# Nested sequences and the permutation test

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Do high and low achievers regulate their group work differently, or do their teams? In `group_regulation_long`, a synthetic dataset generated from the `group_regulation` data of the tna package (Tikka, López-Pernas & Saqr 2025), 2,000 students work in 200 teams of 10, and the achievement level is given to the team, not to the student. A comparison of High and Low is therefore a comparison of teams. The students are nested in teams. The permutation test treats each student's sequence as an independent unit, so a nesting effect, teammates behaving alike, would enter the comparison. The arguments for nested data in Nestimate (Saqr, López-Pernas & Misiejuk 2026) are `actor` in `permutation()`, `sequence_compare()` and `bootstrap_network()`, and `nested` with `actor` in `mosaic_plot()`, `mosaic_analysis()` and `mosaic_test()`. Their defaults treat every sequence as an independent unit.

```
achievers <- build_network(group_regulation_long, method = "relative",
                           actor = "Actor", action = "Action",
                           time = "Time", group = "Achiever")
achievers
```

```
## Group Networks (2 groups, group_col: Achiever)
##
##   Group  Nodes  Edges  Weights
##   High   9      76     [0.001, 0.576]
##   Low    9      75     [0.000, 0.462]
```

`build_network()` builds one transition network per achievement level from the students' action sequences. Both networks have the same nine regulation actions and 75 to 76 non-zero transitions.

## The ordinary test

```
permutation(achievers, iter = 1000, seed = 1)
```

```
## Grouped Permutation Test
## Groups: High vs Low
##
## -- High vs Low --
## Permutation Test: Transition Network (relative probabilities) [directed]
##   Iterations: 1000  |  Alpha: 0.05
##   Nodes: 9  |  Edges tested: 78  |  Significant: 42
##  Global test (networks differ overall?): M = 2.612 (p = 0.000999)  |  S = 0.210 (p = 0.000999)
```

`permutation()` pools the 2,000 sequences, reassigns them to High and Low 1,000 times, and compares the observed differences with the reassigned ones, as in the permutation test of transition network analysis (Saqr et al. 2025). Two kinds of result are reported. The edge tests ask, for each transition, whether the High minus Low difference is larger than the reassignments produce: 42 of 78 transitions are. The global test asks whether the two networks differ at all, with two statistics: M, the sum of all absolute edge differences, and S, the largest one. (These letters follow `permutation()`'s convention; in the Network Comparison Test and in `nct()`, M is the largest edge difference and S the difference in global strength.) Both have $p = 0.000999$, the smallest value 1,000 reassignments can give: no reassignment produced a difference as large as the observed one.

The test assumes that any student could have been in either group. In this design only whole teams could, so the next step accounts for the nesting.

## Reassigning whole teams

```
permutation(achievers, iter = 1000, seed = 1, actor = "Group")
```

```
## Grouped Permutation Test
## Groups: High vs Low
##
## -- High vs Low --
## Permutation Test: Transition Network (relative probabilities) [directed]
##   Iterations: 1000  |  Alpha: 0.05  |  Actor: Group (200 actors)
##   Nodes: 9  |  Edges tested: 78  |  Significant: 42
##  Global test (networks differ overall?): M = 2.612 (p = 0.000999)  |  S = 0.210 (p = 0.000999)
##   Nesting in Group: ICC = -0.002 [95% CI -0.006, 0.002]  |  between design
##   Design effect (1 = nesting does not matter): edges 1.03  |  global 1.20
```

`actor = "Group"` tells the test that the sequences are nested in teams. Each reassignment now moves all ten students of a team together, which is how the achievement levels were actually given. The observed differences are the same; only the reference distribution changes.

The edge tests and the global test give the same result as with student-level reassignment: 42 significant transitions, p = 0.000999 for M and S. The output also reports the intraclass correlation, ICC = −0.002 (95% CI −0.006 to 0.002), and the design effect, 1.03 for the transitions and 1.20 for M. Both are defined and interpreted in the next section.

A low ICC means that sequences from the same team are about as different from each other as sequences from different teams: the observations are close to independent, and an analysis that ignores the nesting gives nearly the same results as one that accounts for it. Accounting for nesting becomes necessary when the ICC is not negligible, and more so when units are large, because the design effect grows with both: Kish's (1965) approximation is $1 + (m - 1) \times \text{ICC}$ for units of size m. A commonly cited rule of thumb (Muthén & Satorra 1995) is that design effects below 2 do not lead to seriously misleading inferences. Here the ICC is −0.002 and the design effect 1.03, so accounting for the nesting was not necessary, and the results with and without it were almost the same.

## The nesting diagnostics

The intraclass correlation (ICC) is the proportion of the total variance that lies between units rather than within them:

$$\text{ICC} = \frac{\sigma^2_{\text{between}}}{\sigma^2_{\text{between}} + \sigma^2_{\text{within}}}.$$

An ICC of 0 means that members of the same unit are no more alike than members of different units; an ICC of 1 means that all members of a unit are identical and all variation lies between units. A value in between is the proportion of variation due to the unit. In `permutation()` the ICC is computed for each transition: for every student, the share of their transitions that is, for example, `plan` to `monitor`; the one-way ANOVA ICC of that share across teams is computed within High and within Low. The transition ICCs are averaged with weights equal to transition frequency. The 95% interval comes from the jackknife, leaving out one team at a time.

The design effect is the ratio of the variance of an estimate under the nested design to its variance had the units been sampled independently. Here it is the variance of the reassigned differences when whole teams move, divided by the variance when single students move. A value of 1 means both reassignments give the same chance variation.

`permutation_diagnostics()` runs the ordinary and the team-level test on the same data and reports both with these two quantities, one row per compared pair:

```
permutation_diagnostics(achievers, actor = "Group", iter = 1000, seed = 1)
```

```
##          pair n_sequences n_actors  design          icc icc_ci_lower
## 1 High vs Low        2000      200 between -0.001697397 -0.005641197
##   icc_ci_upper deff_edges deff_global p_global_sequence p_global_actor
## 1  0.002246402   1.026921    1.200797       0.000999001    0.000999001
##   sig_edges_sequence sig_edges_actor edges_changed min_p_actor
## 1                 42              42             2 0.000999001
```

The comparison involves 2,000 sequences in 200 teams. The design is `between`: every team belongs to one achievement level (`within` would mean units in both groups, as in repeated measures; `mixed`, some of each). The ICC is −0.002 with a 95% interval from −0.006 to 0.002, which indicates little evidence of a nesting effect; a value slightly below zero is sampling variation around zero. The design effect is 1.03 for the transitions (median over edges) and 1.20 for the global statistic M. The global test has p = 0.000999 under both reassignments, and 42 transitions are significant under both. Two transitions change their conclusion. The smallest p-value the team-level test can produce, `min_p_actor`, is 0.000999: with 200 teams the number of iterations sets the limit, not the number of teams.

With `level = "edges"` the same comparison is reported per transition:

```
head(permutation_diagnostics(achievers, actor = "Group", iter = 1000,
                             level = "edges", seed = 1), 6)
```

```
##          pair  from         to         diff          icc null_sd_sequence
## 1 High vs Low adapt   cohesion -0.014762566  0.010118088       0.03863244
## 2 High vs Low adapt  consensus  0.055773975 -0.003796296       0.04560409
## 3 High vs Low adapt coregulate -0.029891304  0.002498496       0.01294589
## 4 High vs Low adapt    discuss -0.032473790 -0.009052931       0.02104505
## 5 High vs Low adapt    emotion  0.030430928 -0.007376103       0.02877059
## 6 High vs Low adapt    monitor -0.006957293 -0.003562251       0.01591287
##   null_sd_actor      deff p_sequence    p_actor changed
## 1    0.04129895 1.1428088 0.68831169 0.72927073   FALSE
## 2    0.04255012 0.8705504 0.21378621 0.18981019   FALSE
## 3    0.01383698 1.1424014 0.01498501 0.02397602   FALSE
## 4    0.01902641 0.8173606 0.11588412 0.09190809   FALSE
## 5    0.02727781 0.8989211 0.32267732 0.26373626   FALSE
## 6    0.01553230 0.9527393 0.66633367 0.66733267   FALSE
```

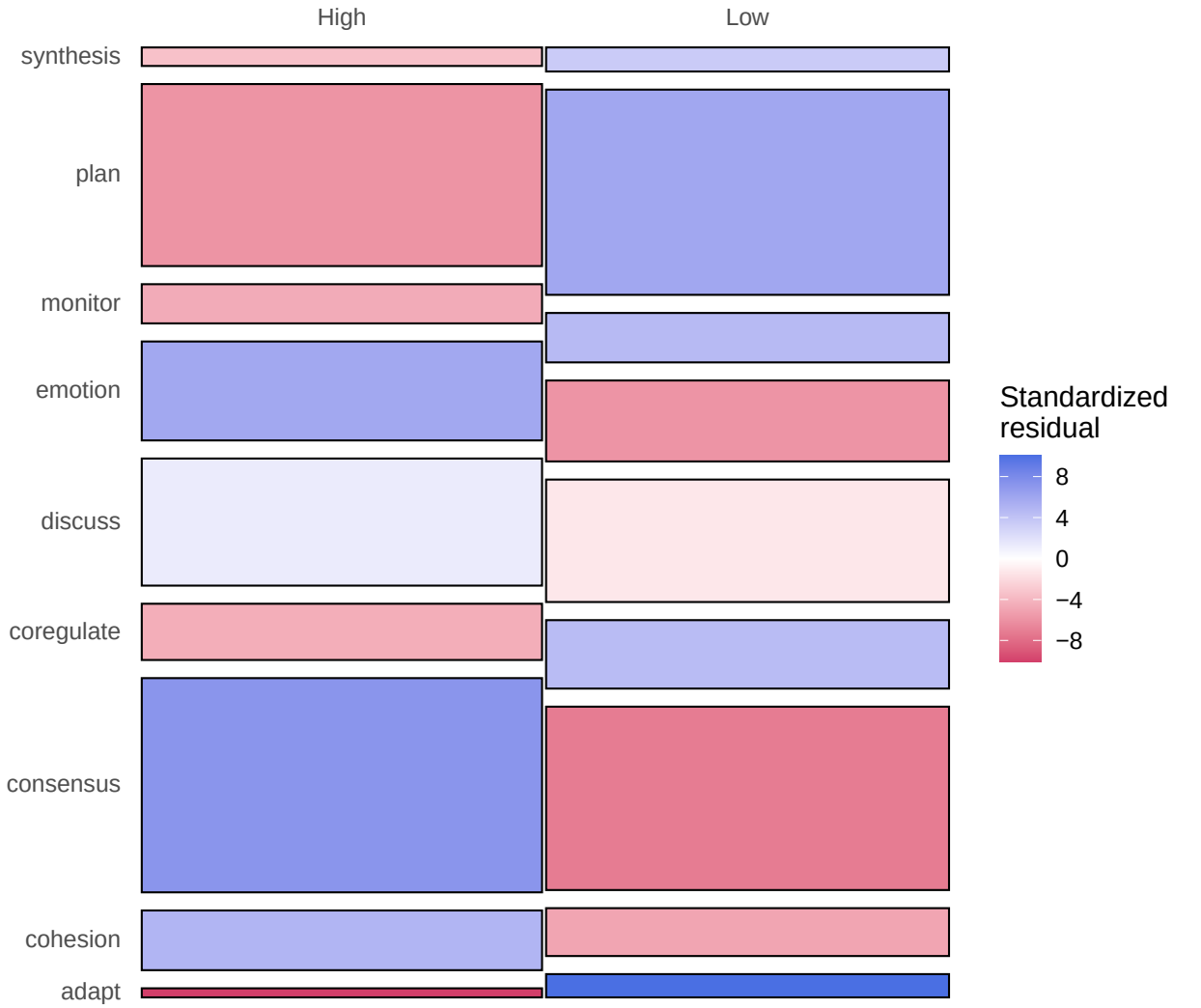
`diff` is the High minus Low transition probability and is the same under both tests. `icc` is the ICC of that transition. `null_sd_sequence` and `null_sd_actor` are the spread of the reassigned differences under student-level and team-level reassignment, and `deff` is the squared ratio of the two. `p_sequence` and `p_actor` are the two edge p-values, and `changed` marks a transition that is significant at 0.05 under one test but not the other. In the six rows shown, the ICCs lie between −0.009 and 0.010 and the design effects between 0.82 and 1.14; the two spreads are close, so the two p-values are close. `adapt` to `coregulate` has p = 0.015 and p = 0.024 and is significant under both.

Over all 78 transitions, two change at this seed (`coregulate` to `adapt`, `emotion` to `plan`), with p-values between 0.047 and 0.072 under both tests. With seeds 2 to 4 a different set of two or three transitions changes, all with p-values between 0.038 and 0.068. These changes come from the finite number of reassignments, not from the nesting. The ICC indicates little evidence of a nesting effect, and the High–Low difference does not depend on the nesting of students in teams.

## Mosaic plots of nested counts

`mosaic_plot()` computes the residuals of a group-by-action table. With `nested = TRUE` the counts are taken team by team (`actor = "Group"`), and the residuals allow for the dependence of actions within a team. `nested_method` selects the method: `"rao_scott"` (default), the chi-square corrected for the design effect of the cluster sample (Rao & Scott, 1984); `"donner_klar"`, the chi-square adjusted by the intracluster correlation (Donner & Klar, 1994); `"cmh"`, the Cochran-Mantel-Haenszel test stratified by team (Landis, Heyman, & Koch, 1978); `"gee"`, a generalized estimating equation with a cluster-robust covariance (Liang & Zeger, 1986); and `"glmm"`, a generalized linear mixed model with a random effect per team (Breslow & Clayton, 1993). `report = TRUE` prints the overall test and adds it to the plot as a subtitle.

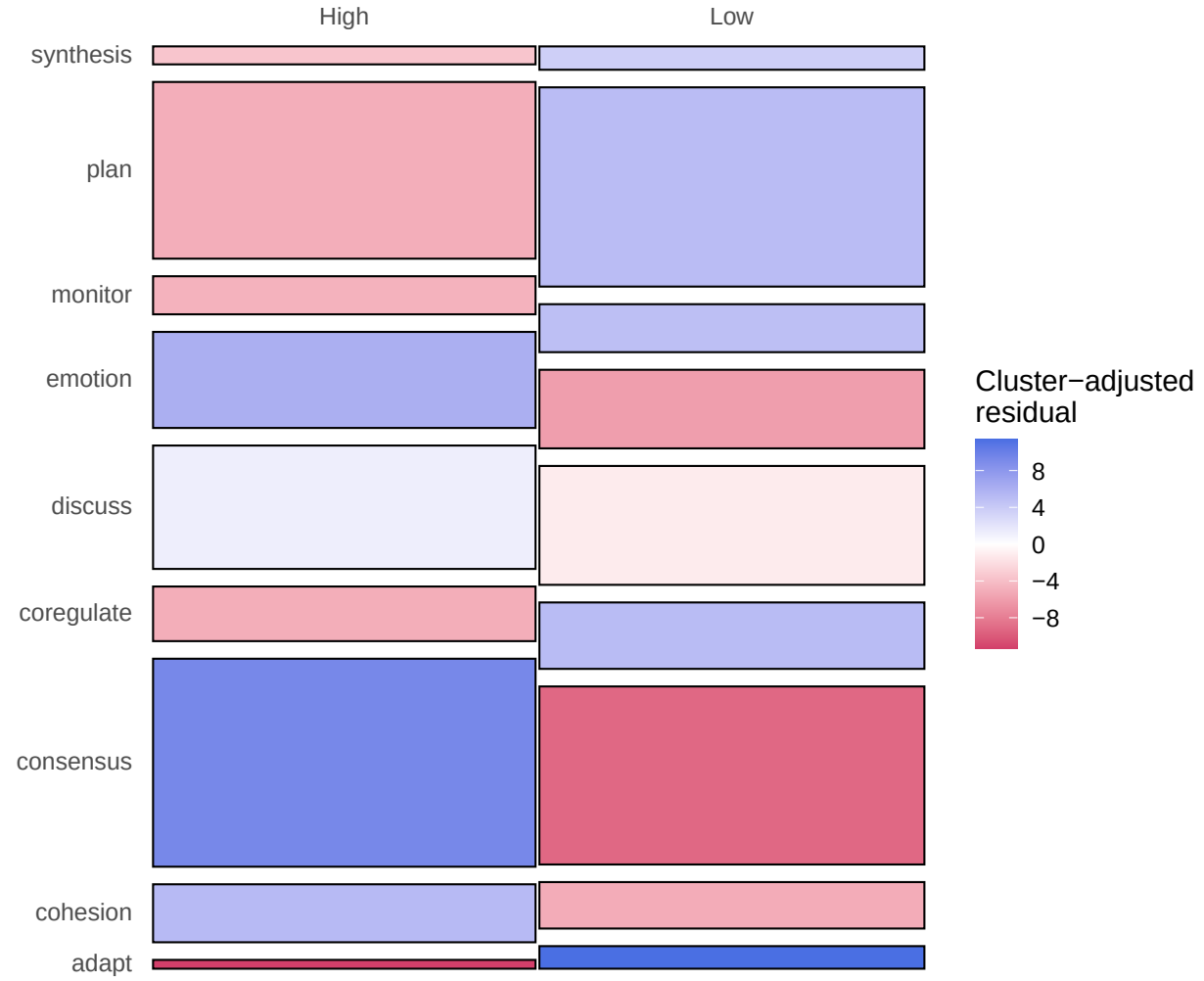
```
mosaic_plot(achievers, seed = 1, left_angle = 0)
```




```
mosaic_plot(achievers, nested = TRUE, actor = "Group", report = TRUE,
            left_angle = 0)
```

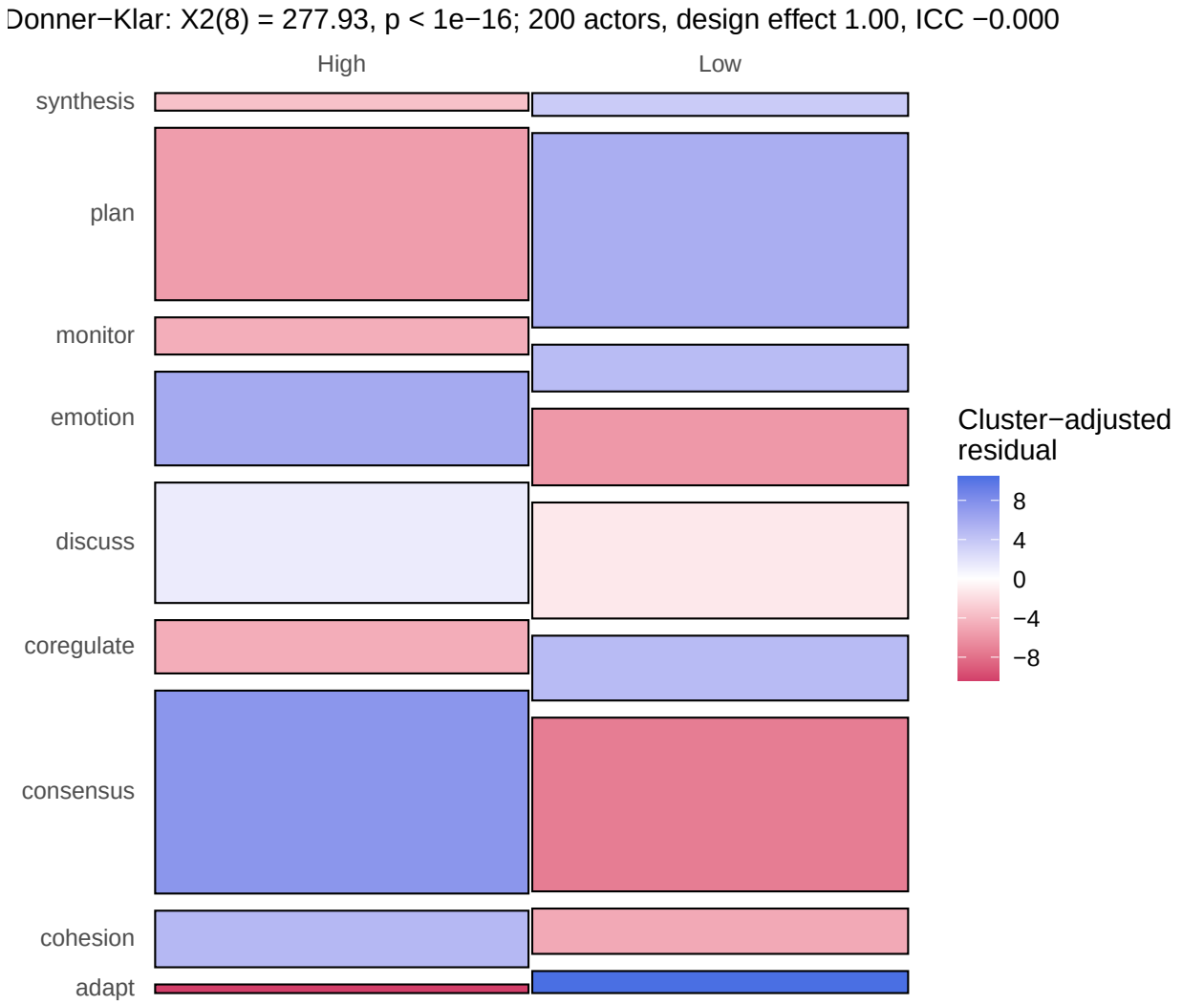
```
##     method      test statistic       df      df2      p_value     n
##  rao_scott Rao-Scott  37.21183 6.955041 1384.053 1.065954e-47 27533
```

```
##  clusters design_effect icc
##       200     0.9335922  NA
```




```
mosaic_plot(achievers, nested = TRUE, nested_method = "donner_klar",
            actor = "Group", report = TRUE, left_angle = 0)
```

```
##       method        test statistic df df2      p_value     n clusters
##  donner_klar Donner-Klar  277.9254  8  NA 2.038053e-55 27533      200
##  design_effect           icc
##              1 -0.0002752021
```




The subtitle and the printed row give the test statistic, its degrees of freedom, the p-value, the number of teams, and the design effect or the intracluster correlation where the method estimates one.

The three plots show the same pattern. Low achievers use `adapt` more often than expected under independence (residual 11.3 with the Rao-Scott method) and High achievers `consensus` (9.2) and `cohesion` (5.2). The Rao-Scott design effect is 0.93 and the Donner-Klar intracluster correlation −0.0003, so counting team by team leaves the residuals and the test close to those of the pooled counts.

## Tests of association for nested counts

```
mosaic_test(achievers, actor = "Group")
```

```
##        method                   test statistic       df      df2
## 1       chisq                Pearson 277.92541 8.000000       NA
## 2   rao_scott              Rao-Scott  37.21183 6.955041 1384.053
## 3 donner_klar            Donner-Klar 277.92541 8.000000       NA
## 4         cmh Cochran-Mantel-Haenszel        NA       NA       NA
## 5         gee                GEE Wald 358.60471 8.000000       NA
```

```
## 6        glmm               GLMM Wald 269.91201 8.000000       NA
##        p_value     n clusters design_effect           icc
## 1 2.038053e-55 27533       NA            NA            NA
## 2 1.065954e-47 27533      200     0.9335922            NA
## 3 2.038053e-55 27533      200     1.0000000 -0.0002752021
## 4           NA 27533       NA            NA            NA
## 5 1.317864e-72 27533      200            NA            NA
## 6 1.026755e-53 27533      200            NA            NA
##                                                                                 note
## 1                                                                               <NA>
## 2                                                                               <NA>
## 3                                                                               <NA>
##  4                                                                 Cochran-Mantel-
Haenszel stratifies by cluster, so both variables must vary within clusters
## 5 Wald test with a cluster-robust covariance; liberal unless the actors are many relative to the degrees of f
## 6                                                                               <NA>
```

`mosaic_test()` returns one row per test: Pearson's chi-square on the pooled counts and the five tests for nested counts. A test that the design does not admit returns `NA` with the reason in `note`. The Cochran-Mantel-Haenszel test stratifies by team, and the achievement level is constant within each team, so it cannot be computed here and returns `NA`. `method` selects tests, and `level = "cells"` returns the residual of every cell.

Every test that can be computed rejects independence: Pearson's chi-square is 277.9 (8 df, $p < 10^{-54}$), the Rao-Scott F is 37.2 (6.96 and 1,384 df, $p < 10^{-46}$), the GEE Wald statistic 358.6 and the GLMM Wald statistic 269.9 (8 df each). The note to the GEE test states that its cluster-robust covariance is liberal unless the teams are many relative to the degrees of freedom; here there are 200 teams for 8 degrees of freedom.

```
head(mosaic_test(achievers, method = "rao_scott", actor = "Group",
                 level = "cells"))
```

```
##      method group     state observed   residual
## 1 rao_scott  High     adapt      155 -11.349878
## 2 rao_scott   Low     adapt      399  11.349878
## 3 rao_scott  High  cohesion     1018   5.193551
## 4 rao_scott   Low  cohesion      821  -5.193551
## 5 rao_scott  High consensus     3651   9.233770
## 6 rao_scott   Low consensus     3146  -9.233770
```

## Sequence patterns

```
set.seed(1)
sequence_compare(achievers, sub = 2:3, iter = 1000, actor = "Group")
```

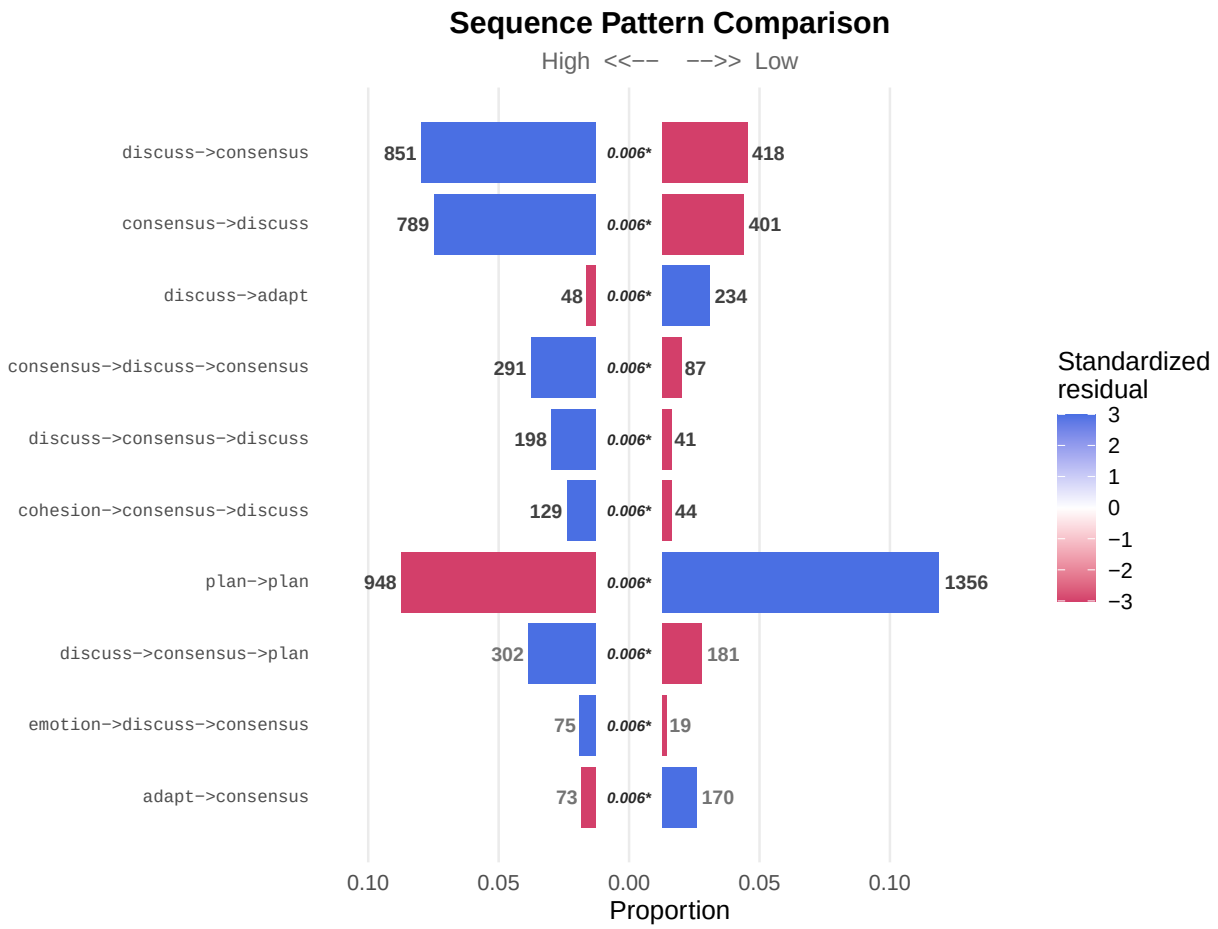
```
## Sequence Comparison  [322 patterns | 2 groups: High, Low]
##  Lengths: 2, 3  |  min_freq: 5  |  permutation: 1000 iter (fdr), actor: Group (200 actors, between)
##
##  pattern                      group count prop resid  effect p
##  discuss->consensus           High   851  0.07  12.60 14.71  0.00564
##  discuss->consensus           Low    418  0.03 -12.60 14.71  0.00564
##  consensus->discuss           High   789  0.06  11.65 14.27  0.00564
```

```
##  consensus->discuss            Low    401  0.03 -11.65 14.27  0.00564
##  discuss->adapt                High    48  0.00 -11.08 12.94  0.00564
##  discuss->adapt                Low    234  0.02  11.08 12.94  0.00564
##  consensus->discuss->consensus High   291  0.02  10.65 12.61  0.00564
##  consensus->discuss->consensus Low     87  0.01 -10.65 12.61  0.00564
##  discuss->consensus->discuss   High   198  0.02  10.27 12.08  0.00564
##  discuss->consensus->discuss   Low     41  0.00 -10.27 12.08  0.00564
##  cohesion->consensus->discuss  High   129  0.01   6.54  9.27  0.00564
##  cohesion->consensus->discuss  Low     44  0.00  -6.54  9.27  0.00564
##  plan->plan                    High   948  0.07  -8.73  9.01  0.00564
##  plan->plan                    Low   1356  0.11   8.73  9.01  0.00564
##  discuss->consensus->plan      High   302  0.03   5.65  8.35  0.00564
##  discuss->consensus->plan      Low    181  0.02  -5.65  8.35  0.00564
##  emotion->discuss->consensus   High    75  0.01   5.83  8.30  0.00564
##  emotion->discuss->consensus   Low     19  0.00  -5.83  8.30  0.00564
##  adapt->consensus              High    73  0.01  -6.20  8.26  0.00564
##  adapt->consensus              Low    170  0.01   6.20  8.26  0.00564
##   ... and 312 more patterns (624 rows); summary() returns them all
```

With `actor = "Group"`, the permutation test of each pattern reassigns whole teams. The header reports the actor column, the number of actors and the design: `between` when each team belongs to one group, `within` when every team has sequences in both groups, `mixed` otherwise.

99 of the 322 patterns of two and three actions differ between High and Low at an FDR-adjusted p below 0.05. `discuss -> consensus` makes up 6.7% of the patterns of High achievers and 3.3% of those of Low achievers, and `discuss -> adapt` 0.4% against 1.8%. With 1,000 reassignments and the FDR adjustment over 322 patterns, the smallest adjusted p-value is 0.0056.

```r
set.seed(1)
plot(sequence_compare(achievers, sub = 2:3, iter = 1000, actor = "Group"))
```




The plot shows the ten patterns with the largest differences. Each bar is the pattern's proportion in one group, labelled with its count, and its colour is the standardized residual: blue where the group uses the pattern more often than expected, red where less. `discuss -> consensus` and `consensus -> discuss` are blue for High achievers; `plan -> plan` and `discuss -> adapt` are blue for Low achievers.

## Bootstrap

```
pooled <- build_network(group_regulation_long, method = "relative",
                        actor = "Actor", action = "Action", time = "Time")
bootstrap_network(pooled, iter = 1000, seed = 1, actor = "Group")
```

```
##   Edge                    Mean     95% CI          p
##   ------------------------------------------------
##   cohesion → consensus    0.498  [0.474, 0.522]  ***
##   adapt → consensus       0.477  [0.437, 0.520]  ***
##   synthesis → consensus   0.466  [0.423, 0.506]  ***
##   consensus → plan        0.396  [0.384, 0.408]  ***
##   monitor → discuss       0.376  [0.353, 0.400]  ***
##   ... and 46 more significant edges
##
## Bootstrap Network  [Transition Network (relative) | directed]
##   Iterations : 1000  |  Nodes : 9
```

```
##   Edges      : 51 significant / 78 total
##   CI         : 95%  |  Inference: stability  |  CR [0.75, 1.25]
##   Actor      : Group (200 actors)
##   Nesting    : ICC = 0.006 [95% CI 0.002, 0.011]  |  Design effect (edges) = 1.03
```

With `actor = "Group"`, `bootstrap_network()` resamples whole teams, and a resampled team contributes all of its sequences. The output adds the intracluster correlation and the design effect of the edges. 51 of the 78 edges keep their size, the ICC is 0.006 (95% CI 0.002 to 0.011) and the design effect 1.03. The ICC is larger than in the permutation test because it is computed on the pooled network, where the difference between High and Low teams is part of the variance between teams.

## Reporting

> Because the data were nested (students in teams; with repeated measurements, sessions in students), the two groups were compared with a permutation test that accounted for the nesting: in each of 1,000 permutations, whole teams rather than single sequences were reassigned between the groups, so that sequences from the same team stayed together. Units that belonged to one group were reassigned as a whole, and units that contributed to both groups, as in a repeated-measures design, had their sequences reassigned within the unit. The nesting effect was quantified with the intraclass correlation (ICC) and the design effect, the ratio of the variance under the nested design to the variance under independent sampling (ICC = −0.002, 95% CI −0.006 to 0.002; design effect 1.03 across 200 teams). The networks of high and low achievers differed overall (M = 2.61, p < .001), and 42 of 78 transitions differed at p < .05.

## Arguments for nested data

| Function | Argument | Effect |
|---|---|---|
| `permutation()` | `actor` | Reassigns whole actors when each actor belongs to one group; reassigns sequences within each actor that has sequences in both groups |
| `permutation_diagnostics()` | `actor` | Reports the test with and without the actor-level reassignment, with the ICC and the design effect |
| `sequence_compare()` | `actor` | The reassignment scheme of `permutation()`, applied to the test of each pattern |
| `bootstrap_network()` | `actor` | Resamples whole actors |
| `mosaic_plot()`, `mosaic_analysis()` | `nested`, `nested_method`, `actor`, `report` | Residuals and overall test from the counts of each actor |
| `mosaic_test()` | `method`, `actor`, `level` | Pearson's test and the five nested tests in one table |

The design effect is the ratio of the variance of an estimate under the nested design to its variance under independent sampling. Kish's approximation is $1 + (m - 1) \times \text{ICC}$ for m observations per actor. `actor` applies to transition networks (`relative`, `frequency`, `co_occurrence`).

## How to cite this article

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