Untitled

Ali Taqi

3/5/2021

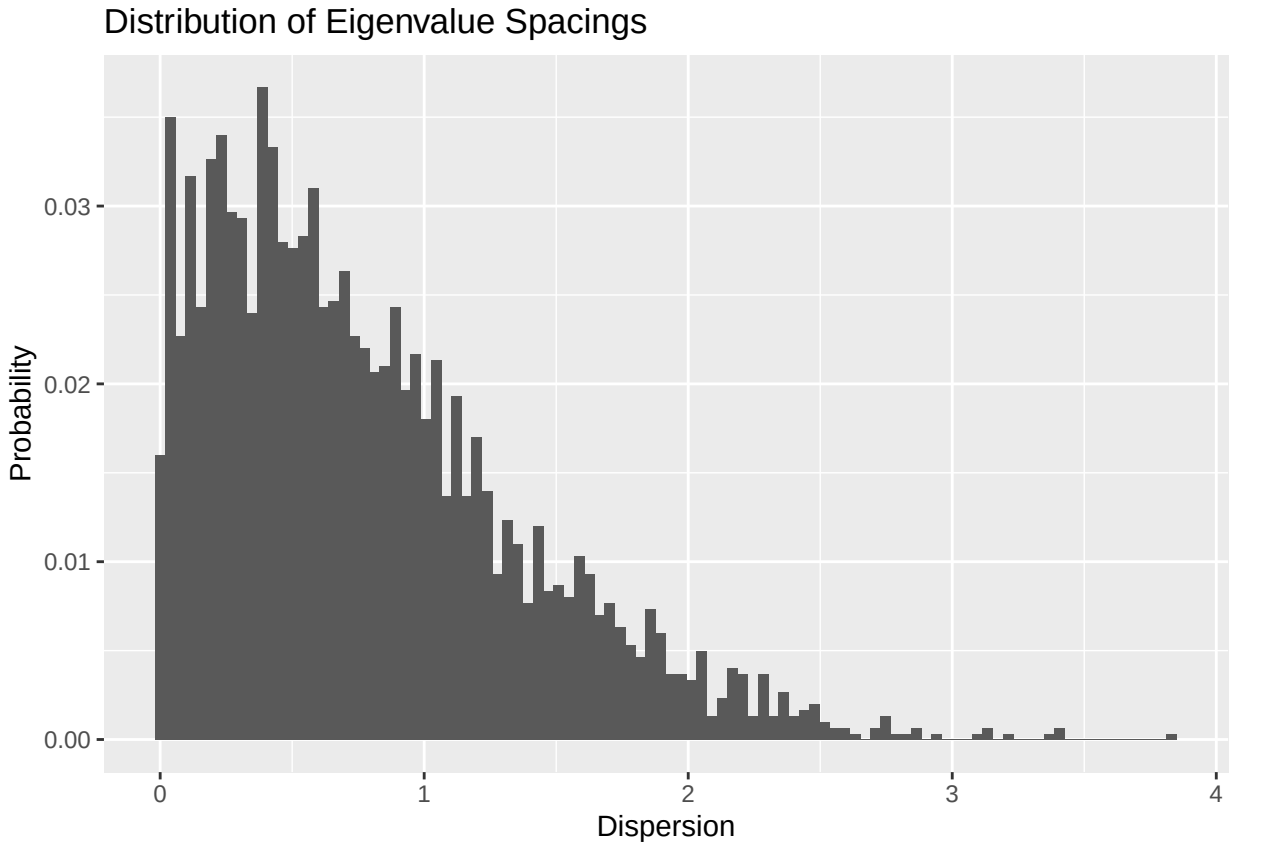
```
P <- RME_norm(N = 25, cplx = T, herm = T, size = 3000)
```

```
#.dispersion_matrix(P[[1]], diff_abs = T)
#.dispersion_matrix(P[[1]], diff_abs = F)
```

Within matrix

Difference of Absolutes

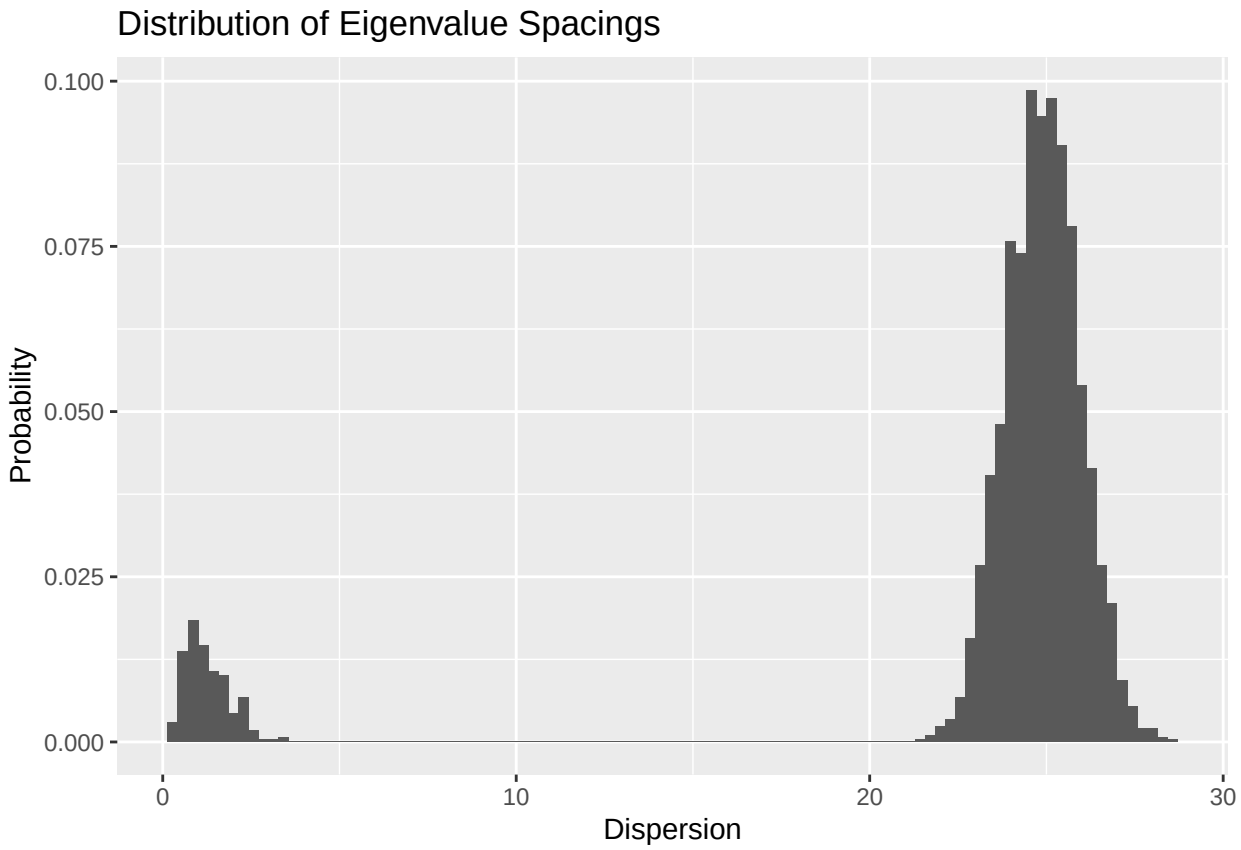
```
pairs_12 <- data.frame(i = 1, j = 2)
disps <- P %>% dispersion(diff_abs = T, components = F, norm = F, pairs = pairs_12)
disps %>% dispersion.histogram()
```



Absolute Difference

Without Resolving Components

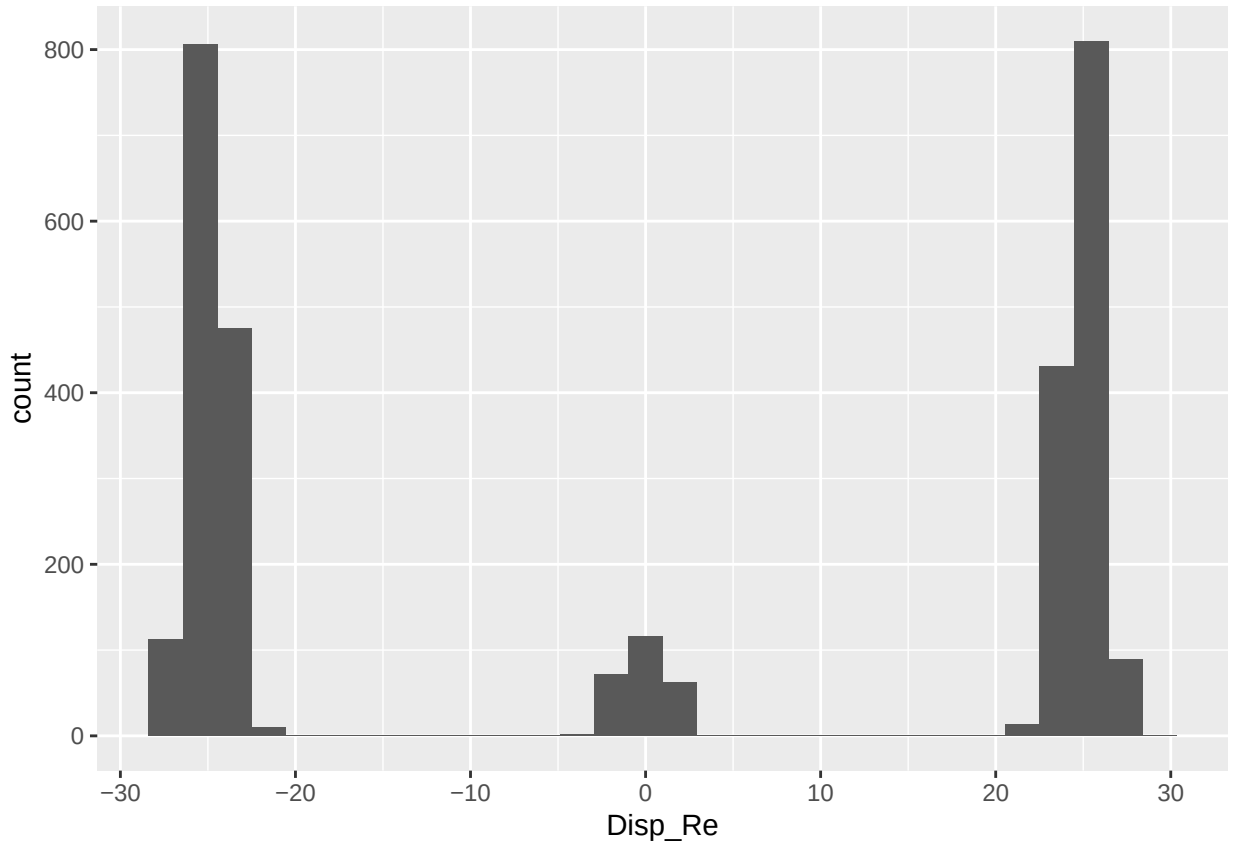
```
pairs_12 <- data.frame(i = 1, j = 2)
disps <- P %>% dispersion(diff_abs = F, components = F, pairs = pairs_12)
disps %>% dispersion.histogram()
```



Resolving Components

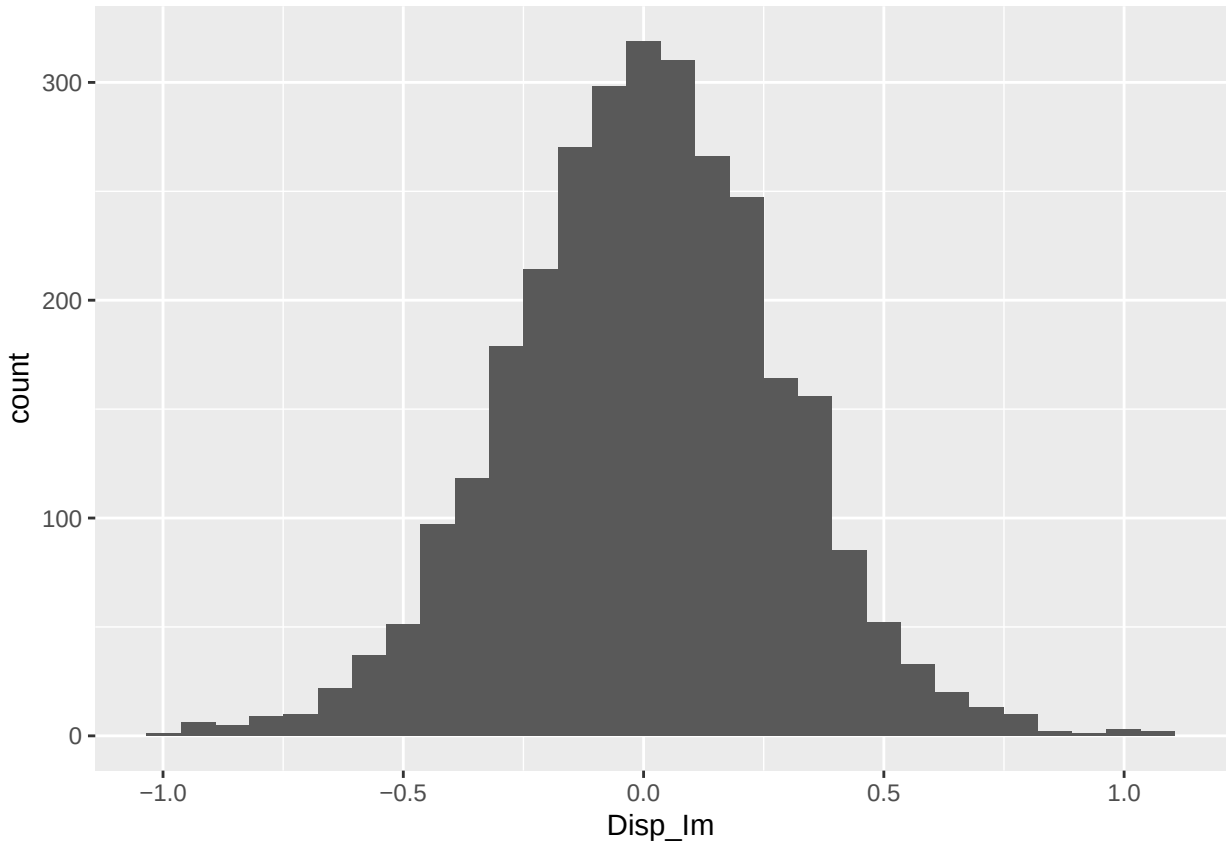
```
disps <- P %>% dispersion(diff_abs = F, components = T, norm = F, pairs = pairs_12)
disps %>%
  ggplot(aes(x = Disp_Re)) +
  geom_histogram()
```

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




```
disps %>%
  ggplot(aes(x = Disp_Im)) +
  geom_histogram()
```

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


300
200
100
0
count
−1.0
−0.5
0.0
0.5
1.0
Disp_Im

Within ensemble

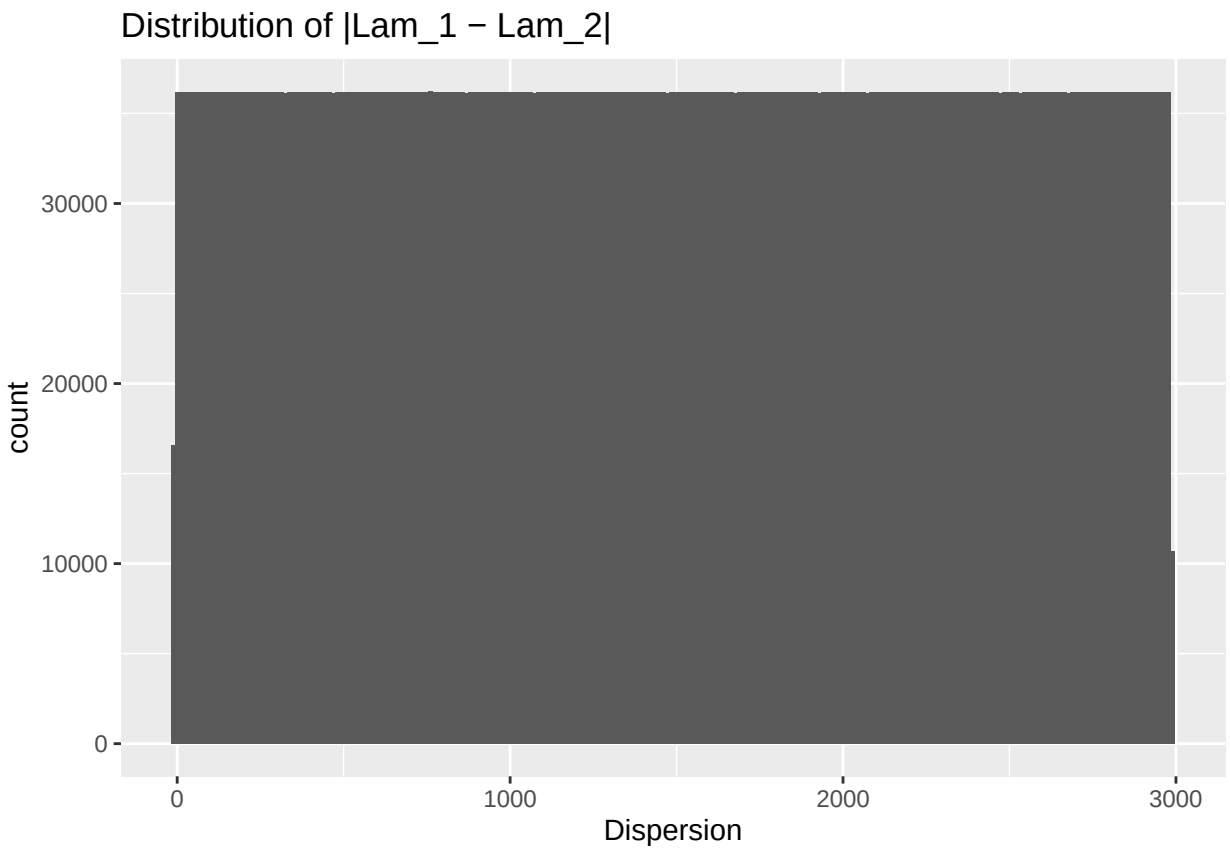
```
specP <- P %>% spectrum()
```

Difference of Absolutes

```
spec1 <- (specP %>% filter(Order == 1))$Norm
spec2 <- (specP %>% filter(Order == 2))$Norm
```

```
disps_cross <- data.frame(Dispersion = do.call("c",map(seq_along(spec1), function(x){x - spec2})))
```

```
disps_cross %>%
  ggplot(mapping = aes(Dispersion)) +
  geom_histogram(bins = 250) +
  labs(title = "Distribution of |Lam_1 - Lam_2|")
```

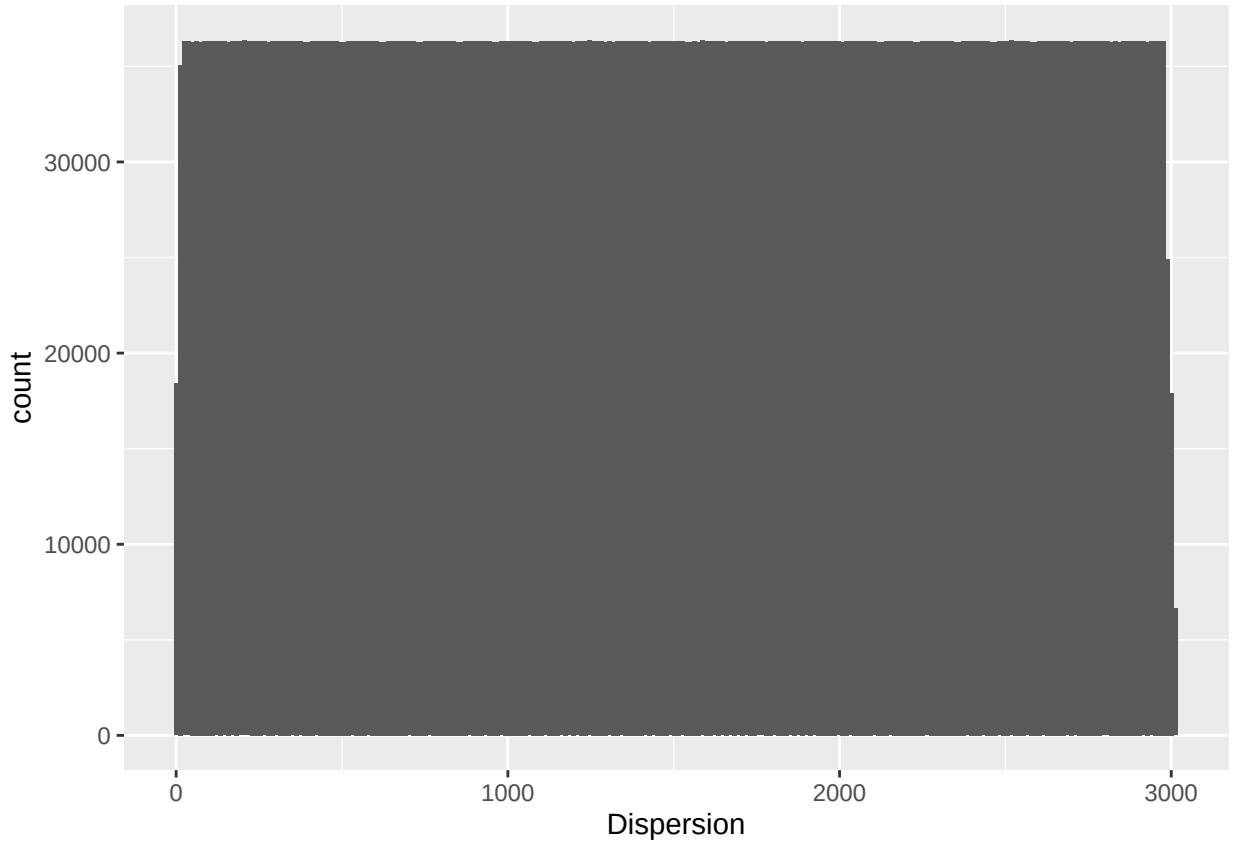


Absolute Difference

```
specP <- P %>% spectrum(components = F)
```

```
spec1 <- (specP %>% filter(Order == 1))$Eigenvalue
spec2 <- (specP %>% filter(Order == 2))$Eigenvalue
```

```
disps_cross2 <- data.frame(Dispersion = do.call("c",map(seq_along(spec1), function(x){abs(x - spec2)})))
```

```
disps_cross2 %>%
  ggplot(mapping = aes(Dispersion)) +
```

```
  geom_histogram(bins = 250)
```