

Untitled

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

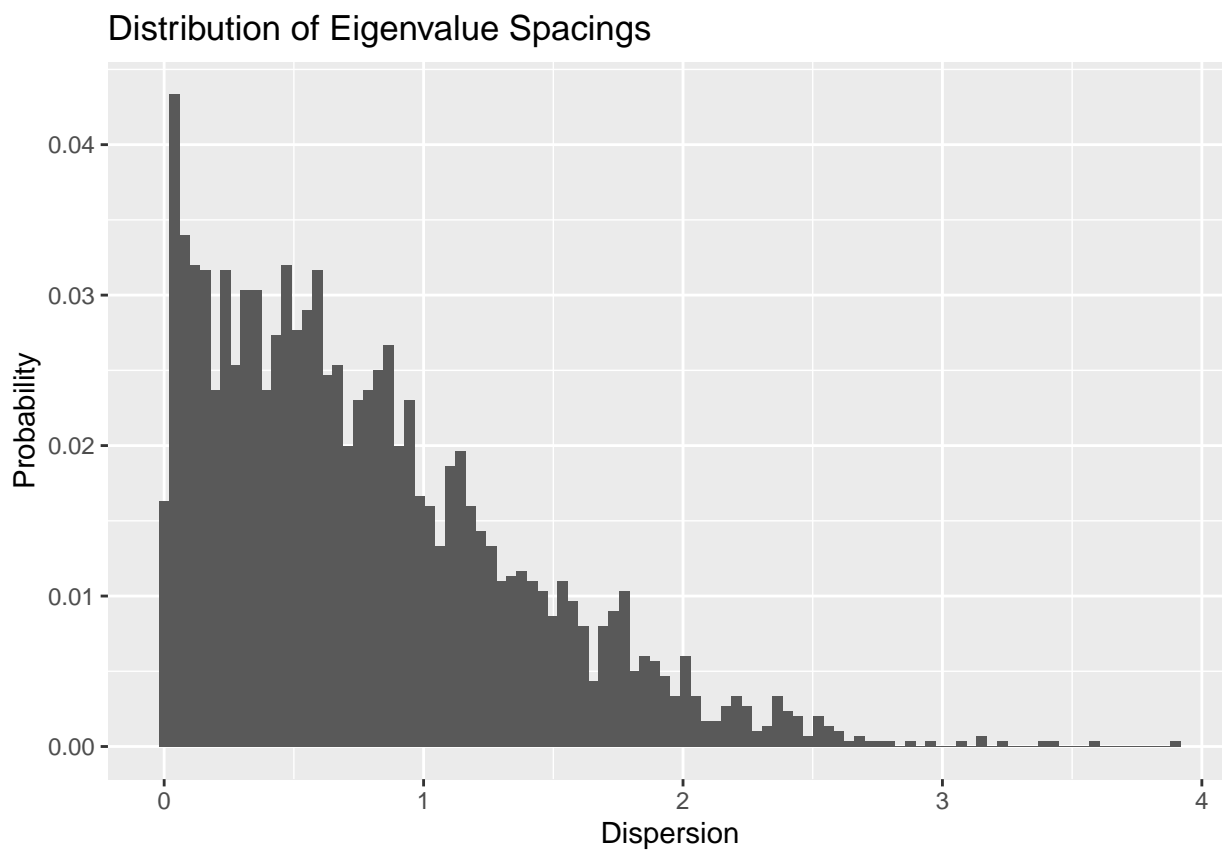
```
#.dispersion_matrix(P[[1]], diff_abs = T)
```

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

Within matrix

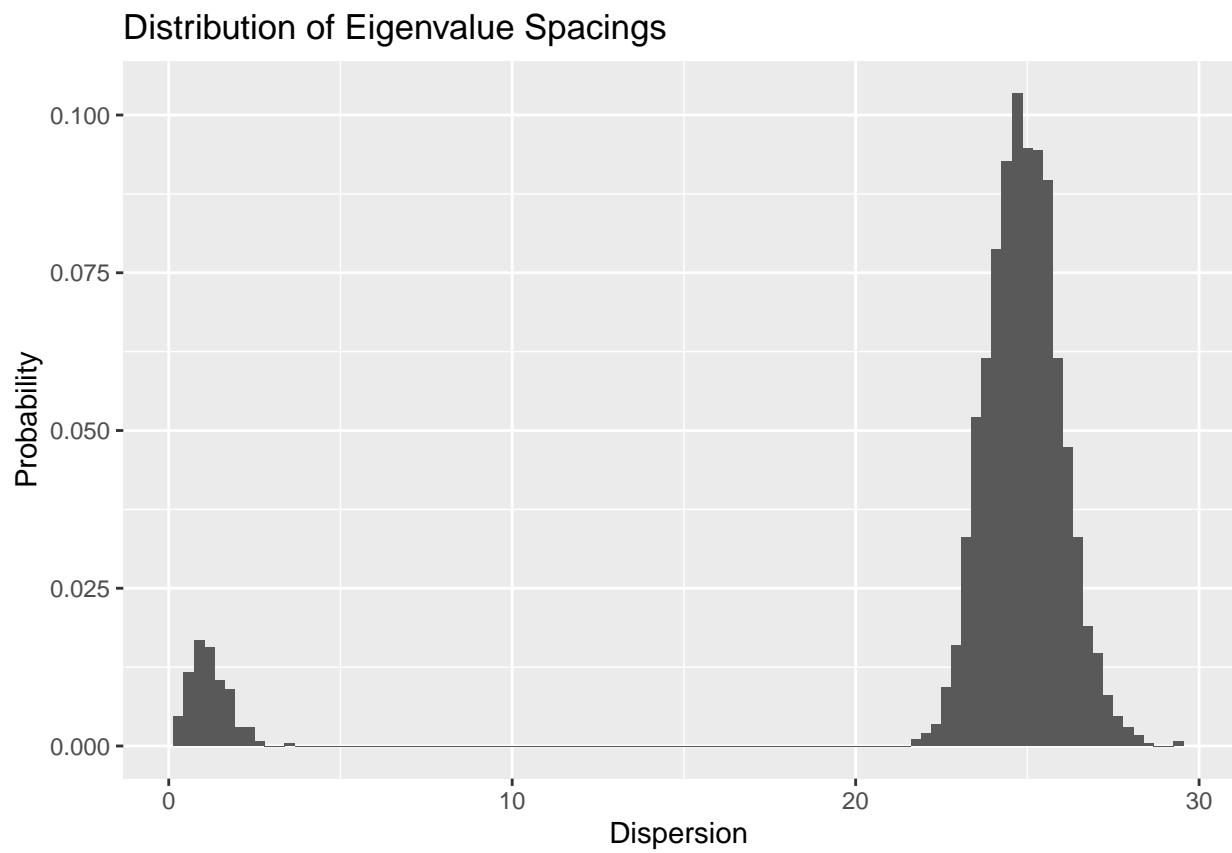
Difference of Absolutes

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



Absolute Difference

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



Within ensemble

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

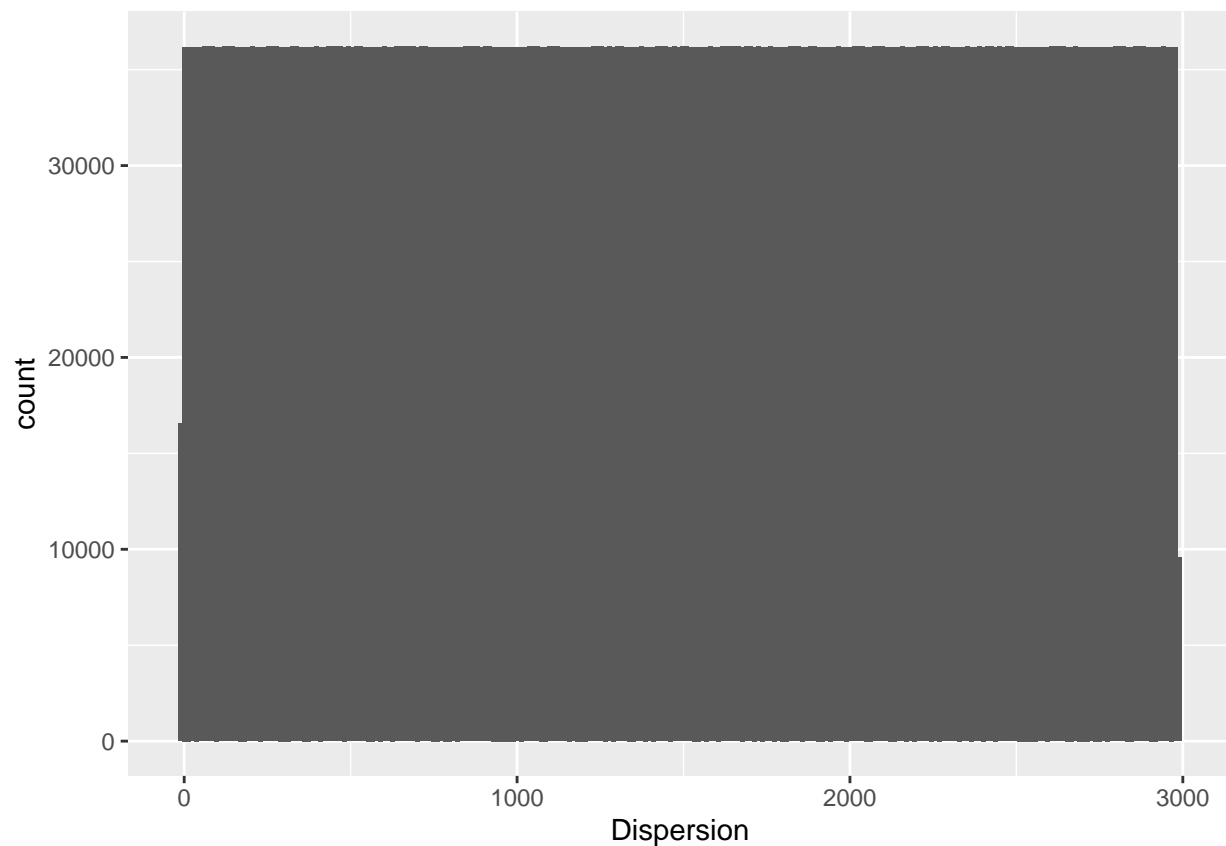
Difference of Absolutes

```
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)
```



Absolute Difference

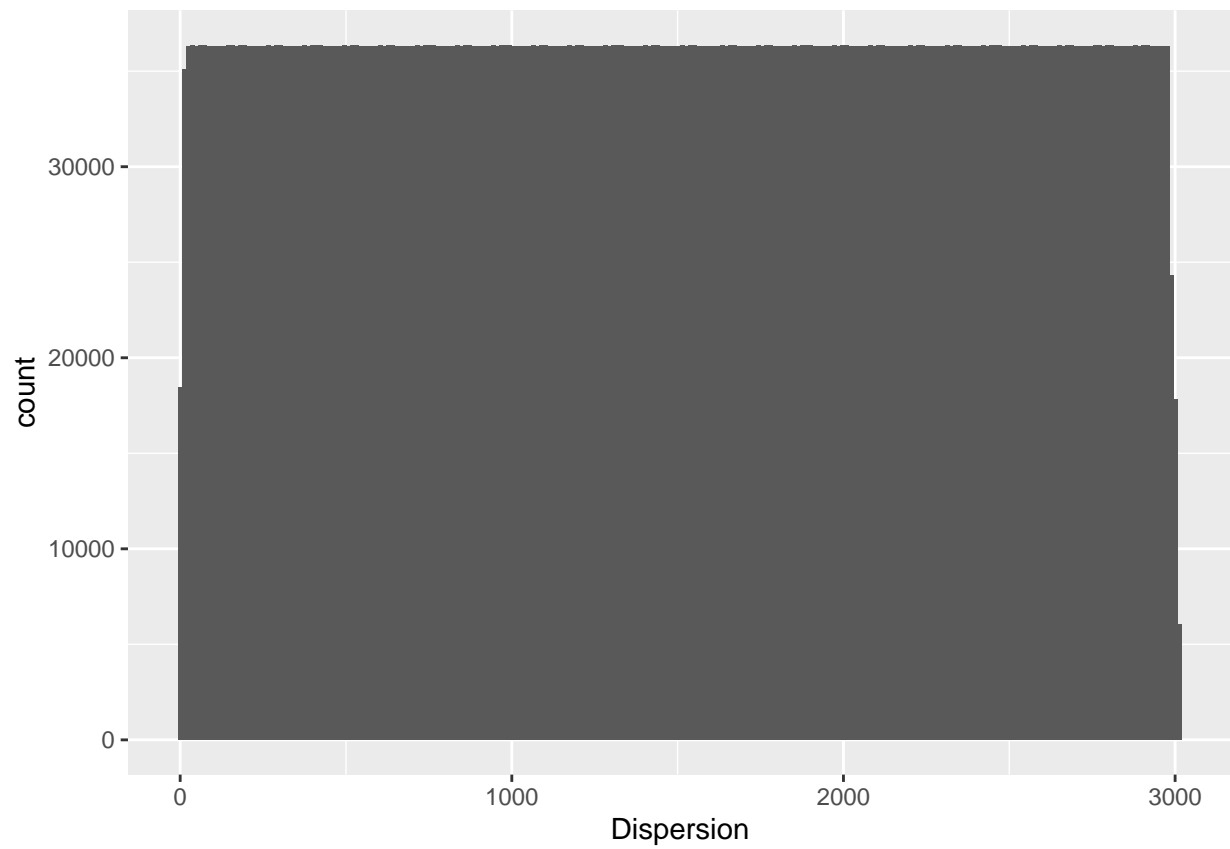
```
specP <- P %>% spectrum(components = F)
```

```
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)
```



```
dispsAD <- P %>% dispersion(diff_abs = F, components = F, norm = T, pairs = pairs_12)
```