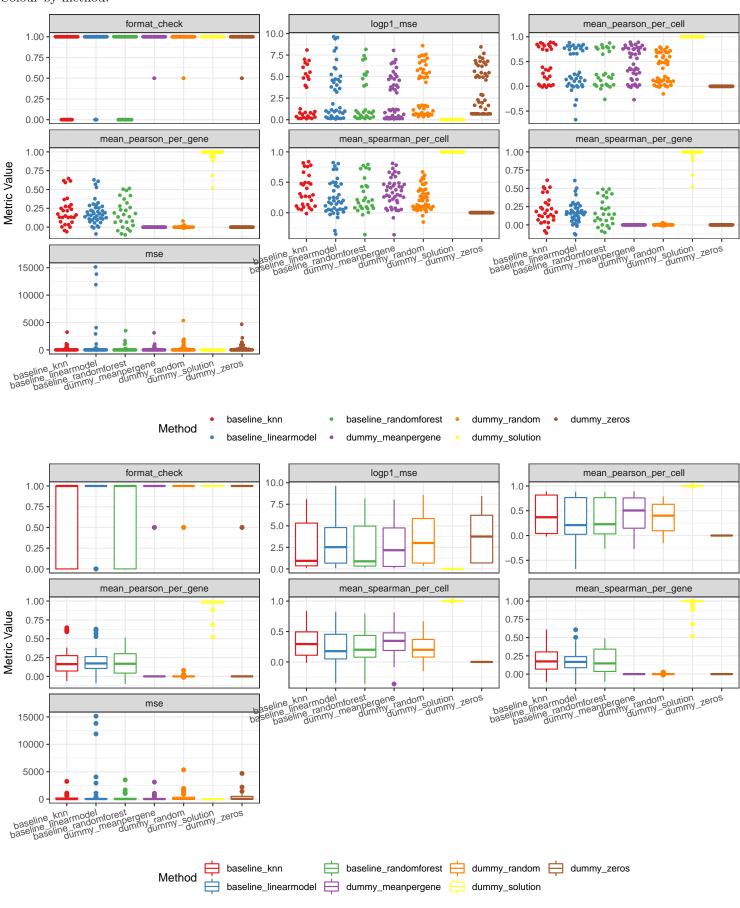
Predict Modality - Pilot Analysis

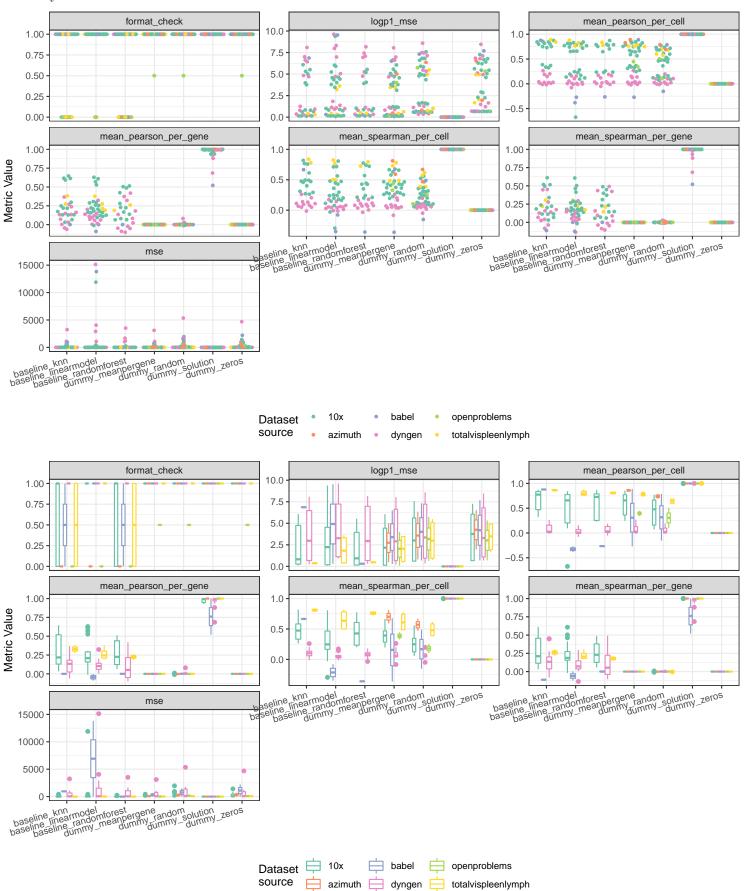
1

Visualise results

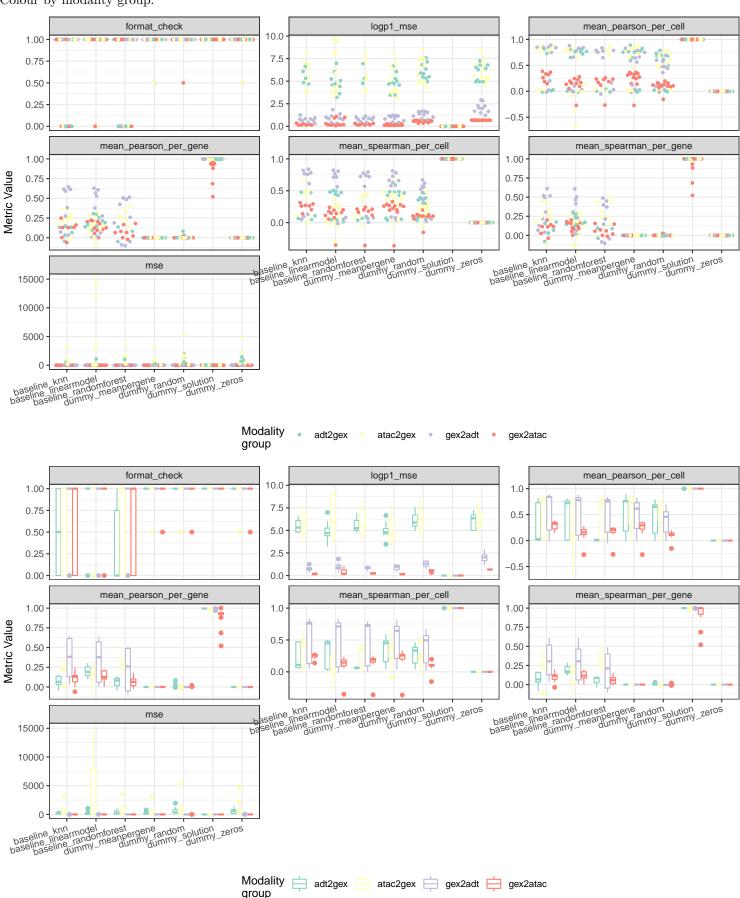
Colour by method.



Colour by dataset source.

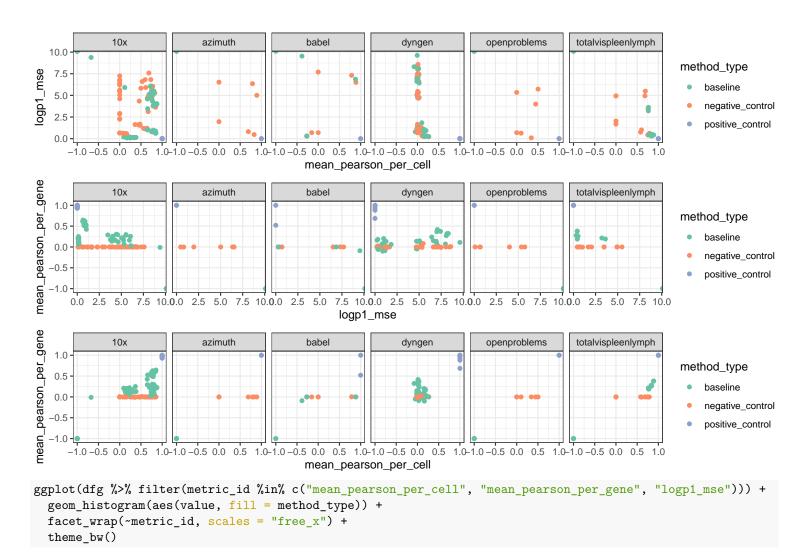


Colour by modality group.



Comparing most interesting metrics.

```
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, logp1_mse)) + geom_point(aes(colour = dataset_source)) + facet_wrap(~met
  ggplot(df, aes(logp1_mse, mean_pearson_per_gene)) + geom_point(aes(colour = dataset_source)) + facet_wrap(~met
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = dataset_source)) + fac
) & theme_bw() & scale_colour_brewer(palette = "Set2")
                    baseline
                                                   negative_control
                                                                                      positive_control
  10.0
                                                                                                                dataset_source
                                                                                                                    10x
   7.5
logp1_mse
                                                                                                                    azimuth
   5.0
                                                                                                                    babel
                                                                                                                    dyngen
   2.5
                                                                                                                    openproblems
                                                                                                                    totalvispleenlymph
   0.0
       -1.0
              -0.5
                      0.0
                                     1.0
                                                -0.5
                                                        0.0
                                                                0.5
                                                                           -1.0
                                                                                   -0.5
                                                                                           0.0
                                                                                                  0.5
                                               mean_pearson_per_cell
                    baseline
                                                   negative_control
                                                                                      positive_control
   1.0
mean_pearson_per_gene
                                                                                                                dataset_source
                                                                                                                    10x
   0.5
                                                                                                                    azimuth
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                                                     logp1_mse
                                                   negative_control
                                                                                      positive_control
                    baseline
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mean_pearson_per_gene
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                                                                                                                    10x
   0.5
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                                                        0.0
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                                                                                   -0.5
                                                                                           0.0
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                                                                        1.0 -1.0
       -1.0
                                                                                                          1.0
                                               mean_pearson_per_cell
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, logp1_mse)) + geom_point(aes(colour = method_type)) + facet_wrap(~datase
  ggplot(df, aes(logp1_mse, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)) + facet_wrap(~datase
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)) + facet
  ncol = 1
) & theme_bw() & scale_colour_brewer(palette = "Set2")
```



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

