ridgeline density plots

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Intro

Here we'll be making the hottest visualization of 2017 - the *joy plot* or *ridgeline plot*.

Ridgelines are partially overlapping density line plots. They are useful for densely showing changes in many distributions over time / condition / etc.

This type of visualization was inspired by the cover art from Joy Division's album Unknown Pleasures and implemented in the R package ggridges by Claus Wilke.

While the original term for this plot took off as *joy plot* it has since been changed to a *ridgeline plot* or *ridges plots*, as discussed at length here.

Anyways, Claus has a *beautiful* intro to his package here. I will not reproduce any of his plots, as I want you to click the link. Plus they are way cooler looking than what we will be making. Which is real(ish) data from people in my division.

Load Davide merged data

This is a highly cut down version of his original data - which is a 160mb csv file. The csv for this exercise can be found here.

It contains cell area size for thousands of cells which have had a drug perturbation, split by wells in a dish. One drug per well.

```
library(tidyverse)
library(ggridges)
merged.df <- read_csv('~/git/Let_us_plot/005_ggridges/davide_cell_size_data.csv')
```

What does the data look like?

```
head(merged.df)
```

```
## # A tibble: 6 × 3
##   Well.names  Area Drug
##   <chr>      <dbl> <chr>
## 1 D07          643 20(S
## 2 D07          388 20(S
## 3 D09          290 20(S
## 4 D08         1174 20(S
## 5 D09          186 20(S
## 6 D09         7062 20(S
```

First we create a fake DMSO to match each drug so we can see the 'null' distribution matched with each drug in the visualization below

I know `for` loops are out of trend, but I find them easier to write *and* read compared to `purrr`. A lot less compact, I concede.

This is a bit hacky, but I want to duplicate the DMSO data and assign it to each drug. Later we'll be splitting the plot by drug, so we can see both the drug data *and* the DMSO data in the section.

```
# for background DMSO plot
fake_DMSO_drug <- data.frame()
for (i in (merged.df$Drug %>% unique())){
  print(i)
  fake_DMSO_drug <- rbind(fake_DMSO_drug, merged.df %>% filter(Drug=='DMSO') %>% mutate(Drug = i, Well.names
=paste0('0DMSO_', i), DMSO='Yes'))
}
```

```
## [1] "20(S"
## [1] "3-Am"
## [1] "Brom"
## [1] "Cili"
## [1] "Ctrl"
## [1] "DMSO"
## [1] "ETP"
## [1] "G-Pr"
## [1] "GANT"
## [1] "HA 1"
## [1] "IMR-"
## [1] "IWP-"
## [1] "IWR-"
## [1] "LGK-"
## [1] "LY41"
## [1] "Metf"
## [1] "PJ 3"
## [1] "SANT"
## [1] "Sodi"
## [1] "Tori"
## [1] "UNC"
## [1] "Valp"
## [1] "Wnt-"
## [1] "WYE"
```

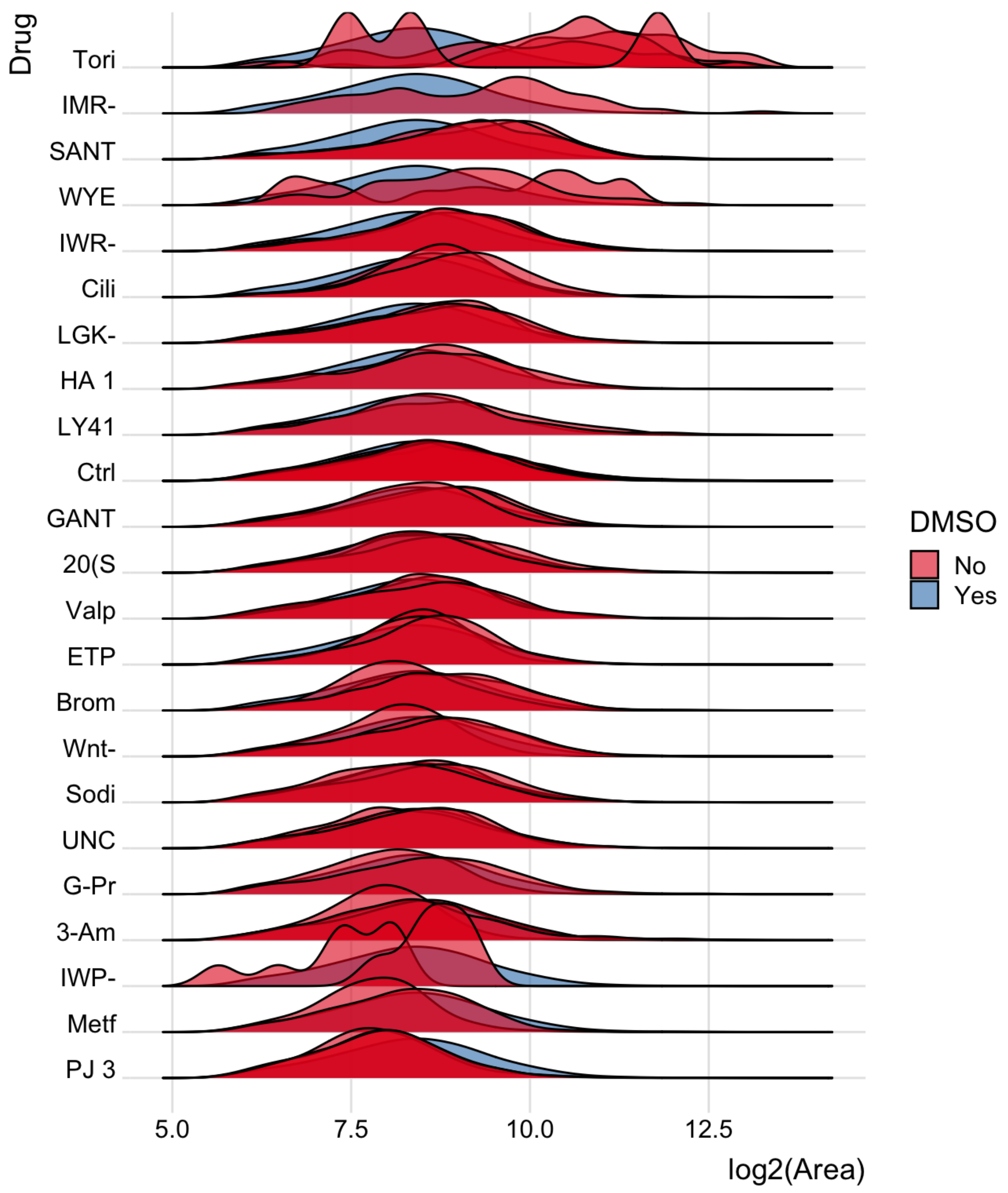
```
# order drugs by median area
drug_order <- merged.df %>% group_by(Drug) %>% summarise(MedianArea=median(Area)) %>% arrange(MedianArea) %>
% pull(Drug)
```

ridgeline plot, showing each well separately

Several wells got the same drugs. So there are multiple plots per drug.

```
bind_rows(merged.df %>% mutate(DMSO='No'),fake_DMSO_drug) %>%
  filter(Drug!='DMSO', Drug!='Pyr') %>% # don't need DMSO plot now and Pyr is empty
  mutate(Drug=factor(Drug, levels=drug_order)) %>% # reorder drugs by drug_order above
  ggplot(aes(y = Drug, x=log2(Area), group=Well.names, fill=DMSO)) +
  geom_density_ridges(alpha=0.6) +
  theme_ridges() +
  scale_fill_brewer(palette = 'Set1')
```

```
## Picking joint bandwidth of 0.258
```

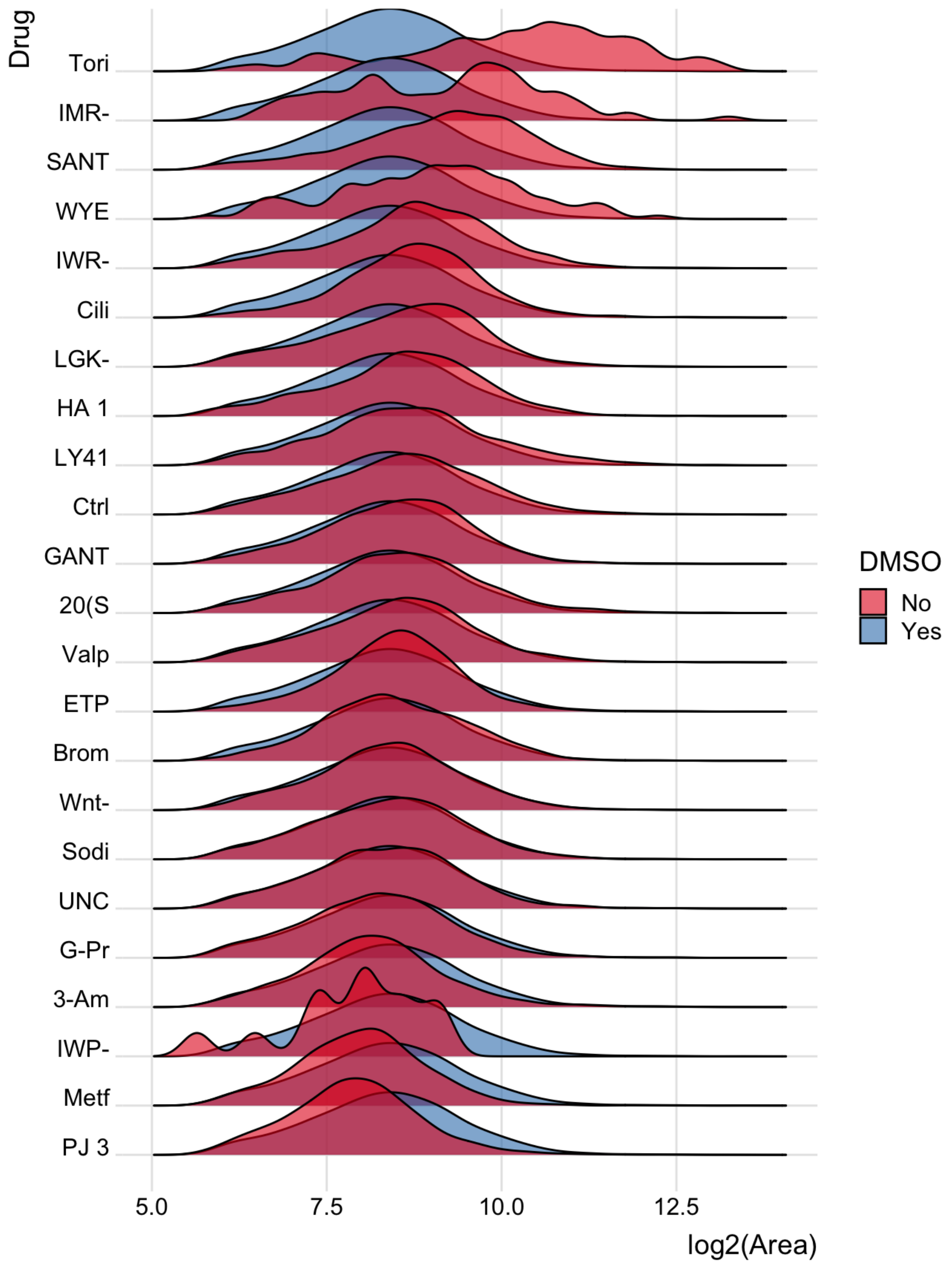


Same, but merging all wells together

Now merge all the wells together. Notice how the group is now `Well.names2`

```
bind_rows(merged.df %>%
            mutate(DMSO='No', Well.names2=paste0('Orig', Drug)),
          fake_DMSO_drug %>%
            mutate(Well.names2 = Well.names)) %>%
  filter(Drug!='DMSO', Drug!='Pyro') %>% # dont' need DMSO plot now and Pyroxamine is empty
  mutate(Drug=factor(Drug, levels=drug_order)) %>% # reorder drugs by drug_order above
  ggplot(aes(y = Drug, x = log2(Area), group=Well.names2, fill=DMSO)) +
  geom_density_ridges(alpha=0.6) +
  theme_ridges() +
  scale_fill_brewer(palette = 'Set1')
```

```
## Picking joint bandwidth of 0.204
```



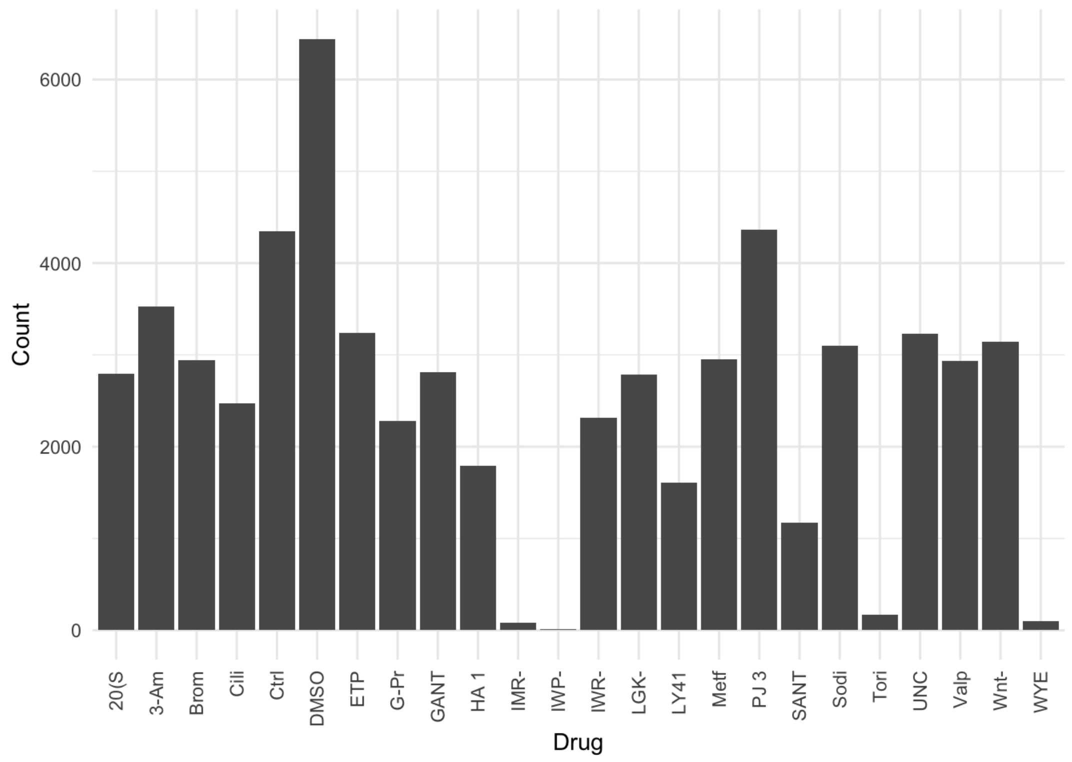
There’s a large variation in the number of counts

How did I know? Because a bunch of the density plots were super wavy - which means (almost always) that the number of counts in that sample is very low. Low numbers = high variance.

So IMR, IMP, Tori, and WYE are *problem* tests. Perhaps they are just killing the cells? Something for Davide to examine.

```
cell_area_counts_by_drug <- merged.df %>%
  group_by(Drug) %>%
  summarise(Count=n())

cell_area_counts_by_drug  %>%
  ggplot(aes(x=Drug, y=Count)) +
  geom_bar(stat='identity') +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```



Count
6000
4000
2000
0
20(S
3-Am
Brom
Cili
Ctrl
DMSO
ETP
G-Pr
GANT
HA 1
IMR-
IWP-
IWR-
LGK-
LY41
Metf
PJ 3
SANT
Sodi
Tori
UNC
Valp
Wnt-
WYE
Drug