

Finalised versions of normalisation and threshold

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1 Idea

Even after excluding clashes, the list of harmonies left could be large and overwhelming for human consumption. Hence, there is a need to rank the harmonies basis how well they capture the variation in the measured variable and additionally reduce the number of harmonies for further exploration/visualization. Assuming a numeric response variable, our graphics are displays of distributions compared across combinations of categorical variables, one placed at x-axis and the other on the facet. Gestalt theory suggests that when items are placed in close proximity, people assume that they are in the same group because they are close to one another and apart from other groups. Hence, displays that capture more variation within different categories in the same group would be important to bring out different patterns of the data. Thus, the idea here is to rate a harmony pair higher if this variation between different levels of the x-axis variable is higher on an average across all levels of facet variables.

2 Computing distances

One of the potential ways to evaluate this variation is by computing the pairwise distances between the distributions of the measured variable. We do this through Jensen-Shannon distance which is based on Kullback-Leibler divergence. Probability distributions are represented through sample quantiles instead of kernel density estimate so that there is minimal dependency on selecting kernel or bandwidth. We call this measure of variation as Median Maximum Pairwise Distances (MMPD)

3 Normalize distances

The harmony pairs could be arranged from highest to lowest average maximum pairwise distances across different levels of the harmonies. But maximum is not robust to the number of levels and is higher for harmonies with higher levels. Thus these maximum pairwise distances need to be normalized for different harmonies in a way that eliminates the effect of different levels. The Fisher-Tippett-Gnedenko theorem in the field of Extreme Value Theory states that the maximum of a sample of iid random variables after proper re-normalization can converge in distribution to only one of Weibull, Gumbel or Fréchet distribution, independent of the underlying data or process. The normalizing constants, however, vary depending on the underlying distribution and hence it is important to assume a distribution of distances in our case.

Suppose d_1, d_2, \dots, d_m be a sequence of independent and identically-distributed pairwise distances and $M_m = \max\{d_1, \dots, d_m\}$. Then Fisher-Tippett-Gnedenko theorem (Haan and Ferreira 2007) suggests that if a sequence of pairs of real numbers (a_m, b_m) exists such that each $a_m > 0$ and $\lim_{m \rightarrow \infty} P\left(\frac{M_m - b_m}{a_m} \leq x\right) = F(x)$, where F is a non-degenerate distribution function, then the limit distribution F belongs to either the Gumbel, Fréchet or Weibull family. The normalizing constants (a_m, b_m) vary depending on the underlying distribution of the pairwise distances. Hence to normalize appropriately, it is important to assume a distribution of these distances.

3.1 Distribution of distances

Theoretical: JS distances are distributed as chi-squared with m df where we discretize the continuous distribution with m discrete values. Taking sample percentiles to approximate the integral would mean taking $m = 99$. With large m , chi-squared is asymptotically normal by the CLT. Thus, by CLT, $\chi^2_m \sim \mathcal{N}(m, 2m)$, which would depend on the number of discretization used to approximate the continuous distribution.

Then $b_n = 1 - 1/n$ quantile of the normal distribution and $a_n = 1/[n * \phi(b_n)]$ where ϕ is the normal density function. n is the number of pairwise comparisons being made.

Empirical: Distribution of JS distances is assumed to be normal but the mean and variance are estimated from the sample, rather than deducing it from the number of discretization used to approximate the continuous distribution.

```
#> # A tibble: 16 x 7
#>   facet_variable x_variable facet_levels x_levels MMPD max_pd r
#>   <chr>          <chr>          <int>    <int>  <dbl>  <dbl> <dbl>
#> 1 wknd_wday     day_month         2      31 3.27   0.0477 13
#> 2 wknd_wday     hour_day          2      24 1.94   0.0574 12
#> 3 wknd_wday     week_month        2       5 1.31   0.0126 16
#> 4 day_week      hour_day          7      24 0.849  0.0868  7
#> 5 day_week      day_month         7      31 0.652  0.251   3
#> 6 week_month    hour_day          5      24 0.560  0.113   5
#> 7 day_week      week_month        7       5 0.489  0.0625 11
#> 8 week_month    day_week          5       7 0.431  0.0637 10
```

```

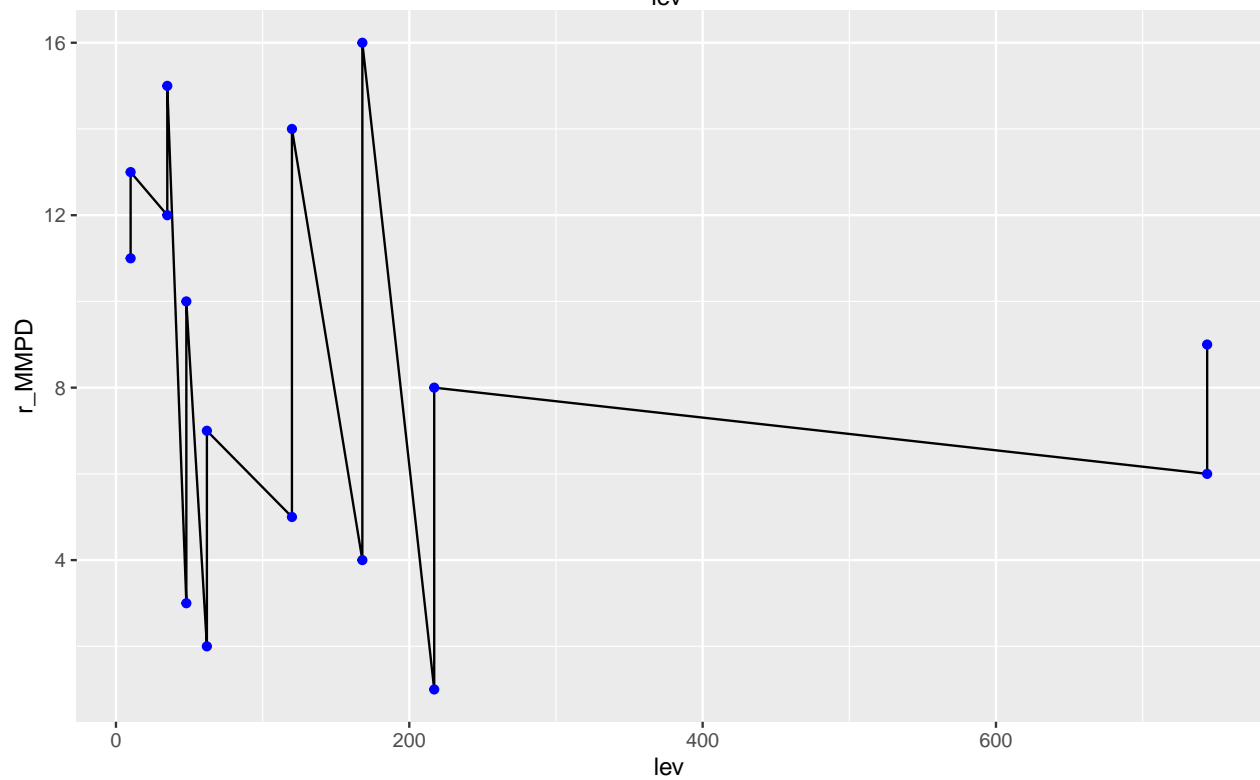
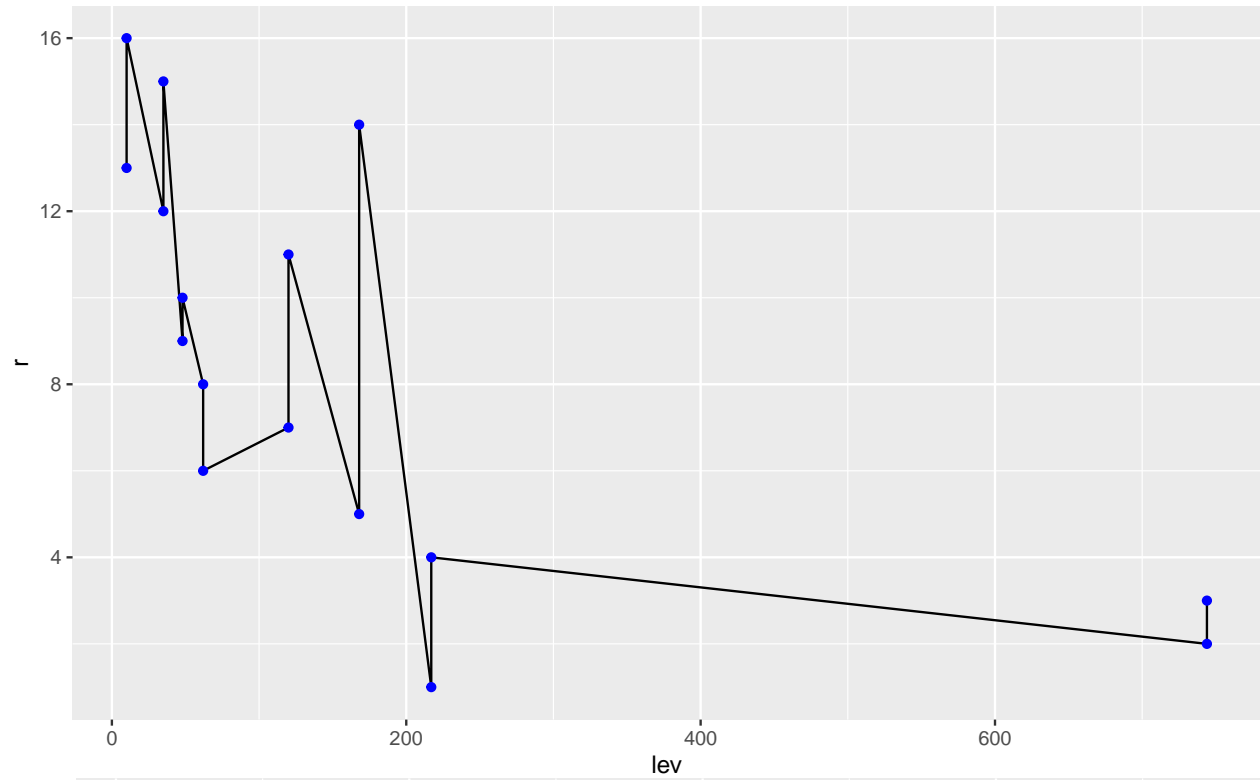
#> 9 hour_day      day_month      24      31 0.301 0.214      4
#> 10 hour_day     week_month     24      5 0.279 0.0890     6
#> 11 day_month    day_week       31      7 0.250 0.253      2
#> 12 day_month    hour_day       31     24 0.223 0.269      1
#> 13 hour_day     day_week       24      7 0.147 0.0766     8
#> 14 day_month    wknd_wday      31      2 0.0136 0.0683     9
#> 15 hour_day     wknd_wday      24      2 0.00879 0.0301    14
#> 16 week_month   wknd_wday      5      2 0.00684 0.0208    15

```

facet_variable	x_variable	facet_levels	x_levels	MMPD	max_pd	rankun	rankn
day_week	day_month	7	31	0.064	0.491	1	1
wknd_wday	day_month	2	31	0.060	0.048	8	2
wknd_wday	hour_day	2	24	0.044	0.041	9	3
day_week	hour_day	7	24	0.024	0.110	5	4
week_month	hour_day	5	24	0.023	0.050	7	5
hour_day	day_month	24	31	0.016	0.248	2	6
day_month	wknd_wday	31	2	0.014	0.069	6	7
day_month	day_week	31	7	0.011	0.115	4	8
day_month	hour_day	31	24	0.009	0.168	3	9
hour_day	wknd_wday	24	2	0.009	0.035	10	10
week_month	wknd_wday	5	2	0.007	0.021	13	11
day_week	week_month	7	5	0.004	0.022	12	12
wknd_wday	week_month	2	5	0.003	0.003	16	13
hour_day	week_month	24	5	0.003	0.026	11	14
week_month	day_week	5	7	0.001	0.003	15	15
hour_day	day_week	24	7	0.001	0.017	14	16

4 Does normalisation work?

4.1 Number of levels and ranking



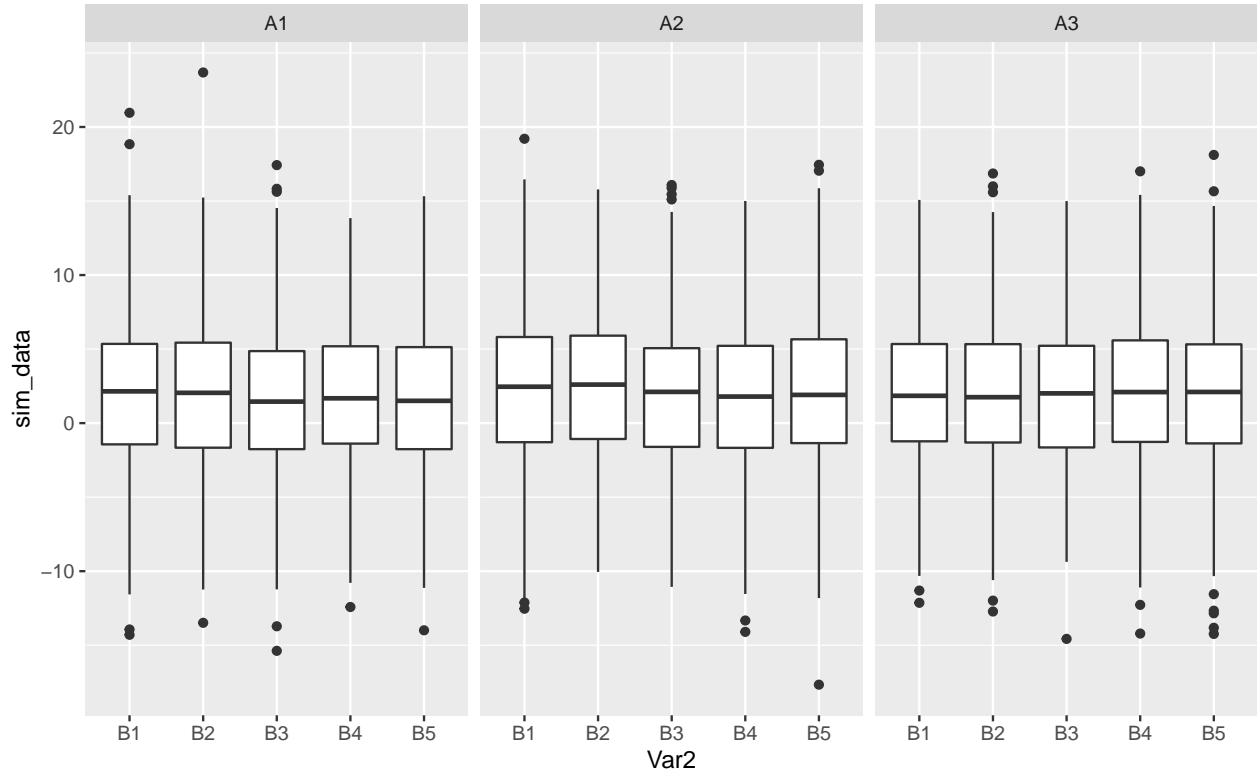
4.2 Comparing levels using simulated data

- MMPD should help choose the significantly different distributions only
- The ranking should be from most different to least different

Both of these should be checked again taking unnormalised statistic

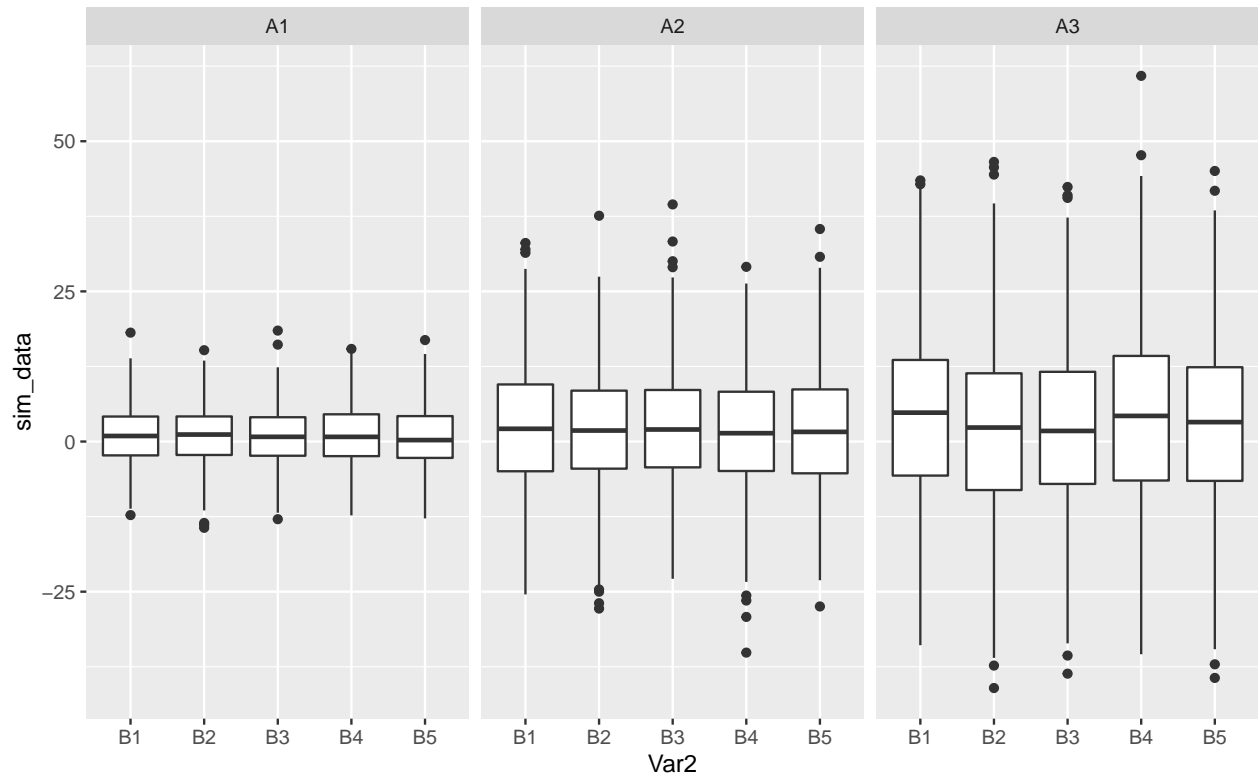
4.3 Scenario 1: Simulated same normal distributions for all combinations of the pair of cyclic granularities

facet_variable	x_variable	facet_levels	x_levels	MMPD	max_pd	r	gt_MMPD	gt_maxpd
A	B	3	5	0.43971	0.05075	1	FALSE	FALSE
C	B	7	5	0.43203	0.04804	3	FALSE	FALSE
D	E	24	31	0.22246	0.04729	4	FALSE	FALSE
D	C	24	7	0.16933	0.04948	2	FALSE	FALSE



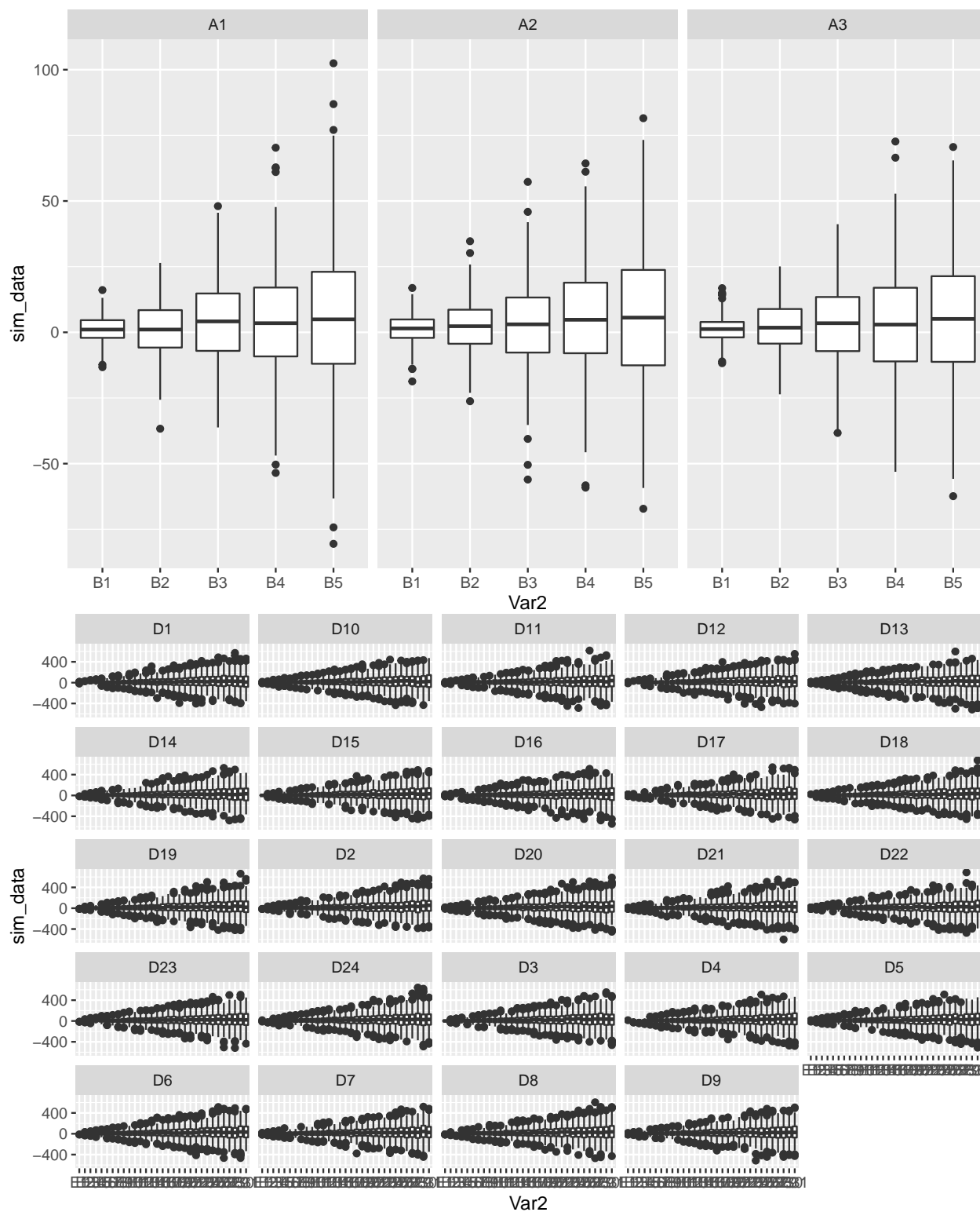
4.4 Scenario 2: Simulated same normal distributions for all x-levels within a facet, but different distributions across facets

facet_variable	x_variable	facet_levels	x_levels	MMPD	max_pd	r	gt_MMPD	gt_maxpd
A	B	3	5	0.49000	0.04612	2	TRUE	FALSE
C	B	7	5	0.33748	0.04531	3	FALSE	FALSE
D	E	24	31	0.25856	0.05473	1	FALSE	TRUE
D	C	24	7	0.15213	0.04260	4	FALSE	FALSE



4.5 Scenario 3: Simulated different normal distributions for different x-levels but they do not vary across facets

facet_variable	x_variable	facet_levels	x_levels	MMPD	max_pd	r	gt_MMPD	gt_maxpd
D	E	24	31	1.84640	0.12771	4	TRUE	FALSE
A	B	3	5	0.79410	0.13663	2	TRUE	FALSE
C	B	7	5	0.48567	0.12987	3	FALSE	FALSE
D	C	24	7	0.45191	0.15607	1	FALSE	FALSE



5 Scenario 4: Mixture of secenario 2 and 3

6 Choose thresholds for harmonies

Permutation test:

Assumption: random permutation without considering ordering (global)

1. Given the data; $\{v_t : t = 0, 1, 2, \dots, T - 1\}$, the MMPD is computed and is represented by $MMPD_{obs}$.
2. From the original sequence a random permutation is obtained: $\{v_t^* : t = 0, 1, 2, \dots, T - 1\}$.
3. MMPD is computed for all random permutation of the data and is represented by $MMPD_{sample}$.
4. Steps (2) and (3) are repeated a large number of times M (e.g. 1000).
5. For each permutation, one $MMPD_{sample}$ value is obtained.
6. 95th percentile of this $MMPD_{sample}$ distribution is computed and stored in $MMPD_{threshold}$.
7. If $MMPD_{obs} > MMPD_{threshold}$, harmony pairs are accepted. Onlyone threshold for all harmony pairs.

Pros: Considering thresholds global for all harmony pairs would imply less computation time.

Cons: Only one threshold for all harmony pairs might not be an appropriate measure but a good benchmark.

Haan, Laurens de, and Ana Ferreira. 2007. *Extreme Value Theory: An Introduction*. Springer Science & Business Media.