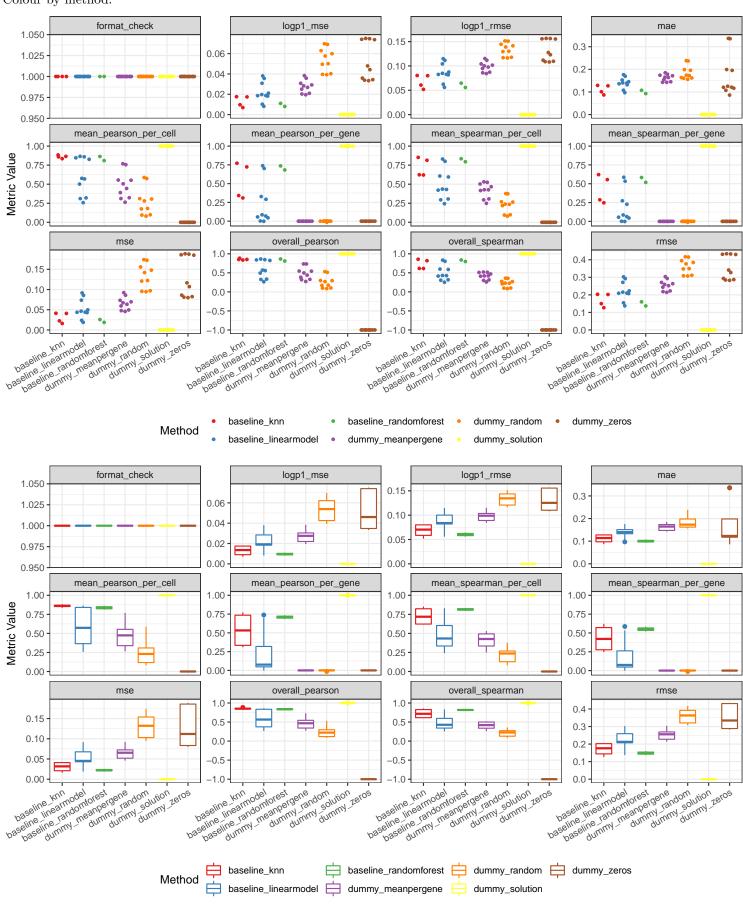
Predict Modality - Pilot Analysis

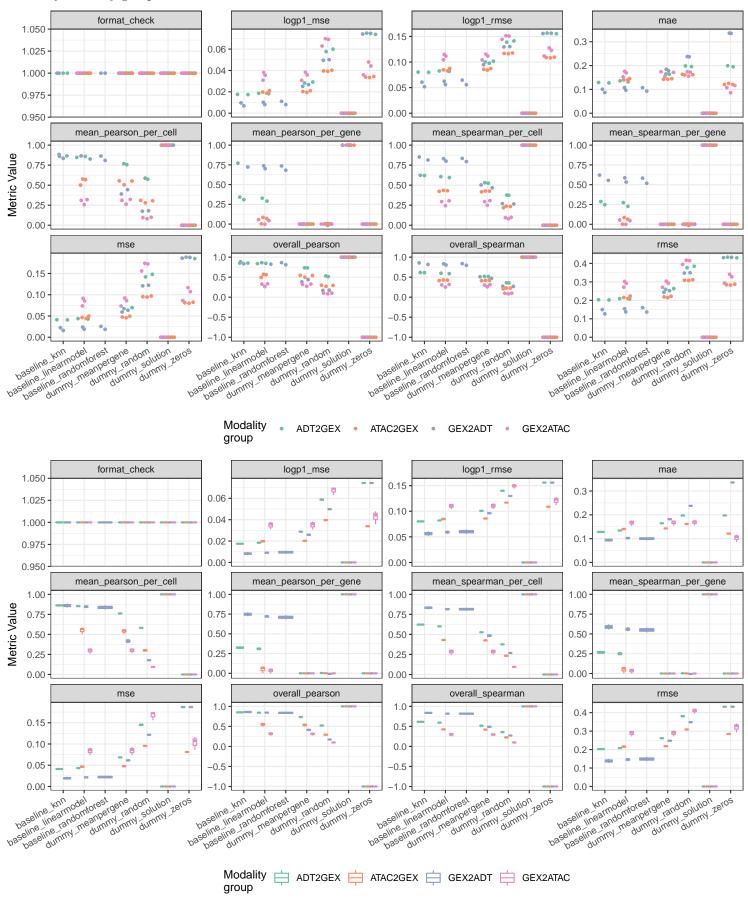
1

Visualise results

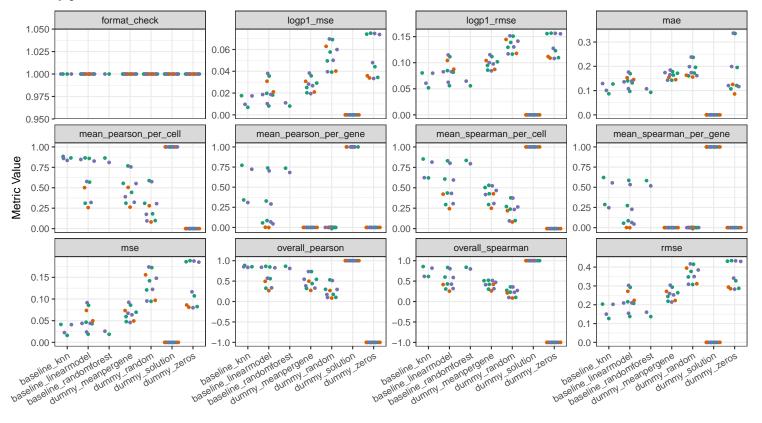
Colour by method.



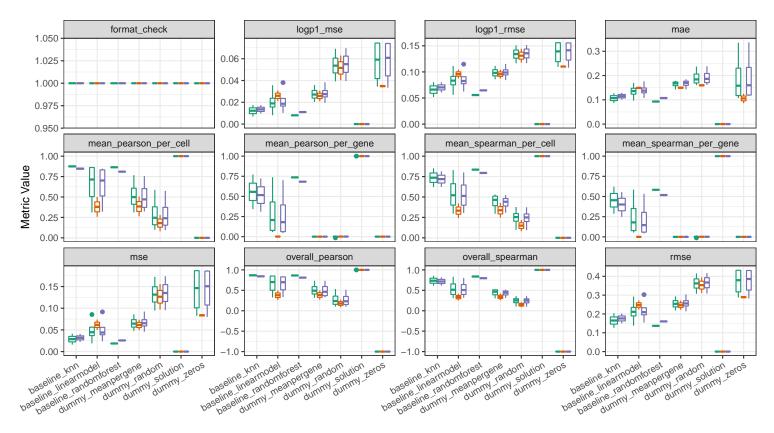
Colour by modality group.



Colour by phase







Phase iid phase1 phase2

Comparing most interesting metrics.

theme_bw()

```
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, rmse)) + geom_point(aes(colour = method_type)),
  ggplot(df, aes(rmse, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)),
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)),
  nrow = 1,
  guides = "collect"
) & theme_bw() & scale_colour_brewer(palette = "Set2")
                                     1.00 -
                                                                         1.00
  0.4
                                                                       gene
                                   mean_pearson_per_gene
0.50
0.25
                                                                         0.75
  0.3
                                                                       mean_pearson_per_
                                                                                                            method_type
B 0.2
                                                                                                                baseline
                                                                         0.50
                                                                                                                negative_control
                                                                                                                positive_control
                                                                         0.25
  0.1
                                     0.00
                                                                         0.00
  0.0
     0.00
           0.25
                 0.50
                        0.75
                              1.00
                                         0.0
                                                     0.2
                                                                 0.4
                                                                             0.00
                                                                                         0.50
                                                                                                0.75
                                               0.1
                                                           0.3
                                                                                   0.25
        mean_pearson_per_cell
                                                     rmse
                                                                                 mean_pearson_per_cell
ggplot(dfg %>% filter(metric_id %in% c("mean_spearman_per_cell", "mean_spearman_per_gene", "rmse"))) +
  geom_histogram(aes(value, fill = method_type)) +
  facet_grid(method_type~metric_id, scales = "free_x") +
```

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

