mortality_analysis

Bohan Zhang

2023-08-21

Evaluation proceduce

1. calculate the ratio between mae/rmse of reconciled forecasts and mae/rmse of base forecasts
2. mae/rmse of the total, mean, max and min mae/rmse of bottom series
3. summarised over specific domains

mint and wlsv vs ols and wlss

OLS and structural scaling are more likely to produce more extreme results.

robustness: wlsv > mint > wlss > ols

```r
ratio %>% group_by(rf_method, accuracy_method) %>%
  summarise(total= mean(total), bottom_max=mean(bottom_max),
            bottom_min=mean(bottom_min), bottom_mean=mean(bottom_mean)) %>%
  arrange(accuracy_method)
```

```
## `summarise()` has grouped output by 'rf_method'. You can override using the
## `.groups` argument.
```

```
## # A tibble: 8 x 6
## # Groups:   rf_method [4]
##   rf_method accuracy_method total bottom_max bottom_min bottom_mean
##   <chr>     <chr>           <dbl>      <dbl>      <dbl>       <dbl>
## 1 mint      mae             0.857       1.63      0.740        1.01
## 2 ols       mae             0.956      27.9       0.589        2.20
## 3 wlss      mae             0.862      13.4       0.642        1.48
## 4 wlsv      mae             0.846       1.41      0.818        1.00
## 5 mint      rmse            0.945       1.51      0.764        1.00
## 6 ols       rmse            0.976      22.9       0.627        2.01
## 7 wlss      rmse            0.940      11.1       0.675        1.40
## 8 wlsv      rmse            0.944       1.36      0.844        1.00
```

In general, the improvement of some series comes with the cost of some other series. It's very unlikely that reconciliation improves all the series.

```r
ratio %>% filter(bottom_max <= 1.01) %>% select(representator, rf_method, distance, cluster, total, bot
  arrange(bottom_max)
```

```
## # A tibble: 26 x 9
##    representator rf_method distance      cluster total bottom_mean bottom_max
##    <chr>         <chr>     <chr>         <chr>   <dbl>       <dbl>      <dbl>
##  1 ""            wlsv      ""            ""       1.04       0.999       1.00
##  2 "forecast"    wlsv      "uncorrelati~ "kmedo~  1.04       0.998       1.00
```

```
##  3 "forecast"       wlsv    "uncorrelati~ "kmedo~  1.04       0.998      1.00
##  4 "forecast"       wlsv    "uncorrelati~ "kmedo~  1.04       0.999      1.00
##  5 ""               wlsv    ""            ""       1.03       1.00       1.00
##  6 "forecast"       wlsv    "uncorrelati~ "kmedo~  1.03       0.998      1.00
##  7 "error.features" wlsv    "dtw"         "kmedo~  1.46       0.992      1.00
##  8 "error.features" wlsv    "dtw"         "kmedo~  1.46       0.991      1.00
##  9 "forecast"       wlsv    "uncorrelati~ "kmedo~  1.03       0.999      1.00
## 10 "error.features" wlsv    "dtw"         "kmedo~  1.45       0.991      1.00
## # i 16 more rows
## # i 2 more variables: bottom_min <dbl>, batch <int>
```

K-medoids (only mint, rmse)

```r
tmp <- ratio %>% filter(startsWith(cluster, "kmedoids"), rf_method == "mint", accuracy_method == "rmse")
  rowwise() %>%
  mutate(n_middle = NROW(other$S)) %>%
  select(representator, distance, cluster, total, bottom_mean, bottom_max, bottom_min, n_middle, batch)
  ungroup()
```
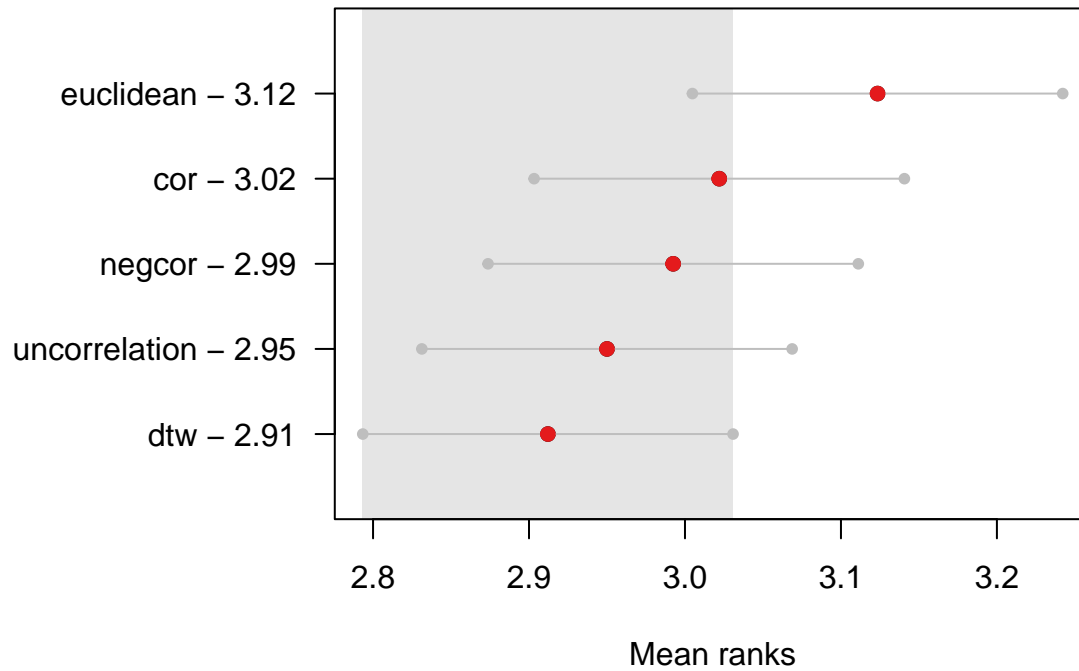
distance

```r
tmp %>% group_by(distance) %>% summarise_at(c("total", "bottom_mean", "bottom_max", "bottom_min"), c(mea
```

```
## # A tibble: 5 x 5
##   distance       total_mean bottom_mean_mean bottom_max_mean bottom_min_mean
##   <chr>               <dbl>            <dbl>           <dbl>           <dbl>
## 1 cor                 0.956            0.998            1.46           0.767
## 2 dtw                 0.952            1.00             1.55           0.776
## 3 euclidean           0.959            0.999            1.49           0.768
## 4 negcor              0.946            1.00             1.60           0.757
## 5 uncorrelation       0.951            1.01             1.52           0.760
```

```r
mcb <- function(x) {
  tsutils::nemenyi(x, plottype = "vmcb")
}

## total
tmp %>% select(representator, cluster, batch, distance, total) %>%
  tidyr::pivot_wider(names_from = "distance", values_from = "total") %>%
  select(-representator, -cluster, -batch) %>%
  mcb()
```
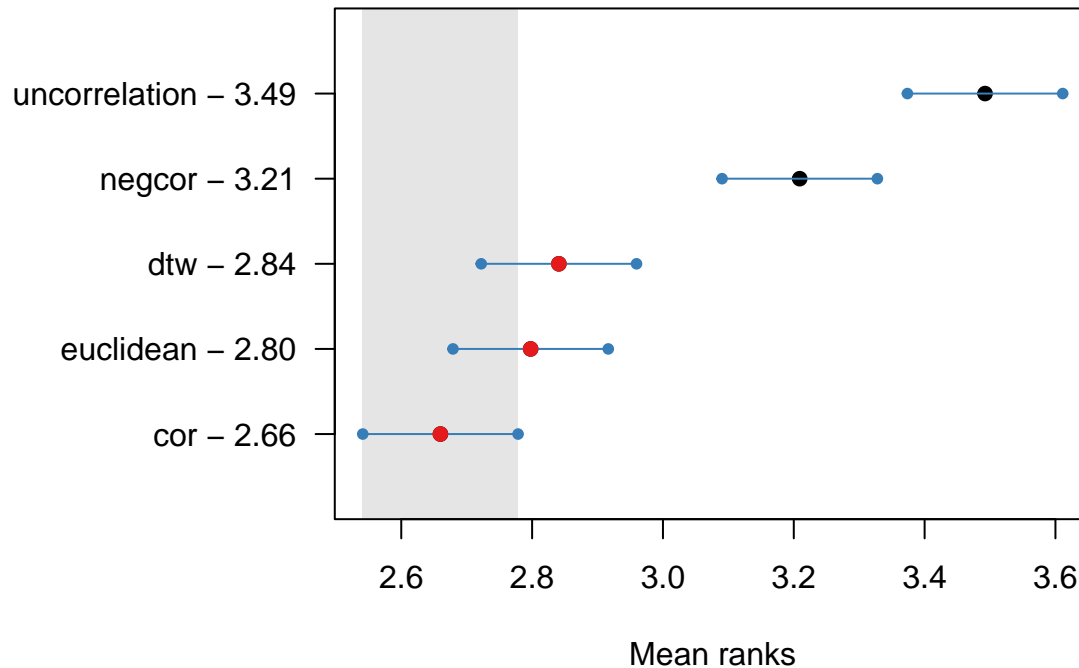
Friedman: 0.139 (H0: Identical)
Critical distance: 0.237


```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 660 and number of methods is 5
## Friedman test p-value: 0.1394 - H0: Identical
## Critical distance: 0.2374
```

```r
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "distance", values_from = "bottom_mean") %>%
  select(-representator, -cluster, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 0.237


```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 660 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.2374
```
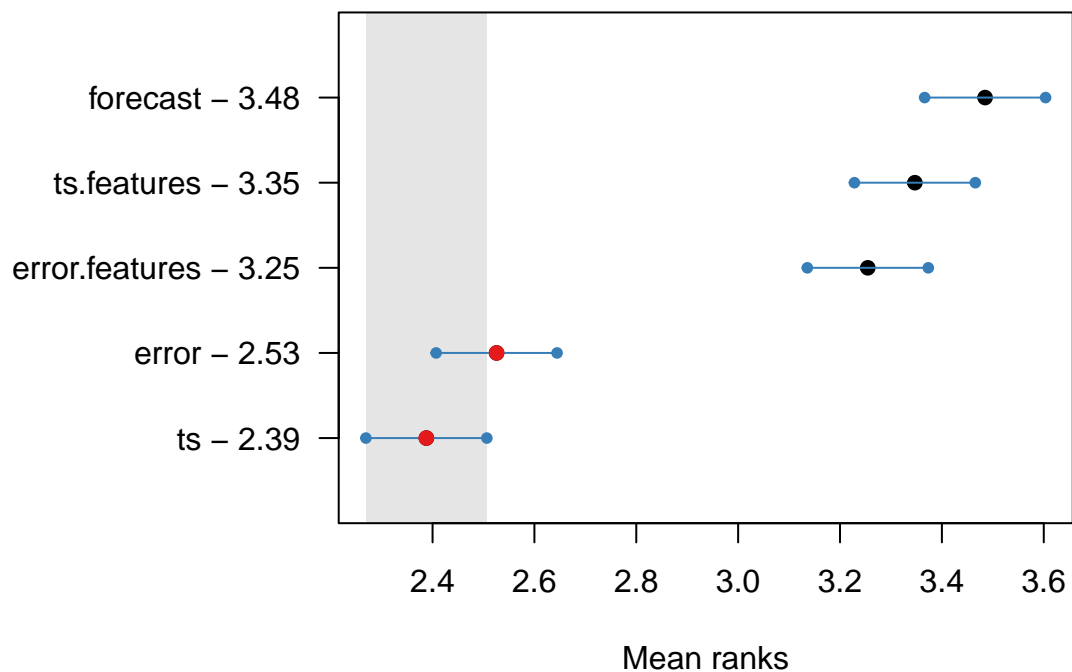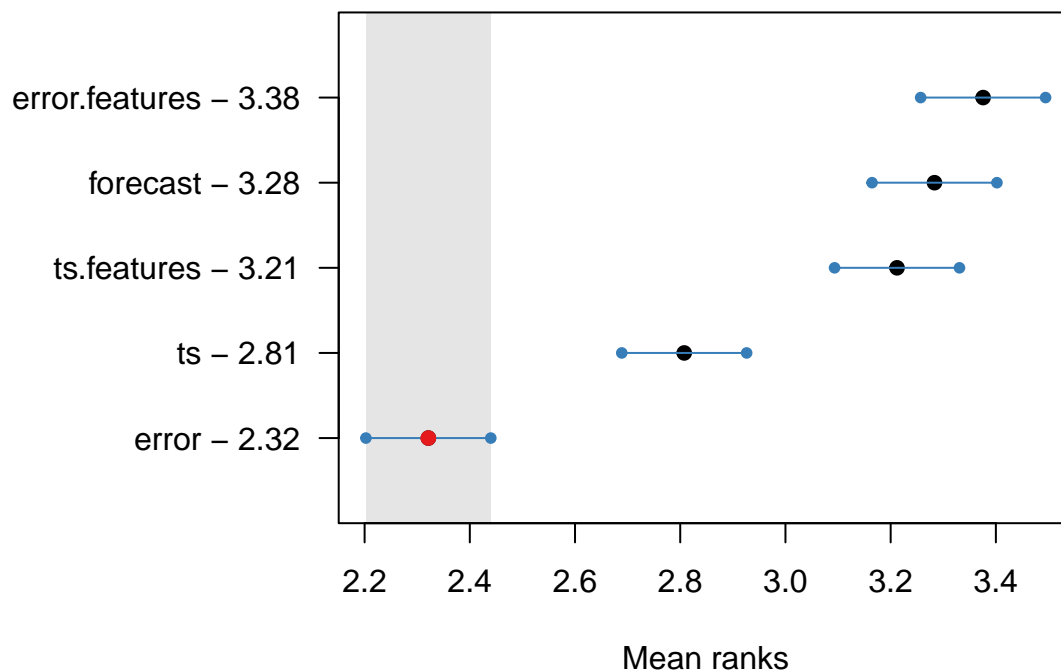
representator

```r
tmp %>% group_by(representator) %>% summarise_at(c("total", "bottom_mean", "bottom_max", "bottom_min"),
```

```
## # A tibble: 5 x 5
##   representator  total_mean bottom_mean_mean bottom_max_mean bottom_min_mean
##   <chr>               <dbl>            <dbl>           <dbl>           <dbl>
## 1 error               0.931            0.996            1.54           0.758
## 2 error.features      0.966            1.01             1.54           0.755
## 3 forecast            0.975            1.00             1.53           0.789
## 4 ts                  0.924            1.00             1.47           0.779
## 5 ts.features         0.968            1.01             1.55           0.747
```

```r
tmp %>% select(representator, cluster, batch, distance, total) %>%
  tidyr::pivot_wider(names_from = "representator", values_from = "total") %>%
  select(-distance, -cluster, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
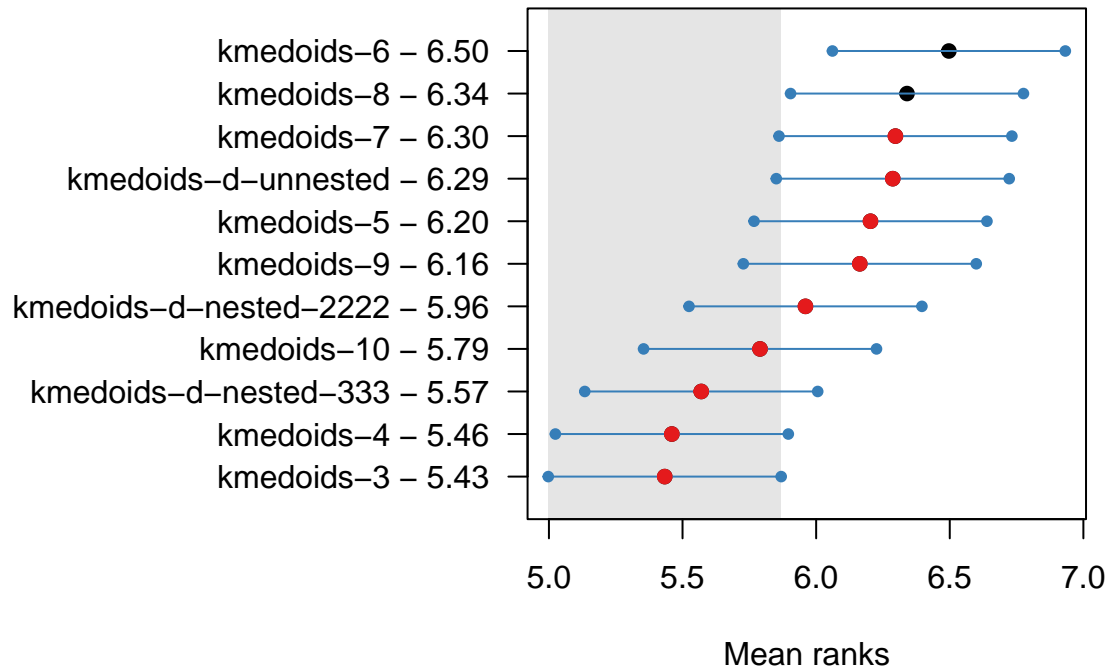## Critical distance: 0.237

Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 660 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.2374
```

```r
# bottom
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "representator", values_from = "bottom_mean") %>%
  select(-distance, -cluster, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 0.237


```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 660 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.2374
```

cluster

```r
tmp %>% select(representator, cluster, batch, distance, total) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "total") %>%
  select(-representator, -distance, -batch) %>%
  mcb()
```
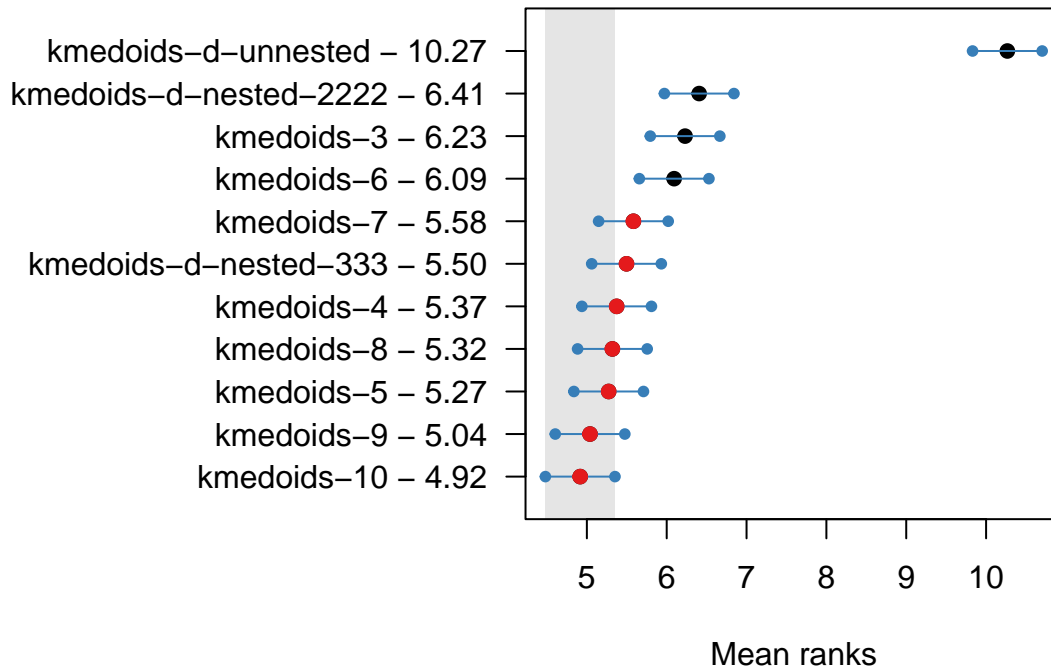
Friedman: 0.000 (Ha: Different)
Critical distance: 0.872

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 11
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.8716
```

```
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "bottom_mean") %>%
  select(-representator, -distance, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 0.872


```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 11
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.8716
```

HCluster

```r
tmp <- ratio %>% filter(startsWith(cluster, "hcluster"), rf_method == "mint", accuracy_method == "rmse"
  rowwise() %>%
  mutate(n_middle = NROW(other$S)) %>%
  select(representator, distance, cluster, total, bottom_mean, bottom_max, bottom_min, n_middle, batch)
  ungroup()
```

representator

```r
tmp %>% group_by(distance) %>% summarise_at(c("total", "bottom_mean", "bottom_max", "bottom_min"), c(mea
```

```
## # A tibble: 5 x 5
##   distance      total_mean bottom_mean_mean bottom_max_mean bottom_min_mean
##   <chr>              <dbl>            <dbl>           <dbl>           <dbl>
## 1 cor                0.958             1.02            1.98           0.569
## 2 dtw                0.944             1.02            2.00           0.575
## 3 euclidean          0.965             1.02            1.97           0.569
## 4 negcor             0.956             1.02            1.96           0.566
## 5 uncorrelation      0.950             1.02            1.89           0.583
## total
```
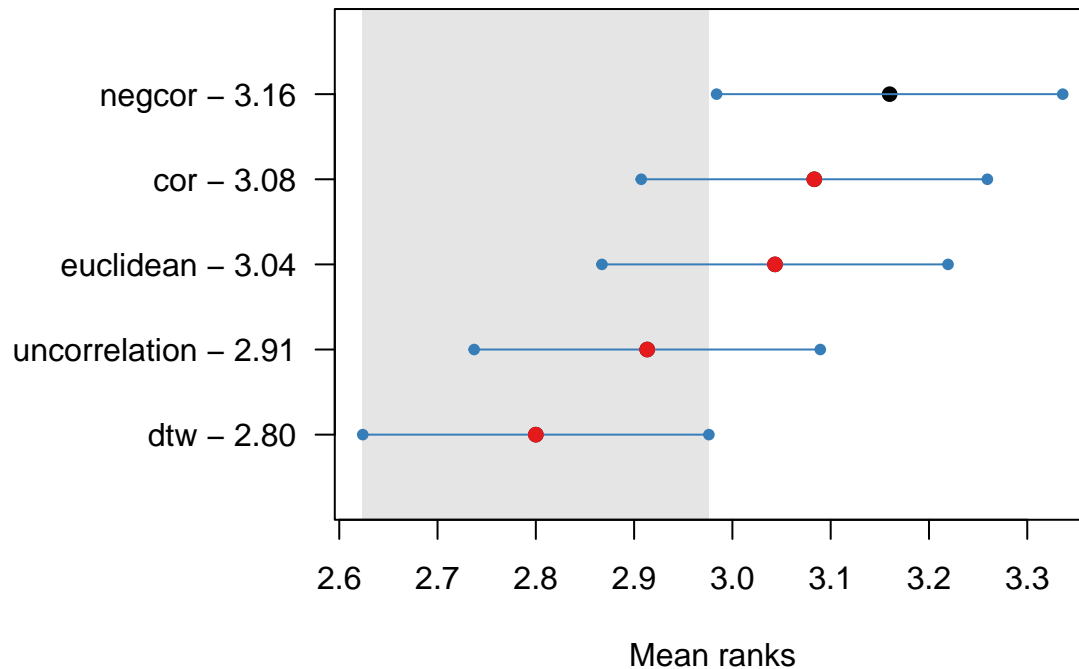
```r
tmp %>% select(representator, cluster, batch, distance, total) %>%
```

```
tidyr::pivot_wider(names_from = "distance", values_from = "total") %>%
select(-representator, -cluster, -batch) %>%
mcb()
```
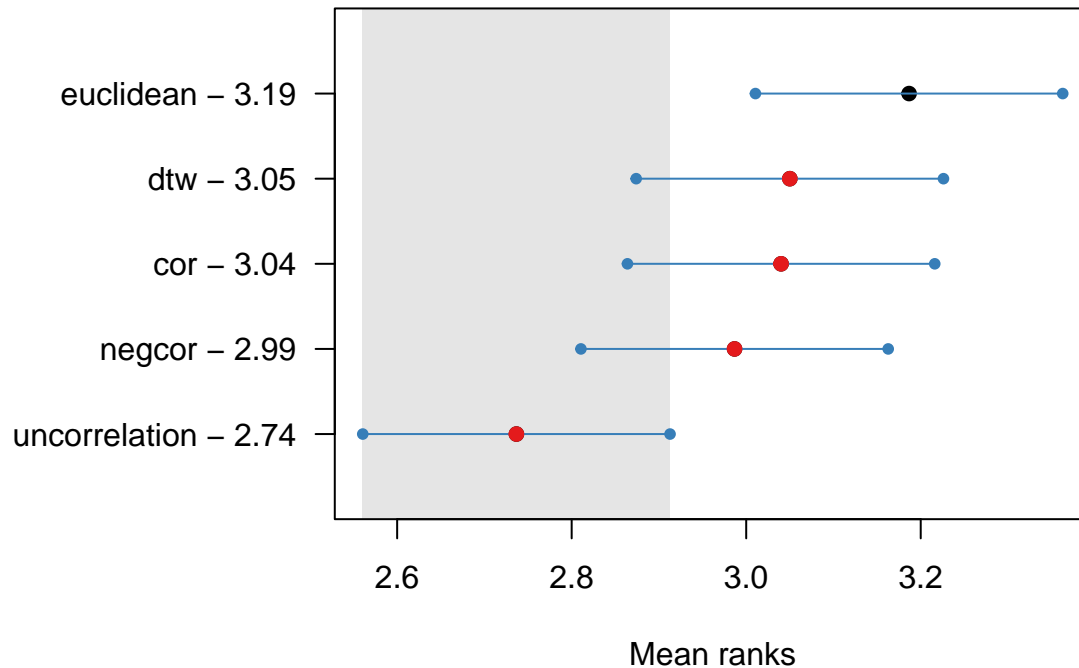
Friedman: 0.038 (Ha: Different)
Critical distance: 0.352

Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 5
## Friedman test p-value: 0.0382 - Ha: Different
## Critical distance: 0.3522
```

```
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "distance", values_from = "bottom_mean") %>%
  select(-representator, -cluster, -batch) %>%
  mcb()
```

Friedman: 0.009 (Ha: Different)
Critical distance: 0.352

Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 5
## Friedman test p-value: 0.0094 - Ha: Different
## Critical distance: 0.3522
```
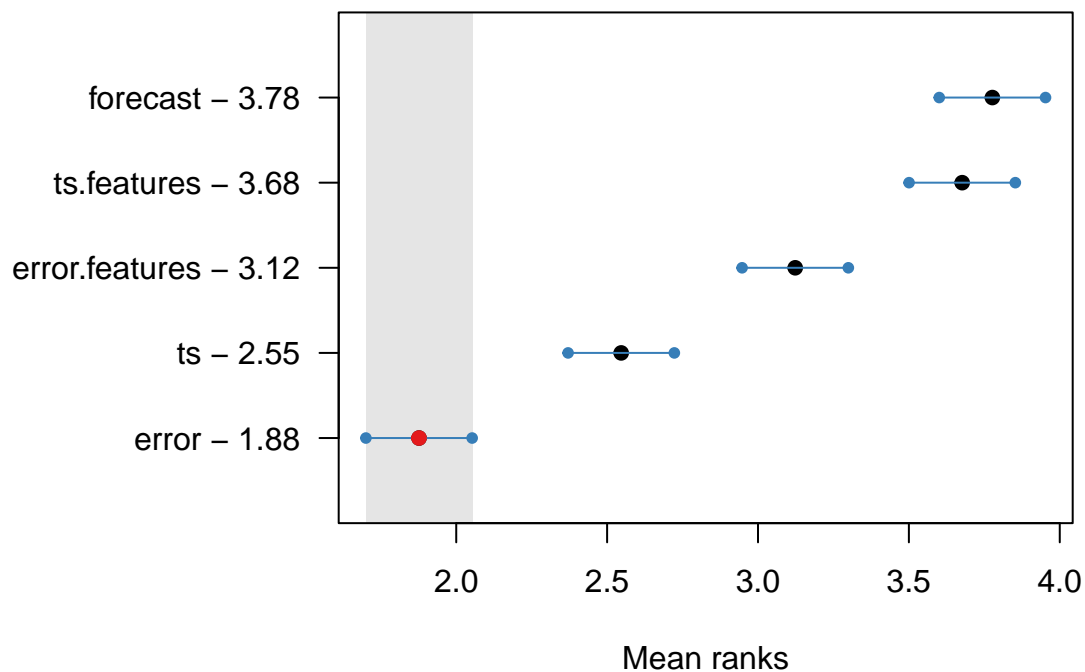
representator

```r
tmp %>% group_by(representator) %>% summarise_at(c("total", "bottom_mean", "bottom_max", "bottom_min"),
```

```
## # A tibble: 5 x 5
##   representator  total_mean bottom_mean_mean bottom_max_mean bottom_min_mean
##   <chr>               <dbl>            <dbl>           <dbl>           <dbl>
## 1 error               0.841             1.01            2.03           0.565
## 2 error.features      0.971             1.03            2.01           0.590
## 3 forecast            1.04              1.03            1.93           0.518
## 4 ts                  0.906             1.01            1.89           0.596
## 5 ts.features         1.01              1.02            1.94           0.592
```

```r
tmp %>% select(representator, cluster, batch, distance, total) %>%
  tidyr::pivot_wider(names_from = "representator", values_from = "total") %>%
  select(-distance, -cluster, -batch) %>%
  mcb()
```
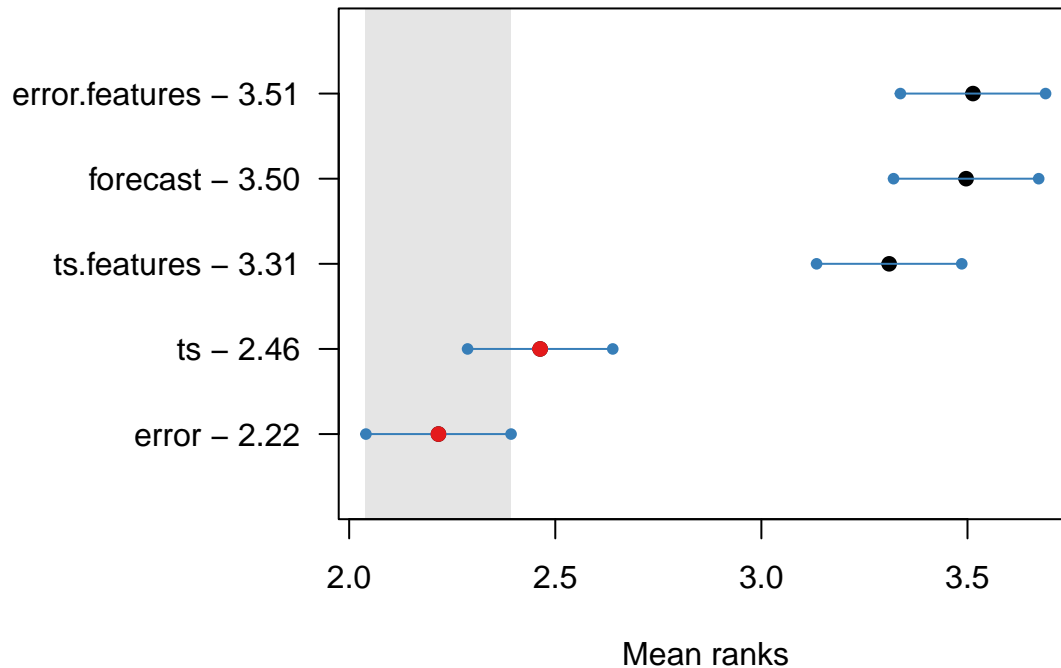
Friedman: 0.000 (Ha: Different)
Critical distance: 0.352


```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.3522
```

```r
# bottom
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "representator", values_from = "bottom_mean") %>%
  select(-distance, -cluster, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 0.352

Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.3522
```
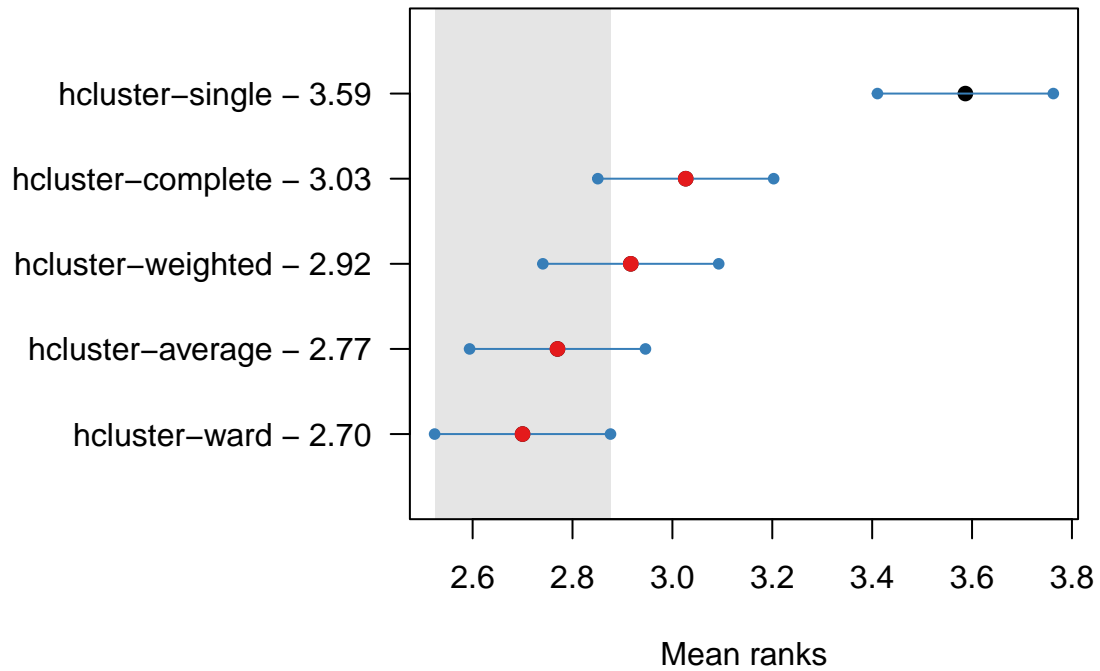
cluster

```r
tmp %>% group_by(cluster) %>% summarise_at(c("total", "bottom_mean", "bottom_max", "bottom_min"), c(mea
```

```
## # A tibble: 5 x 5
##   cluster           total_mean bottom_mean_mean bottom_max_mean bottom_min_mean
##   <chr>                  <dbl>            <dbl>           <dbl>           <dbl>
## 1 hcluster-average       0.940             1.02            1.94           0.572
## 2 hcluster-complete      0.951             1.02            1.96           0.571
## 3 hcluster-single        1.00              1.03            1.97           0.576
## 4 hcluster-ward          0.934             1.02            1.93           0.574
## 5 hcluster-weighted      0.947             1.02            2.00           0.569
```

```r
tmp %>% select(representator, cluster, batch, distance, total) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "total") %>%
  select(-representator, -distance, -batch) %>%
  mcb()
```
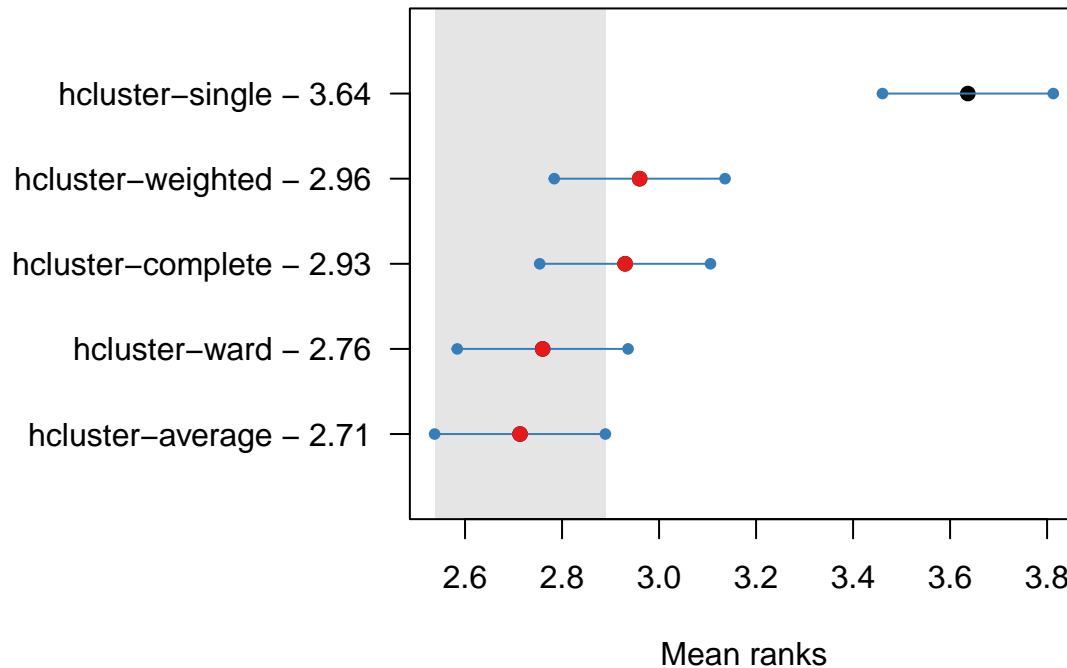
Friedman: 0.000 (Ha: Different)
Critical distance: 0.352

Friedman and Nemenyi Tests
The confidence level is 5%
Number of observations is 300 and number of methods is 5
Friedman test p-value: 0.0000 - Ha: Different
Critical distance: 0.3522

```
tmp %>% select(representator, cluster, batch, distance, bottom_mean) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "bottom_mean") %>%
  select(-representator, -distance, -batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 0.352

Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 300 and number of methods is 5
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 0.3522
```

natural hierarchy, random

```r
tmp <- ratio %>% filter((cluster == "natural") | (startsWith(cluster, "random-average") | (startsWith(c
  filter(rf_method == "mint", accuracy_method == "mae") %>%
  select(-representator, -distance) %>%
  select(batch, cluster,total, bottom_mean)
```

```r
tmp %>% group_by(cluster) %>% summarise_at(c("total", "bottom_mean"), c(mean=function(x){mean(x)})) %>%
  arrange(bottom_mean_mean)
```

```
## # A tibble: 27 x 3
##    cluster                  total_mean bottom_mean_mean
##    <chr>                         <dbl>            <dbl>
##  1 random-average-natural-100    0.850            0.983
##  2 random-average-natural-20     0.857            0.984
##  3 random-average-9-100          0.844            0.989
##  4 random-average-10-100         0.831            0.990
##  5 natural                       0.847            0.990
##  6 random-average-10-20          0.819            0.990
##  7 random-average-10-50          0.831            0.990
##  8 random-average-8-100          0.840            0.991
##  9 random-average-7-20           0.831            0.992
## 10 random-average-9-50           0.843            0.992
```

```
## # i 17 more rows
tmp %>% select(-total) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "bottom_mean") %>%
  select(-batch) %>%
  mcb()
```

Friedman: 0.000 (Ha: Different)
Critical distance: 11.978
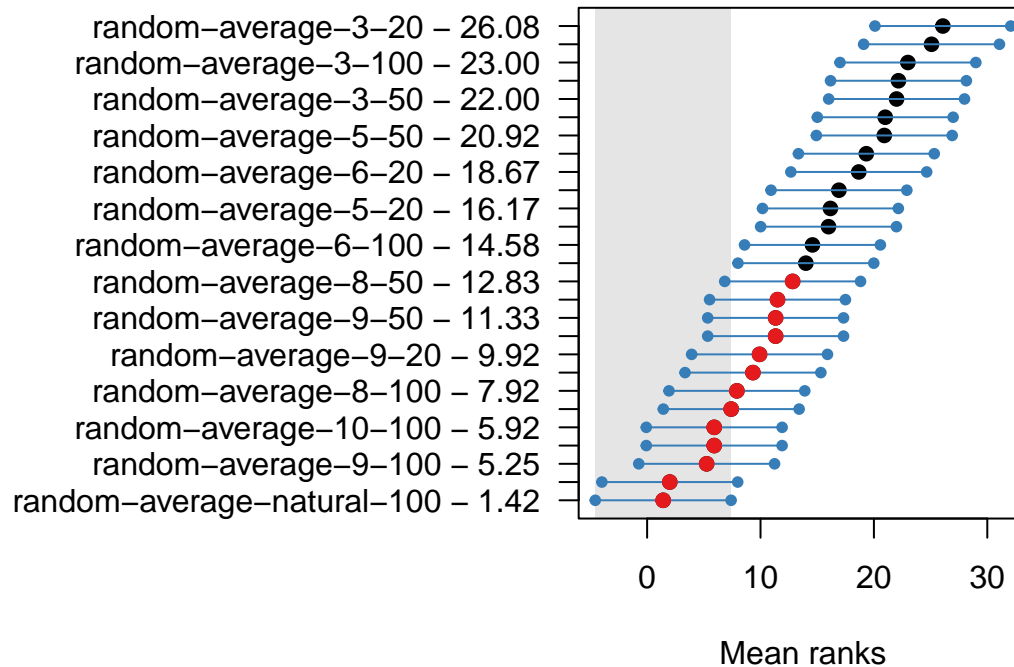
Mean ranks

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 12 and number of methods is 27
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 11.9777
```

```
tmp %>% select(-bottom_mean) %>%
  tidyr::pivot_wider(names_from = "cluster", values_from = "total") %>%
  select(-batch) %>%
  mcb()
```
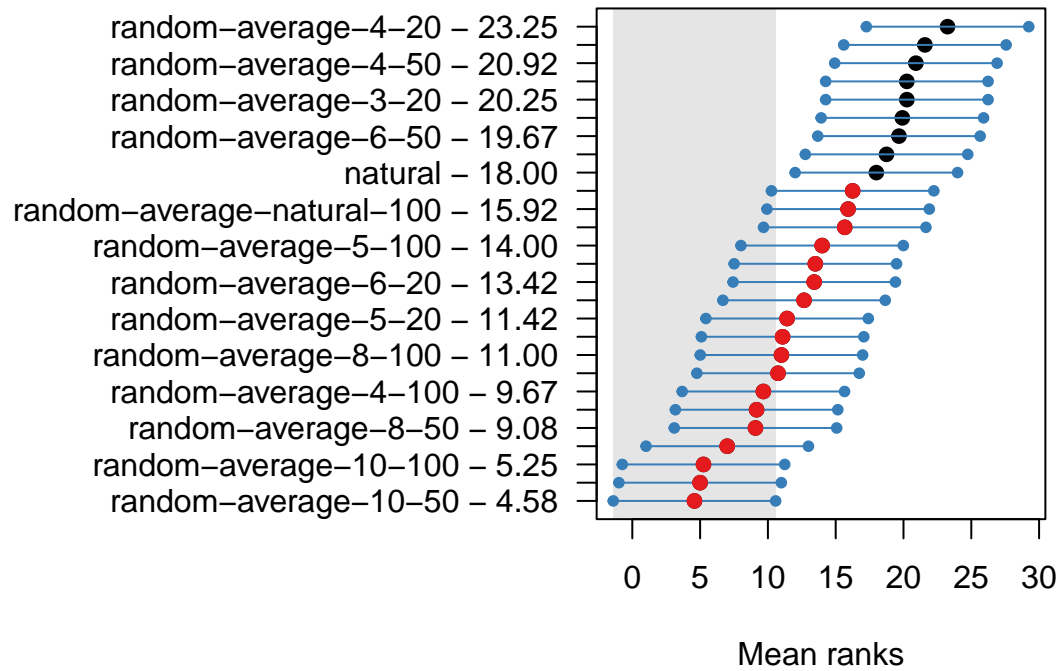
Friedman: 0.000 (Ha: Different)
Critical distance: 11.978

```
## Friedman and Nemenyi Tests
## The confidence level is 5%
## Number of observations is 12 and number of methods is 27
## Friedman test p-value: 0.0000 - Ha: Different
## Critical distance: 11.9777
```