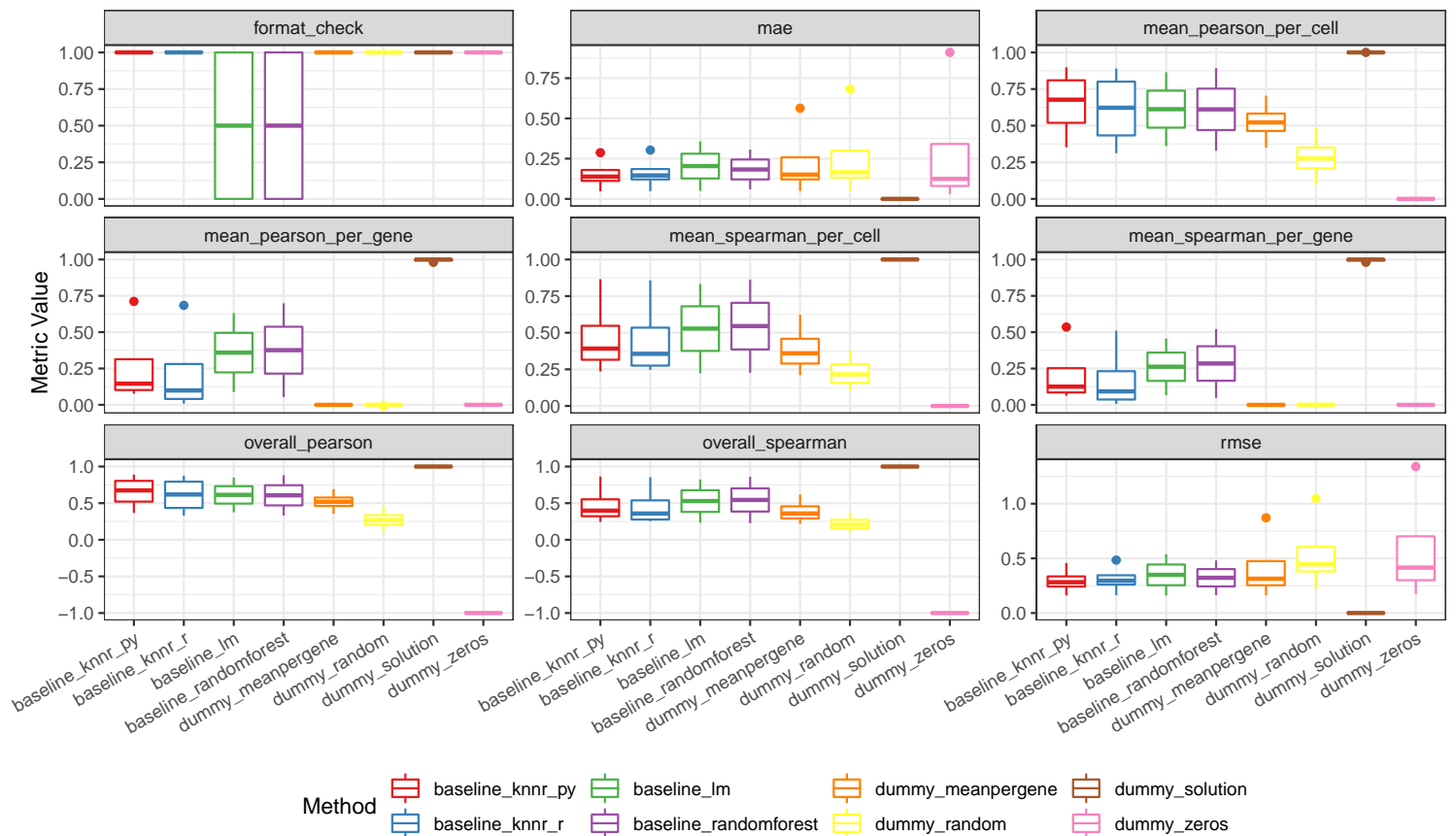
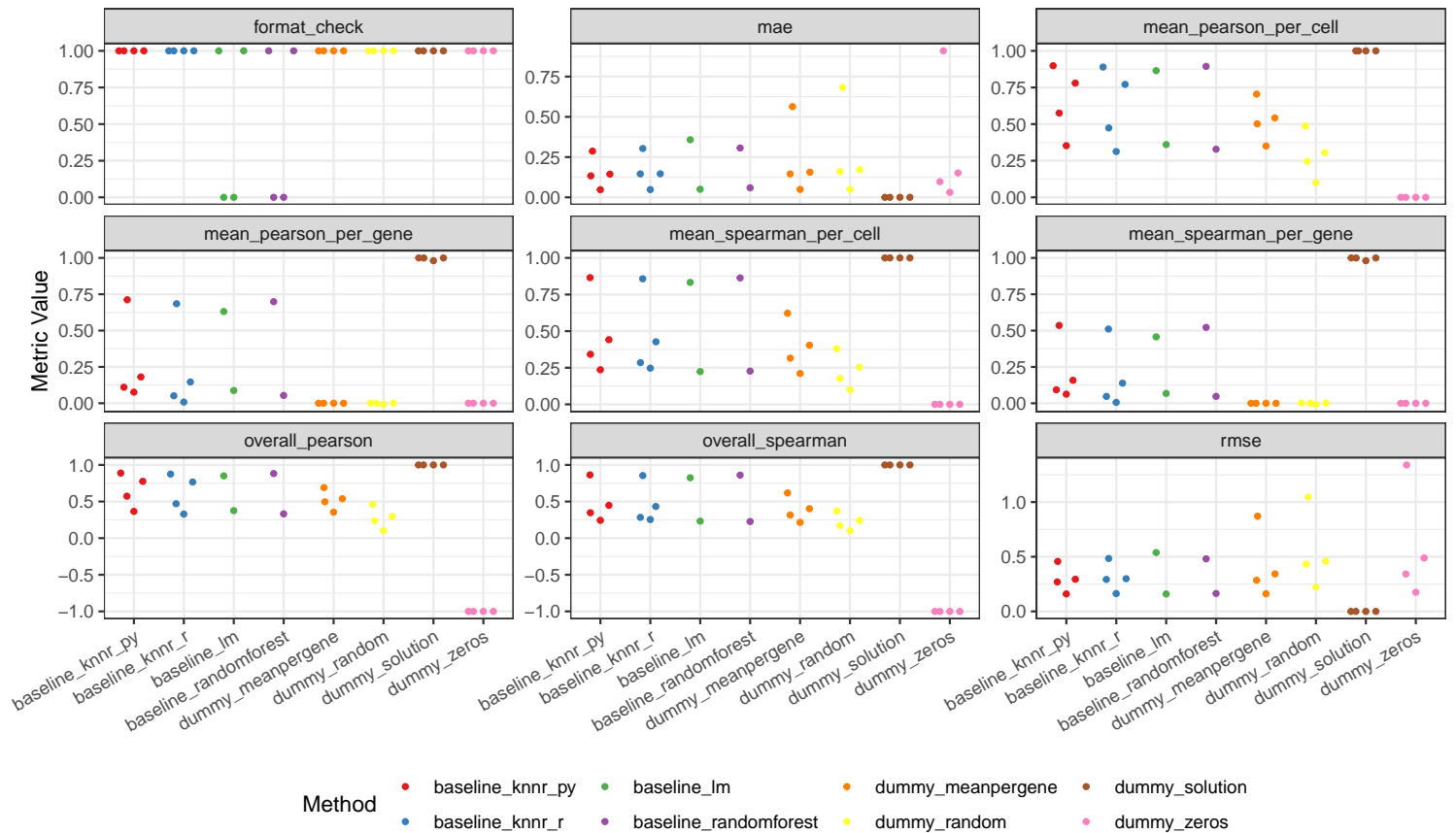


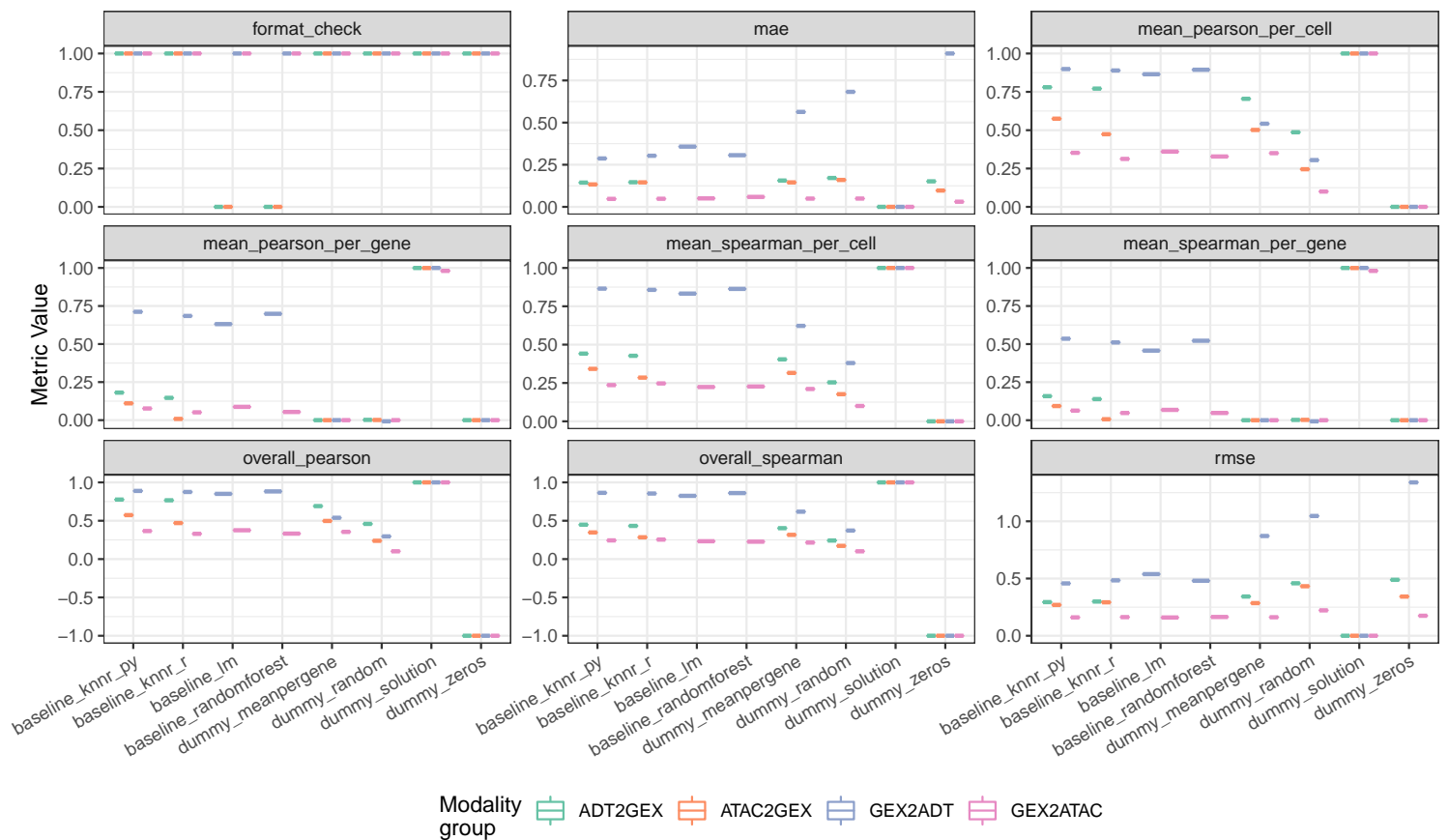
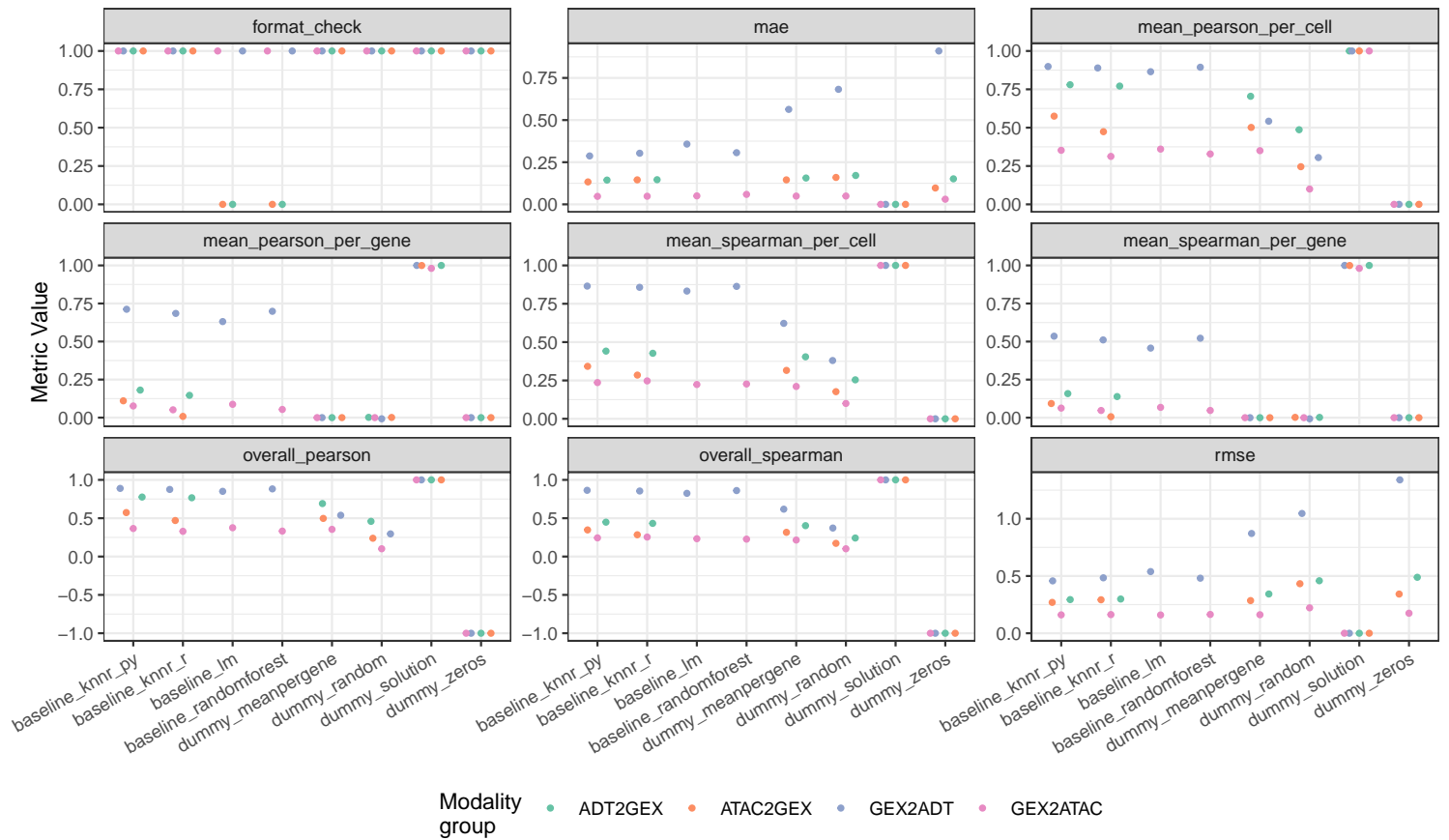
Predict Modality - Pilot Analysis

Visualise results

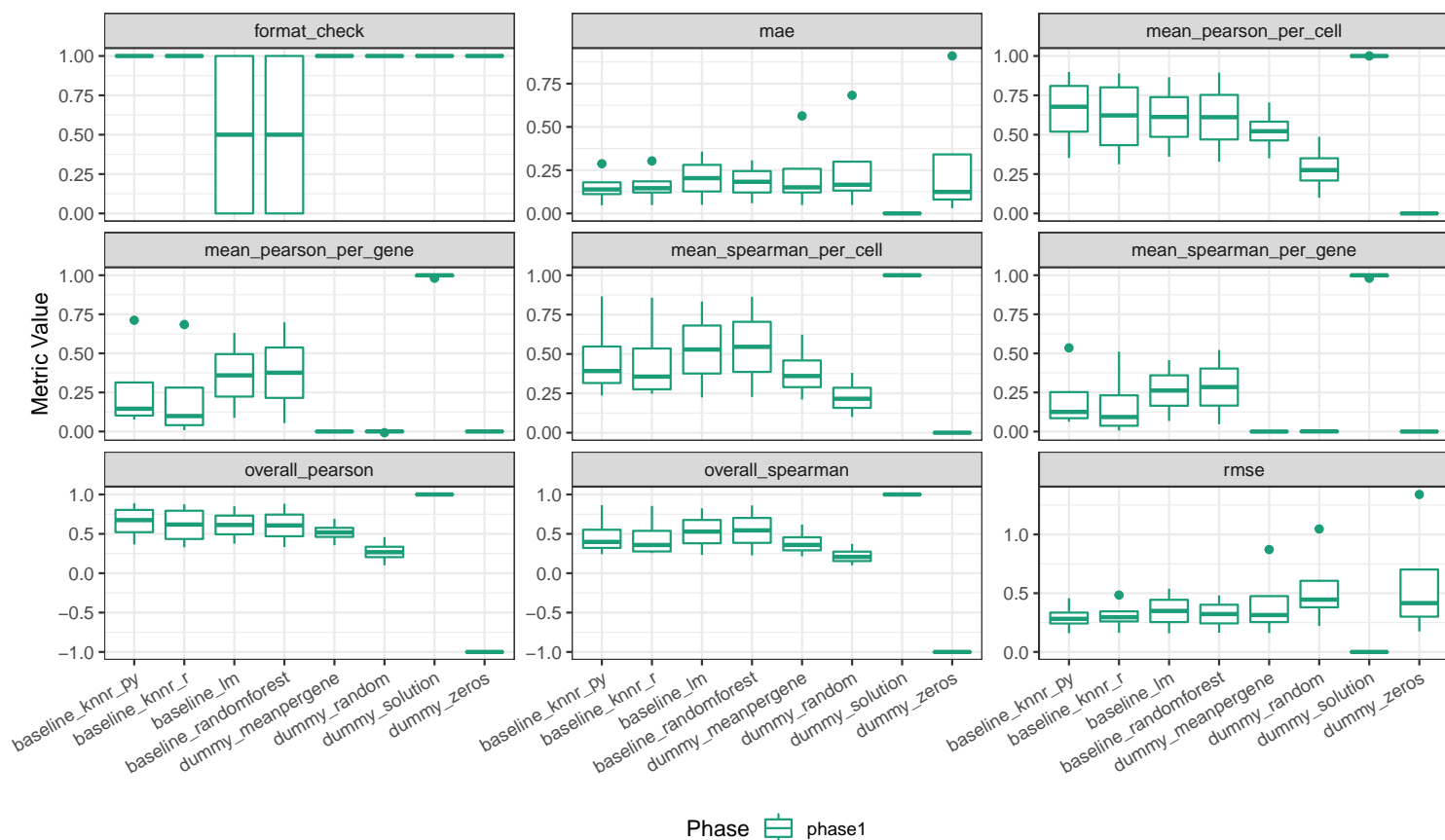
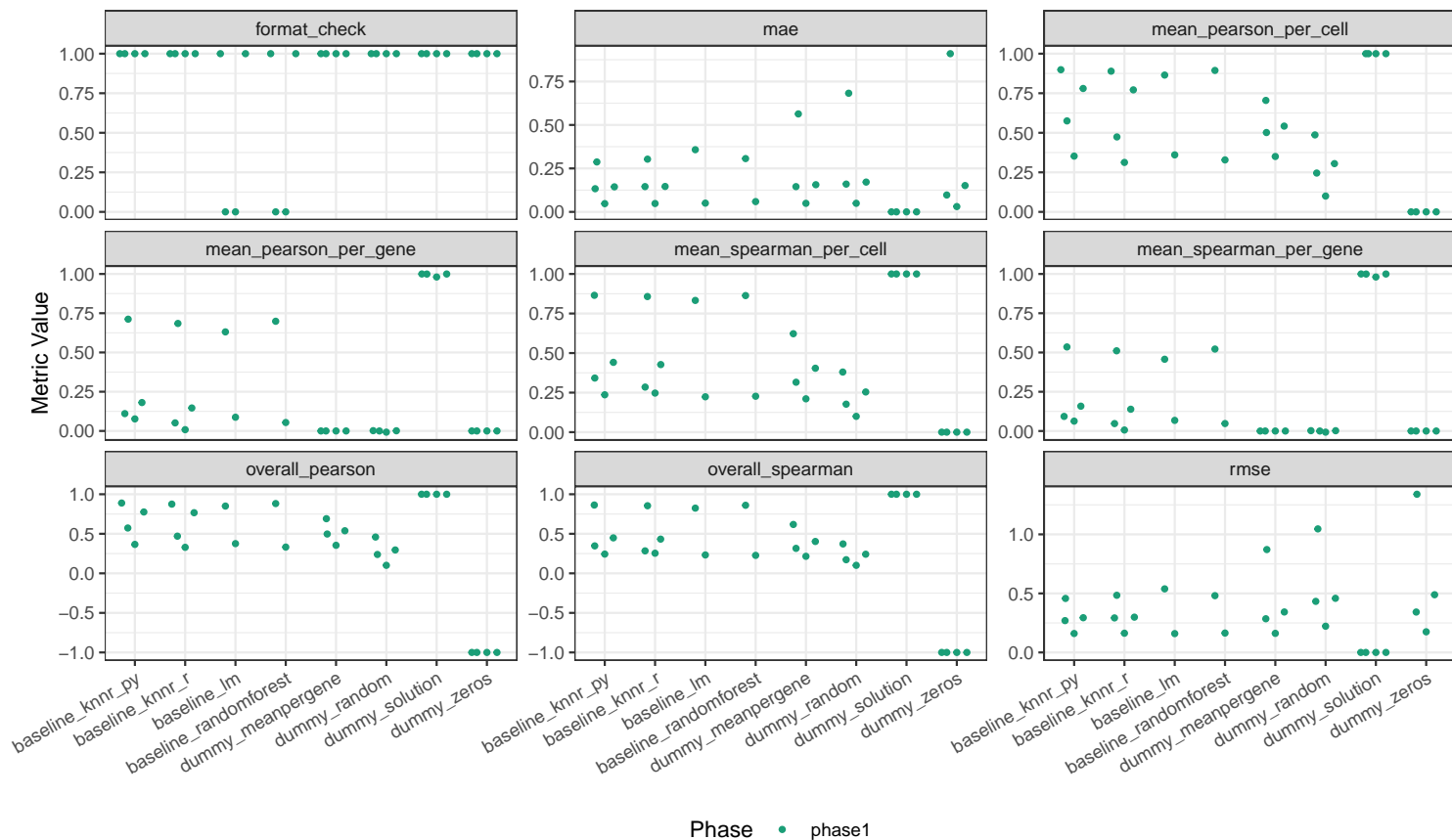
Colour by method.



Colour by modality group.



Colour by phase



Comparing most interesting metrics.

```
selected_metrics <- c("rmse", "mae", "mean_spearman_per_cell", "mean_spearman_per_gene", "overall_spearman")
```

```
GGally::ggpairs(  
  df,  
  mapping = aes(colour = method_type, fill = method_type),  
  columns = selected_metrics,  
  diag = list(continuous = "barDiag", discrete = "barDiag", na = "naDiag")  
) & theme_bw() &  
  scale_colour_brewer(palette = "Set2") &  
  scale_fill_brewer(palette = "Set2")
```

```
## Registered S3 method overwritten by 'GGally':
```

```
##   method from
```

```
##   +.gg    ggplot2
```

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

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

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

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

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

