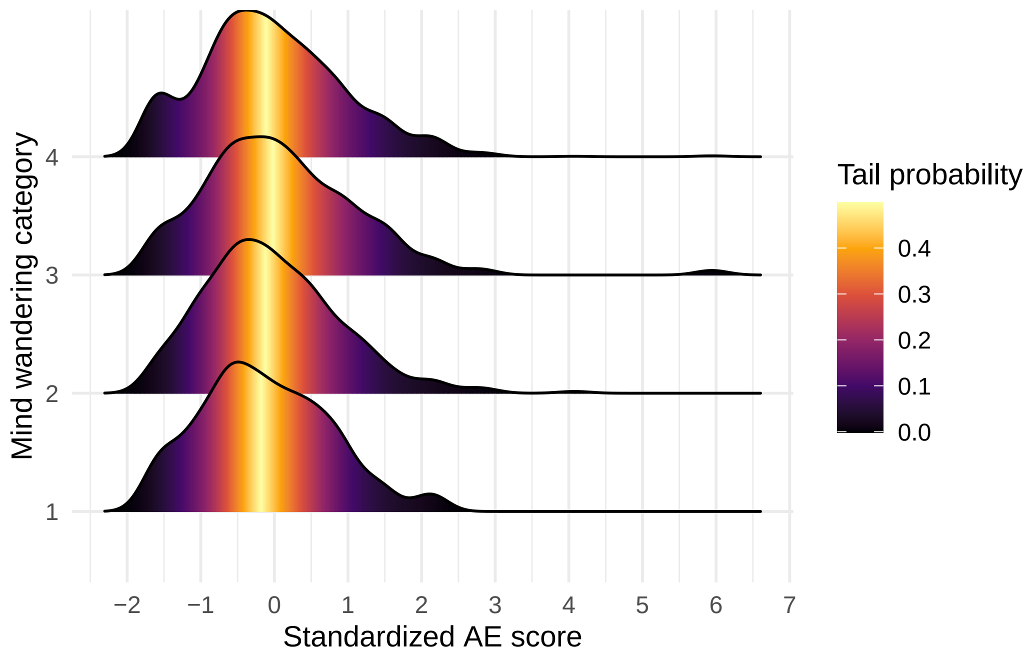


In the plot above, it is a bit easier to grasp the width of the quantiles, and the height of the density function. For this reason, this plot may be preferred over the raincloud - at least when it comes to quantile visualization.

Moreover, it is also possible to colour the ridges according to the probability of obserivng a data point in a certain band range:

```
trans_mw |>
  ggplot(aes(x=zlogapen, y=probe1, fill = 0.5 - abs(0.5 - after_stat(ecdf))))+
  geom_density_ridges_gradient(scale = 1.3, calc_ecdf = T)+
    # https://wilkelab.org/ggridges/articles/introduction.html
  scale_fill_viridis_c(name = "Tail probability", option = "inferno")+
  theme_minimal()+
  scale_x_continuous(breaks = seq(-8,8,1))+
  labs(y = "Mind wandering category", x = "Standardized AE score")
```

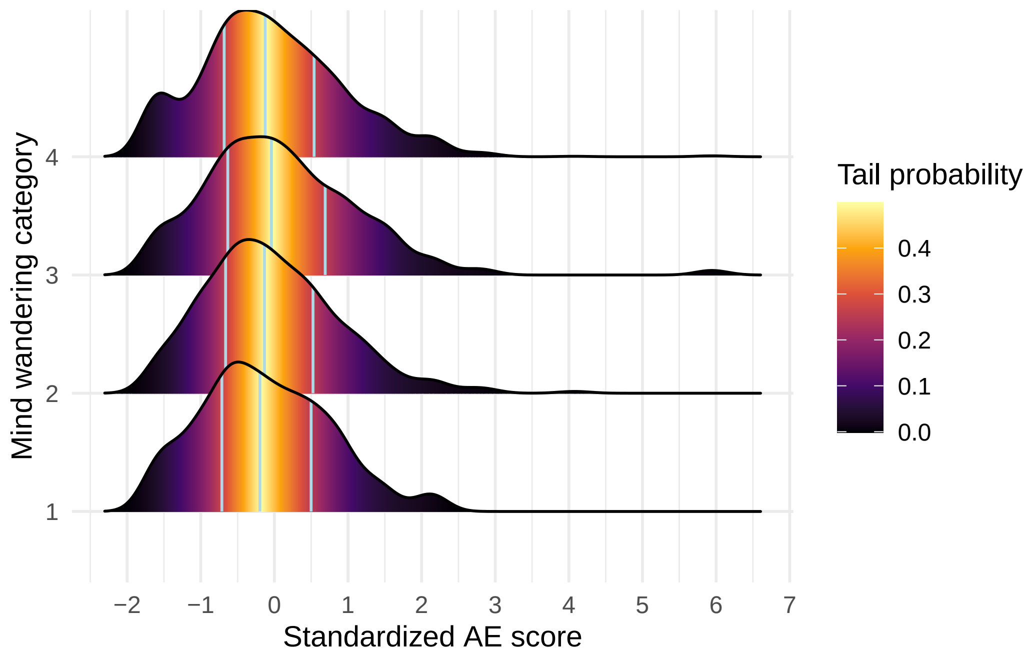
```
Picking joint bandwidth of 0.221
```



In the above plot, I visualize the density distribution over each categorical response of mind wandering and colouring the plot according to the probability of observing an observation within a band. We can easily add quantiles lines to also indicate where most of the data is found - although, this might be obvious from the plot in itself.

```
trans_mw |>
  ggplot(aes(x=zlogapen, y=probe1, fill = 0.5 - abs(0.5 - after_stat(ecdf))))+
  geom_density_ridges_gradient(scale = 1.3, calc_ecdf = T,
                               quantile_lines = T,
                               vline_color="lightblue")+
  scale_fill_viridis_c(name = "Tail probability", option = "inferno")+
  theme_minimal()+
  scale_x_continuous(breaks=seq(-8,8,1))+
  labs(y="Mind wandering category", x="Standardized AE score")
```

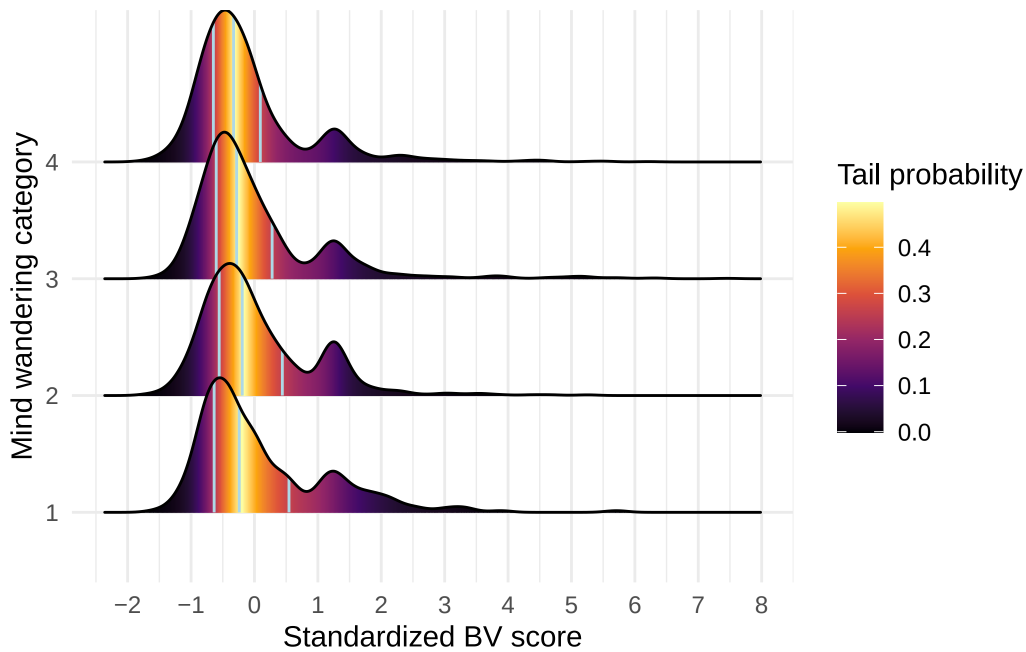
```
Picking joint bandwidth of 0.221
```



In the above plot, there are both quantile lines and coloured probability of observing a value within a range. Due to the colouring, it might not be necessary with the quantile lines. Although, I would say that the colour adds an element that is missing in the prior plots. At any rate, there is not much to suggest that there is any difference between the categorical response and the distribution of AE. To check whether the plot works, I will quickly turn to BV.

```
trans_mw |>
  ggplot(aes(x=zlogbv, y=probe1, fill = 0.5 - abs(0.5 - after_stat(ecdf))))+
  geom_density_ridges_gradient(scale = 1.3, calc_ecdf = T,
                               quantile_lines = T,
                               vline_color = "lightblue")+
  scale_fill_viridis_c(name = "Tail probability", option = "inferno")+
  theme_minimal()+
  scale_x_continuous(breaks=seq(-8,8,1))+
  labs(y = "Mind wandering category", x = "Standardized BV score")
```

```
Picking joint bandwidth of 0.175
```

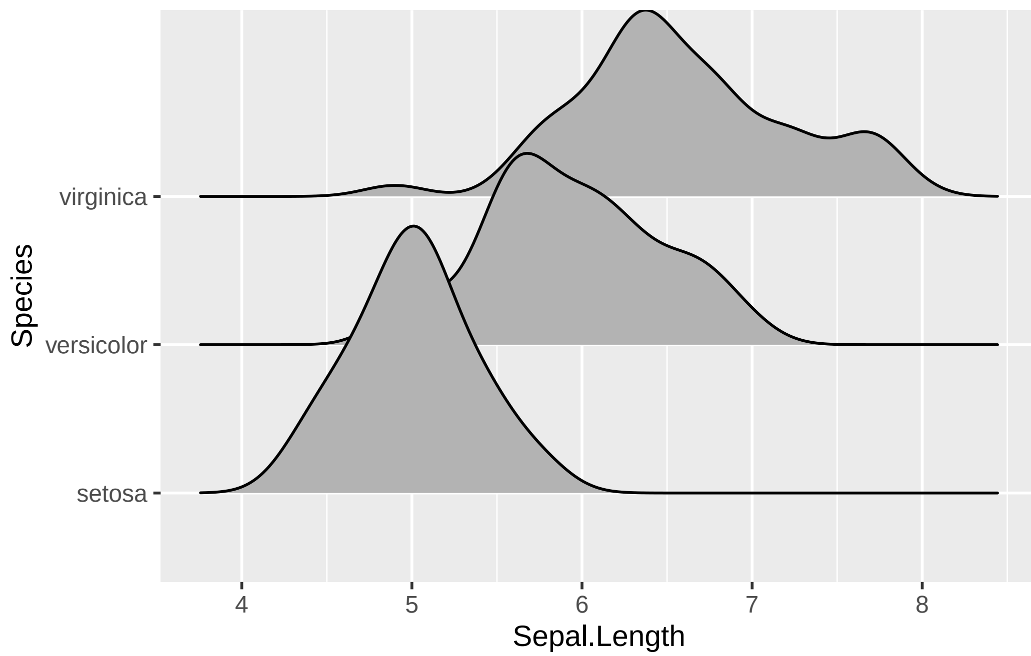


In the above plot, it is a bit more evident that there is a difference between the categorical responses. The lowest categories (1 and 2) seem to have a bit wider bands and distributions than the higher categories (3 and 4). We can, for instance, see that the quantiles for the fourth category are more normally distributed than the first. Thus, more data is observed closer to 0, which indicates better task performance. Similarly, the distribution seems to be wider for the first category than the fourth, suggesting that there might be some differences (albeit not that big, perhaps).

The former plots have not been apparent regarding whether there is any difference between the categorical response, and the behavioural performance measures. To illustrate, I will use an entirely different data set called "iris", which is found in base R. The data set includes measures of flowers of the petal length and width, sepal width and length, and species of the flower. Making it possible to visualize a categorical (species) variable over various continuous variables (width/length).

```
iris |>
  ggplot(aes(x = Sepal.Length, y = Species))+
  geom_density_ridges()
```

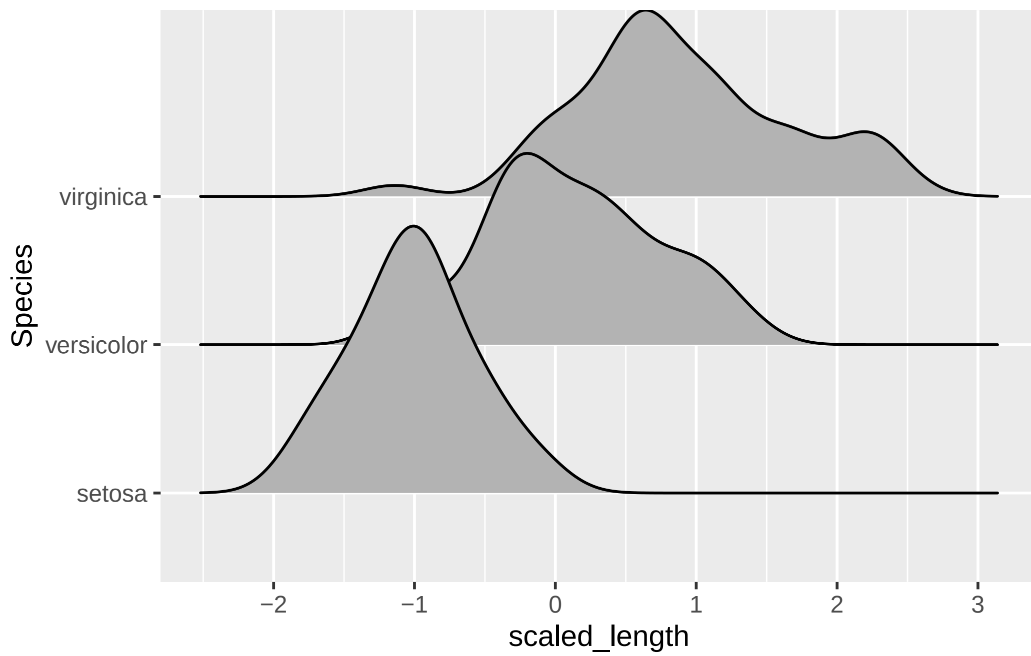
```
Picking joint bandwidth of 0.181
```



With this data set, we can clearly see that these species have different sepal length. Although, the length is not standardized, but to do so, we can use the *scale* function.

```
iris |>
  mutate(scaled_length = scale(Sepal.Length)) |>
  ggplot(aes(x = scaled_length, y = Species))+
  geom_density_ridges()
```

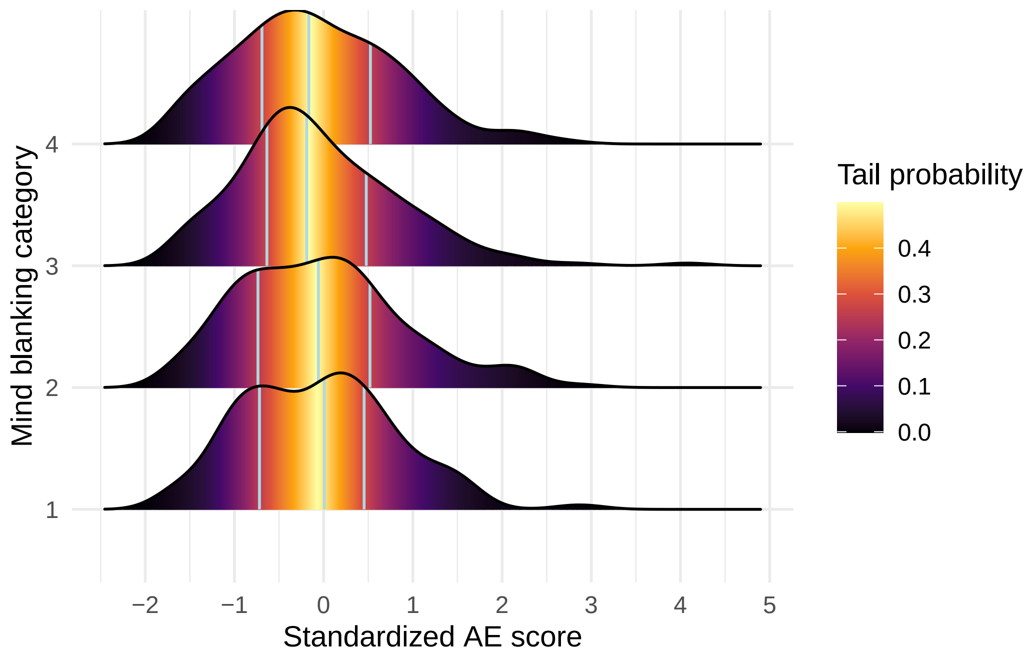
```
Picking joint bandwidth of 0.218
```



In the above plot, we can see that a setosa's length is about one standard deviation below vericolor, and 1.7 (or so) below the virginica flower. These datasets can make differences more obvious by visualizing a distribution over a categorical response. In the case of the randomness (AE) score, it is not as clear whether there is a difference between the categorical responses. This might be expected by the fact that the categorical responses are related to a more continuous scale (focused or not), wherein there can be a wide range of different states. Indeed, we could try to visualize AE/BV score over mind blanking, which is a different variable.

```
trans_mw |>
  filter(probe1<3) |>
  ggplot(aes(x = zlogapen, y = probe2, fill = 0.5 - abs(0.5 - after_stat(ecdf))))+
  geom_density_ridges_gradient(scale = 1.3, calc_ecdf = T,
                               quantile_lines = T,
                               vline_color = "lightblue")+
  scale_fill_viridis_c(name = "Tail probability", option = "inferno")+
  theme_minimal()+
  scale_x_continuous(breaks = seq(-8,8,1))+
  labs(y = "Mind blanking category", x = "Standardized AE score")
```

```
Picking joint bandwidth of 0.274
```



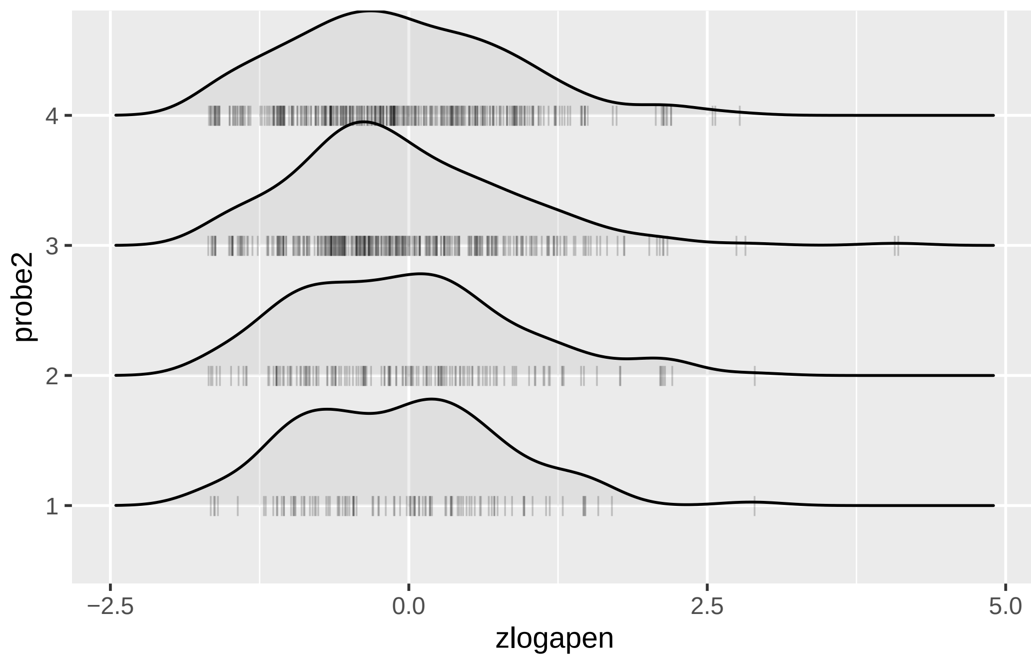
(Lower category indicate more blanking.) In the above plot, I have plotted the mind blanking response only for those who reported to mind wandering (1 and 2). We might expect those who mind blanked (1 and 2) to produce worse AE than those who did not report to mind blank (3 and 4). Such a trend is not obvious from the distribution. In fact, it might seem that mind wandering (4) seems to have a second peak at a reduced AE score. Although this might be the case because it has more cases (however, this is not entirely clear, see below).

At any rate, it paints a rather similar pattern to the previous plots. It is not entirely clear whether there is any difference between the categorical responses (there is a lot of overlap). Nevertheless, we can see that the categorical response 3 and 4 have a second peak at around -1.7 (or so).

```
trans_mw |>
  filter(probe1<3) |>
  ggplot(aes(x = zlogapen, y = probe2))+
  geom_density_ridges(
    jittered_points = T, scale = .95,
    position = position_points_jitter(width = 0.05, height = 0),
      # Creates a rug position of the "points"
    alpha = .2,
      # This sets the transparency of the Density distribution (the points
      # ("|") are drawn behind the distribution).
```

```
    # Point changes:
    point_shape = '|',  # Shape of the point
    point_size = 2.5,
    point_alpha = .2 )
```

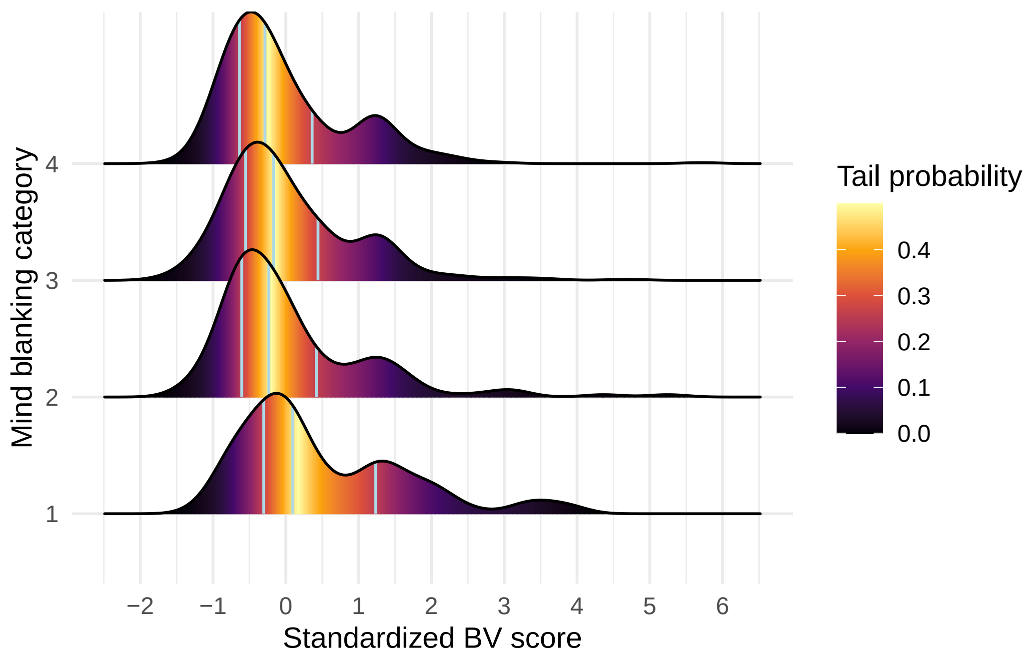
```
Picking joint bandwidth of 0.274
```



Even though AE (randomness) score did not have any clear differences, maybe BV has any clearer differences:

```
trans_mw |>
  filter(probe1 < 3) |>
  ggplot(aes(x = zlogbv, y = probe2, fill = 0.5 - abs(0.5 - after_stat(ecdf))))+
  geom_density_ridges_gradient(scale = 1.3, calc_ecdf = T,
                               quantile_lines = T,
                               vline_color = "lightblue")+
  scale_fill_viridis_c(name = "Tail probability", option = "inferno")+
  theme_minimal()+
  scale_x_continuous(breaks = seq(-8,8,1))+
  labs(y = "Mind blanking category", x = "Standardized BV score")
```

```
Picking joint bandwidth of 0.269
```



It might seem as though categorical response 3 and 4 (indicating mind wandering or content) have a more normal distribution. Moreover, they seem to have a slightly reduced second peak (at around 1.35). While the lower category (1 and 2) seem to have a bit wider distribution and a higher second peak. It should be noted that only the higher categories (3, 4) seem to sometimes become more task disengaged by some higher scores. In this way, it can appear as though most people are more consistent when reporting to have content (mind blanking - 3/4), but might (sometimes) be more disconnected. While, mind blanking (1, 2) might have a wider distribution, they do not seem to have very high (albeit some observation) scores. Thus, it might be said that when people think about nothing in particular, they are generally less task focused, but might not entertain these ideas as much - hence not observing fewer high-value cases.