# Compare permutation and scalar transformation approaches on simulated and real data

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## 1 Simulated data

#### 1.1 Data generation

Observations are generated from a Gamma(2,1) distribution for each combination of nx and nfacet from the following sets:  $nx = nfacet = \{2, 3, 5, 7, 14, 20, 31, 50\}$  to cover a wide range of levels from very low to moderately high. Each combination is being referred to as a panel. That is, data is being generated for each of the panels  $\{nx = 2, nfacet = 2\}, \{nx = 2, nfacet = 3\}, \{nx = 2, nfacet = 5\}, \dots, \{nx = 50, nfacet = 31\}, \{nx = 50, nfacet = 50\}$ . For each of the 64 panels, ntimes = 500 observations are drawn for each combination of the categories. That is, if we consider the panel  $\{nx = 2, nfacet = 2\}, 500$  observations are generated for each of the combination of categories from the panel, namely,  $\{(1,1), (1,2), (2,1), (2,2)\}$ . The values of  $\lambda$  is set to 0.67 and values of raw wpd  $wpd_{raw}$  is obtained.

## 1.2 Scalar transformation approach to normalisation

A log-linear model is fitted to see how the values of  $wpd_{raw}$  changes with the values of nx and nfacet. The model is of the form

$$y = a + b * log(x) + e$$

, where  $y = median(wpd_{raw})$  and x = nx \* nfacet.  $wpd_{norm}$  is a transformation on  $wpd_{raw}$  which should be designed to remove the effect of nx \* nfacet on  $wpd_{raw}$  and thus is defined as follows:  $wpd_{norm} = wpd_{raw} - b * log(nx * nfacet)$ 

## 1.3 Permutation approach to normalisation

The simulated data for each of the panels is permuted/shuffled nperm = 200 times and for each of those permutations  $wpd_{norm}$  is computed as follows:  $wpd_{norm} = (wpd_{raw} - mean(wpd_{raw}))/sd(wpd_{raw})$ . This is done so that the distribution of the normalised measure  $wpd_{norm}$  has the same mean and standard deviation across different nx and nfacet.

## 1.4 Comparing the two approaches

In Figure 1, we see that the distribution of  $wpd_{norm2} = wpd_{raw} - b * log(nx * nfacet)$  is similar when normalised with true or approximate estimate of b. Morever, the distributions are pretty similar across different nx and nfacet.

```
##
## Call:
## lm(formula = actual ~ poly(log(`nx * nfacet`), 1, raw = TRUE),
```

```
##
       data = G21_median)
##
##
  Residuals:
##
         Min
                      1Q
                            Median
                                            3Q
                                                     Max
##
   -2.946e-03 -2.240e-04 5.135e-05 4.147e-04
##
## Coefficients:
##
                                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                                           4.003e-02
                                                     4.171e-04
                                                                  95.97
                                                                          <2e-16
  poly(log(`nx * nfacet`), 1, raw = TRUE) 2.826e-03 8.796e-05
                                                                  32.13
                                                                          <2e-16
## (Intercept)
## poly(log(`nx * nfacet`), 1, raw = TRUE) ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0007881 on 32 degrees of freedom
## Multiple R-squared: 0.9699, Adjusted R-squared: 0.969
## F-statistic: 1032 on 1 and 32 DF, p-value: < 2.2e-16
```

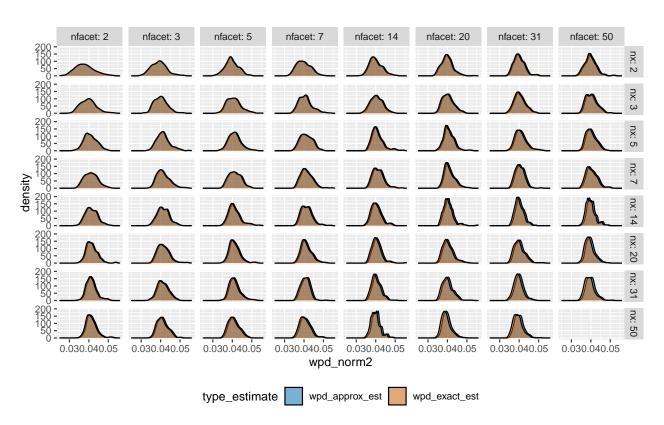


Figure 1: The distribution of  $wpd_{norm2}$  is plotted for approximate estimate of b. The distributions are similar when plotted against true and approximate estimate and b.

## 1.5 Ranking different designs

```
## # A tibble: 5,000 x 11
## type nx nfacet w nperm ntimes perm_id null vary_f vary_x right_order
```

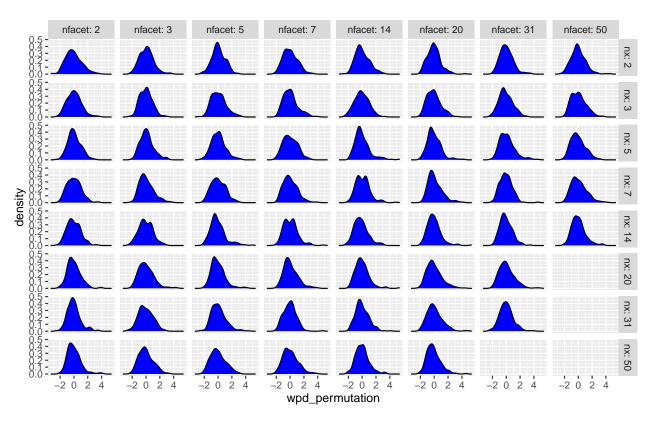


Figure 2: The distribution of  $wpd_{permutation}$  is plotted. The distributions are more similar across different nx and nfacet (specially for small nx and nfacet) but this approach has the downside of more computational time.

##		<chr>&gt;</chr>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<int></int>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<lg1></lg1>
##	1	raw	14	14	1	10	100	1	0.177	0.177	0.157	FALSE
##	2	raw	14	14	1	10	100	2	0.173	0.159	0.171	FALSE
##	3	raw	14	14	1	10	100	3	0.175	0.176	0.179	FALSE
##	4	raw	14	14	1	10	100	4	0.171	0.218	0.163	FALSE
##	5	raw	14	14	1	10	100	5	0.184	0.154	0.156	FALSE
##	6	raw	14	14	1	10	100	6	0.159	0.176	0.168	FALSE
##	7	raw	14	14	1	10	100	7	0.175	0.19	0.16	FALSE
##	8	raw	14	14	1	10	100	8	0.159	0.178	0.175	FALSE
##	9	raw	14	14	1	10	100	9	0.173	0.164	0.165	FALSE
##	10	raw	14	14	1	10	100	10	0.156	0.169	0.159	FALSE
##	#	wit	-h 4 990	) more	roug							

## # ... with 4,990 more rows