Higher-Order Network Analysis with Simplicial Complexes

From Transition Networks to Topological Analysis

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25 November 2026

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Introduction

A transition network is a first-order Markov model: the probability of the next state depends only on the current state (Saqr et al., 2025; Saqr, López-Pernas, & Tikka, 2025). When the states before the current one also change what comes next, the process has higher-order dependencies, and a first-order network averages over them. For example, a programmer who specifies a task after a frustrated message may continue differently from one who specifies it after a request, while a first-order model treats both as the same transition out of *Specify*.

This tutorial tests whether a process has higher-order dependencies, finds the paths where they occur, and describes the shape of the network with simplicial complexes, which represent groups of states rather than pairs (Battiston et al., 2020). Nestimate (Saqr, López-Pernas, & Misiejuk, 2026) estimates the models and cograph draws them.

The data come from vibe coding, programming by conversation with an AI assistant (Sarkar & Drosos, 2025). Sarkar and Drosos describe it as a cycle: the programmer prompts, evaluates the result quickly and edits by hand, and prompts again, with prompts that mix vague directives and detailed specifications. In students' conversations with AI assistants, direct instructions and specifications of the output dominate, and context or iterative refinement is rare (López-Pernas et al., 2025). A transition network analysis of student-AI problem solving found an instructive pattern, in which students give orders and the AI follows them rather than negotiating, and long threads in which the prompts and the output of the AI do not match (Saqr, Misiejuk, & López-Pernas, 2026). Misiejuk et al. (2026) profiled the processes of student-AI programming and their higher-order structure. A cycle of prompting, checking and correcting is a pattern of several steps, and whether it is more than a chain of single transitions is the question the methods below answer.

Question	Function
Is a first-order model enough?	`build_mogen()`, `markov_order_test()`
How predictable is the next state?	`transition_entropy()`
Where does the preceding context matter?	`build_hon()`, `path_counts()`
Which paths are more or less frequent than expected?	`build_hypa()`
Which groups of states are connected?	`build_simplicial()`, `simplicial_degree()`
Which structure holds across thresholds?	`persistent_homology()`
How are the groups of states connected to each other?	`q_analysis()`
Drawing paths as groups of states	`plot_simplicial()` (cograph)

Data

`human_long` holds the coded human turns of 425 human-AI pair-programming ("vibe coding") sessions, one row per action, coded into nine actions: `Command`, `Correct`, `Frustrate`, `Inquire`, `Interrupt`, `Refine`, `Request`, `Specify` and `Verify`. The network holds one sequence per session, ordered by `order_in_session`.

```
library(Nestimate)
library(cograph)
```

```
##
## Attaching package: 'cograph'
```

```
## The following objects are masked from 'package:Nestimate':
##
##     as_tna, centrality, get_theme
```

```
net <- build_network(human_long, method = "relative", action = "code",
                     actor = "session_id", time = "order_in_session")
```

```
## Metadata aggregated per session: ties resolved by first occurrence in 'cluster' (10 sessions)
```

```
net
```

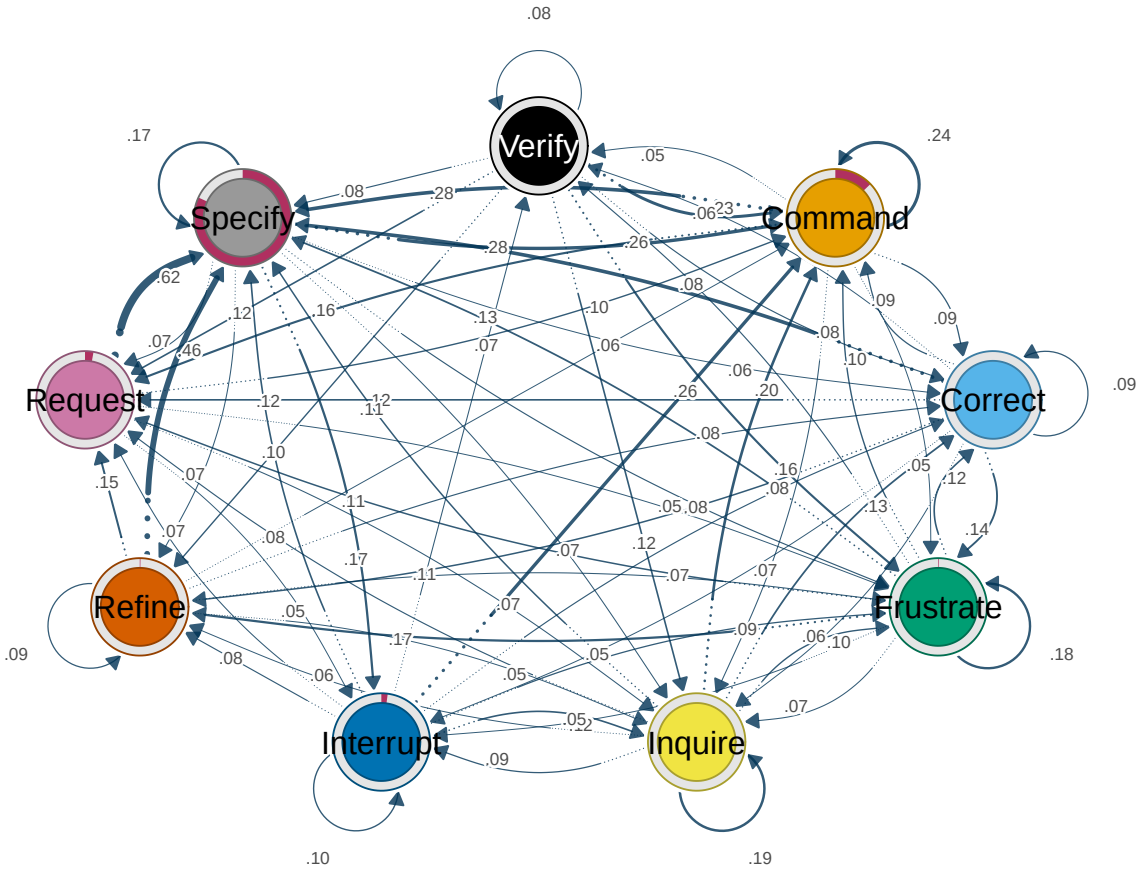
```
## Transition Network (relative probabilities) [directed]
##   Weights: [0.018, 0.616]  |  mean: 0.111
##
##   Strongest edges (10 of 81):
##    from      to      weight
##    Request   Specify 0.616
##    Refine    Specify 0.455
##    Correct   Specify 0.279
##    Command   Specify 0.277
##    Specify   Command 0.264
##    Interrupt Command 0.261
##    Command   Command 0.239
##    Verify    Command 0.226
##    Inquire   Command 0.200
##    Inquire   Inquire 0.187
##
##  extract_edges(include_self = TRUE) lists every edge; extract_transition_matrix() gives the weight matrix;
##   extract_initial_probs() the initial probabilities.
```

```
extract_initial_probs(net)
```

```
##     Command     Correct   Frustrate     Inquire   Interrupt      Refine
## 0.128205128 0.000000000 0.002331002 0.000000000 0.020979021 0.002331002
##     Request     Specify      Verify
## 0.027972028 0.818181818 0.000000000
```

Most sessions open with `Specify` (82%) or `Command` (13%). The strongest transitions lead back to `Specify`: from `Request` (0.62) and from `Refine` (0.46).

```
splot(net, minimum = 0.05)
```



Is a first-order model enough?

Multi-order model

The multi-order generative model (MOGen) fits Markov models of order 0 (no memory) up to `max_order` and compares them with information criteria (Scholtes, 2017). A higher order always fits better; the AIC and the BIC weigh the improvement against the number of parameters, which multiplies by nine with every order.

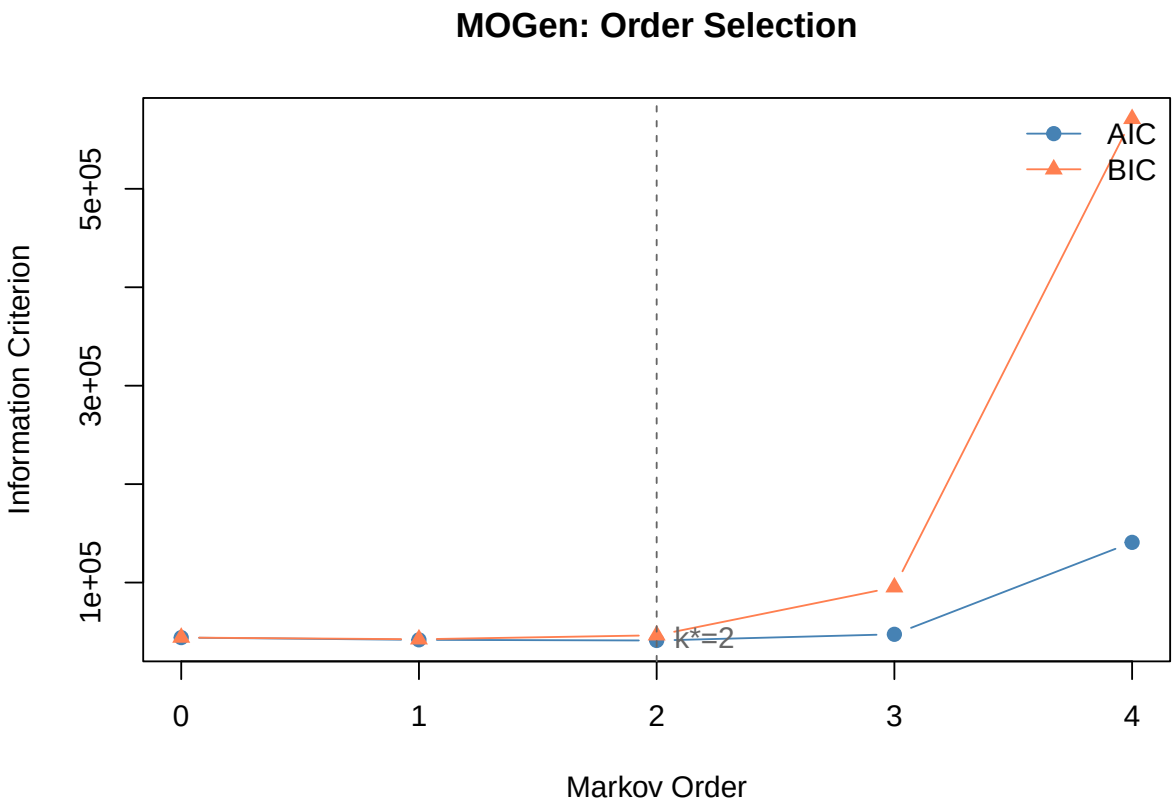
```
mogen <- build_mogen(net, max_order = 4)
summary(mogen)
```

```
## Multi-Order Generative Model (MOGen) Summary
##
##   States: Command, Correct, Frustrate, Inquire, Interrupt, Refine, Request, Specify, Verify
##    Paths: 425 | Observations: 10792
##    Best by AIC: order 2  |  Best by BIC: order 1
##    Selected:    order 2 (by aic)

##         order layer_dof cum_dof    loglik       aic       bic best selected
## order_0     0         8       8 -22031.34  44078.69  44136.98
## order_1     1        72      80 -20829.39  41818.79  42401.71  BIC
## order_2     2       648     728 -19841.13  41138.25  46442.87  AIC      <--
```

```
## order_3     3      5832    6560 -17163.27  47446.54  95246.37
## order_4     4     52488   59048 -11365.83 140827.66 571084.48
```

```
plot(mogen)
```



The AIC is lowest at order 2 and the BIC, which penalises parameters more, at order 1. The order-2 model has 728 parameters against 80 for order 1.

Permutation test of the order

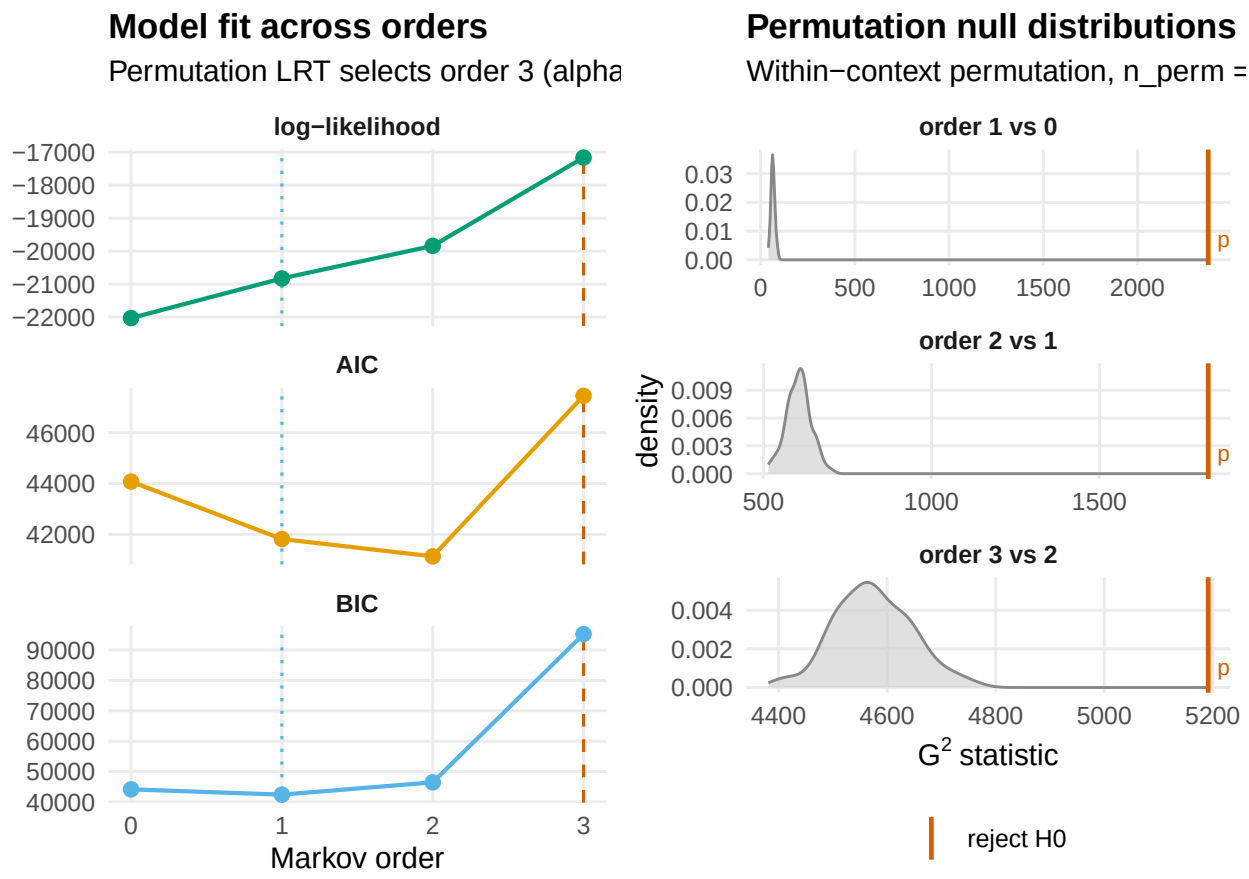
`markov_order_test()` tests at each order k whether order k describes the sequences better than order $k-1$. The statistic is a likelihood ratio G^2, and its null distribution comes from permuting the next state within each context of the preceding $k-1$ states. The permutation is conditional rather than exact, because the overlapping windows of one sequence are not independent (Besag & Mondal, 2013).

```
order_test <- markov_order_test(net, max_order = 3, n_perm = 200, seed = 1)
order_test
```

```
## Markov Order Test  [within-w permutation, n_perm = 200, alpha = 0.050]
##   425 sequences / 10792 observations / 9 states
##
##   Selected order  BIC: 1   AIC: 2   permutation-LRT: 3
##
##  order    loglik      AIC      BIC   df      g2 p_permutation  p_asymptotic
```

```
##       0 -22031.34 44078.69 44136.98   NA      NA            NA            NA
##       1 -20829.39 41818.79 42401.71   64 2375.35   0.004975124  0.000000e+00
##       2 -19841.13 41138.25 46442.87  576 1823.84   0.004975124 1.707029e-129
##       3 -17163.27 47446.54 95246.37 4721 5191.45   0.004975124  1.324824e-06
##   significant
##            NA
##          TRUE
##          TRUE
##          TRUE
```

```r
plot(order_test)
```



All three orders are significant: each observed G^2 (2375, 1824 and 5191) lies above all 200 permuted values, so the p-value of 0.005 is the smallest the test can give with 200 permutations. The test selects order 3, the AIC order 2, and the BIC order 1. The criteria agree that the previous state alone does not describe the sequences; they differ on how much more memory is worth the parameters.

Second-order transitions

`mogen_transitions()` returns the transitions of one order: the two preceding states (`from`), the next state (`to`), the count and the conditional probability.

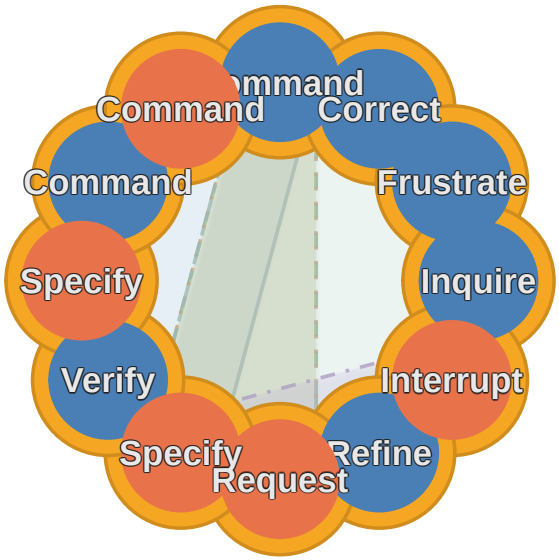
```r
second_order <- mogen_transitions(mogen, order = 2)
head(second_order, 8)
```

```
##                              path count probability              from
## 1   Specify -> Command -> Specify   284      0.3901 Specify -> Command
## 2   Command -> Request -> Specify   231      0.7649 Command -> Request
## 3   Specify -> Command -> Request   199      0.2734 Specify -> Command
## 4 Request -> Specify -> Interrupt   189      0.3259 Request -> Specify
## 5   Command -> Command -> Command   177      0.3882 Command -> Command
## 6 Command -> Specify -> Interrupt   149      0.2770 Command -> Specify
## 7   Specify -> Request -> Specify   128      0.6564 Specify -> Request
## 8   Specify -> Specify -> Specify   123      0.2662 Specify -> Specify
##          to
## 1   Specify
## 2   Specify
## 3   Request
## 4 Interrupt
## 5   Command
## 6 Interrupt
## 7   Specify
## 8   Specify
```

The most frequent context is `Specify -> Command`, which is followed by `Specify` with probability 0.39 and by `Request` with probability 0.27. `Command -> Request` is followed by `Specify` with probability 0.76: after a command and a request, the next action is usually a new specification.

`plot_simplicial()` draws the most frequent paths as shaded regions over the states they pass through, the earlier states in blue and the last state in red.

```
plot_simplicial(net, pathways = second_order, max_pathways = 6)
```



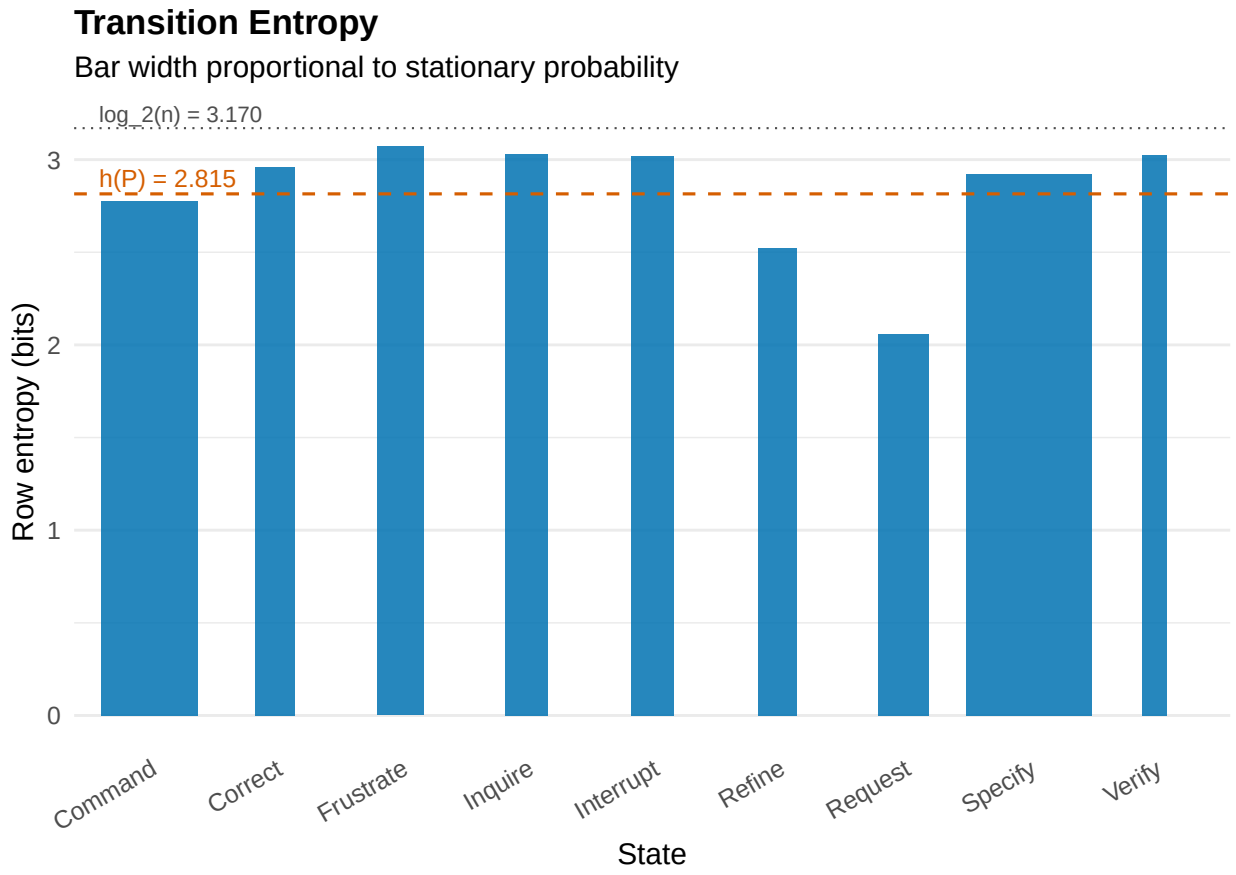
Predictability of the next state

`transition_entropy()` measures how uncertain the next state is (Cover & Thomas, 2006). The entropy of a state's row of transition probabilities is 0 bits when the next state is certain and $\log_2 9 = 3.17$ bits when all nine are equally likely; the entropy rate weights the rows by how often each state occurs.

```
entropy <- transition_entropy(net)
entropy
```

```
## Transition Entropy (9 states, bits; ceiling = 3.170)
##
##                             raw            normalised
##   Entropy rate    h(P)  = 2.815 bits    0.888
##   Stationary    H(pi)  = 2.982 bits    0.941
##   Redundancy   H(pi)-h = 0.167 bits    0.056
##
## Normalised: h(P) and H(pi) are raw / log_2(n_states) (0 = deterministic, 1 = uniform);
##   redundancy is the relative redundancy (H(pi) - h(P)) / H(pi), not raw / log_2(n_states).
```

```
plot(entropy)
```



The entropy rate is 2.82 bits, 89% of the maximum: knowing the current action reduces the uncertainty about the next one by 0.17 bits. In the plot, each bar is one state's entropy and its width the state's share of the actions.

Where the context matters: higher-order networks

A higher-order network (HON) adds a node for a preceding context whenever that context changes the distribution of the next state (Xu, Wickramarathne, & Chawla, 2016); `build_hon()` uses the BuildHON+ algorithm (Saebi et al., 2020). `max_order` limits the length of the contexts and `min_freq` the number of times a transition must occur to be kept.

```
hon <- build_hon(net, max_order = 3, min_freq = 5)
hon
```

```
## Higher-Order Network (HON)
##   Nodes:        233 (9 first-order states)
##   Edges:        819
##   Max order:    3 (requested 3)
##   Min freq:     5
##   Trajectories: 425
```

```
pathways(hon, top = 10)
```

```
##  [1] "Specify Command -> Specify"
```

```
##  [2] "Command Request -> Specify"
##  [3] "Specify Command -> Request"
##  [4] "Request Specify -> Interrupt"
##  [5] "Specify Command Request -> Specify"
##  [6] "Command Command -> Command"
##  [7] "Command Specify -> Interrupt"
##  [8] "Command Request Specify -> Interrupt"
##  [9] "Specify Request -> Specify"
## [10] "Specify Specify -> Specify"
```

The network has 233 nodes, the 9 actions and 224 contexts of two or three actions, and 819 edges, 738 of them from a context. `pathways()` lists the higher-order edges by frequency: `Specify Command -> Specify` reads "after `Specify` then `Command`, the next action is `Specify`".

`path_counts()` counts the paths of `k` states in the sequences, whether or not they are higher-order.

```
path_counts(net, k = 3, top = 10)
```

```
##                               path count proportion
## 1    Specify -> Command -> Specify   284     0.0286
## 2    Command -> Request -> Specify   231     0.0232
## 3    Specify -> Command -> Request   199     0.0200
## 4  Request -> Specify -> Interrupt   189     0.0190
## 5    Command -> Command -> Command   177     0.0178
## 6  Command -> Specify -> Interrupt   149     0.0150
## 7    Specify -> Request -> Specify   128     0.0129
## 8    Specify -> Specify -> Specify   123     0.0124
## 9     Specify -> Refine -> Specify   122     0.0123
## 10 Specify -> Interrupt -> Command   113     0.0114
```

`Specify -> Command -> Specify` is the most frequent three-action path (284 times, 2.9% of all paths of three actions).

Paths more or less frequent than expected: HYPA

HYPA compares the frequency of each path with the frequency expected from the transitions it is made of (LaRock et al., 2020). The expectation comes from a hypergeometric model of the network of paths that keeps how often each shorter path starts and ends a longer one. A path observed more often than expected is over-represented, and one observed less often under-represented.

```
hypa <- build_hypa(net)
hypa
```

```
## HYPA: Path Anomaly Detection
##   Order(s):     2
##   Edges:        729
##   Anomalous:    149 (alpha=0.05, p_adjust=none)
##     Over-repr:  103
##     Under-repr: 46
```

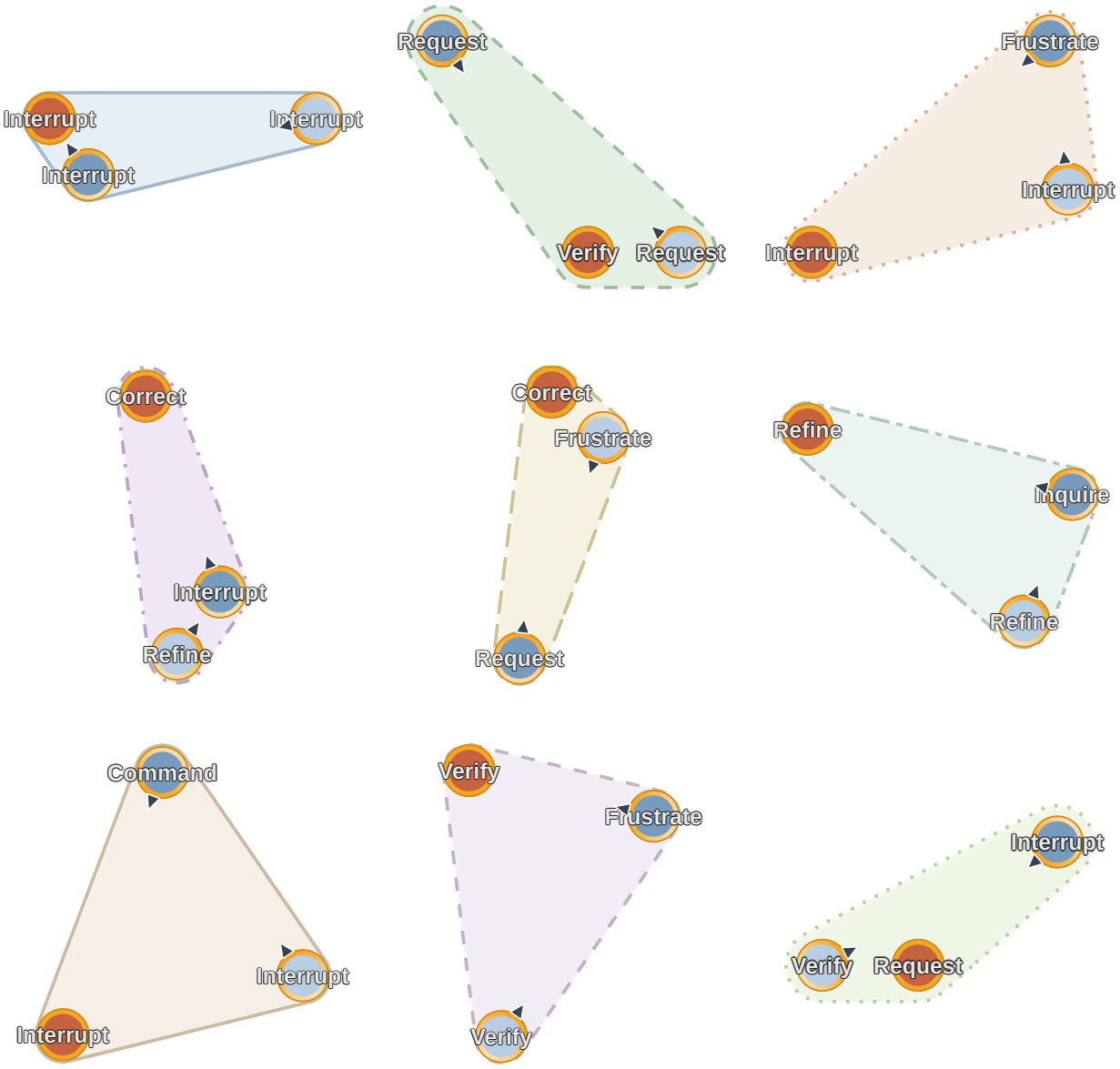
Of the 729 paths of three actions, 149 differ from the expectation at the 5% level: 103 are over-represented and 46 under-represented. The p-values are not adjusted for the number of paths (`p_adjust = "none"`).

```r
summary(hypa, type = "over", order_by = "ratio", n = 8)
```

```
## HYPA Summary
##
##   Order(s): 2 | Edges: 729
##   Alpha: 0.05 | p_adjust: none
##   Anomalous: 149 (over: 103, under: 46) | order_by: ratio
##
##   Over-represented (top 8 ):
##                                  path observed expected    ratio
##  Interrupt -> Interrupt -> Interrupt       29 5.457995 5.313307
##         Request -> Request -> Verify        5 1.287834 3.882488
##  Interrupt -> Frustrate -> Interrupt       12 3.114595 3.852829
##       Refine -> Interrupt -> Correct        6 1.626016 3.690000
##      Frustrate -> Request -> Correct        7 1.899110 3.685937
##          Refine -> Inquire -> Refine        8 2.176329 3.675916
##    Interrupt -> Command -> Interrupt       23 6.257631 3.675513
##        Verify -> Frustrate -> Verify       22 6.063784 3.628098
##        p_tail
##  2.428322e-13
##  2.126592e-03
##  2.353580e-05
##  1.459766e-03
##  7.891460e-04
##  4.335950e-04
##  5.237408e-08
##  1.187755e-07
```

Three interruptions in a row occur 29 times against 5.5 expected (ratio 5.3), and `Interrupt -> Command -> Interrupt` 23 times against 6.3. Interruptions cluster: once a programmer interrupts the assistant, further interruptions follow more often than the single transitions predict.

```r
plot_simplicial(hypa, anomaly = "over", max_pathways = 9,
                dismantled = TRUE, ncol = 3)
```

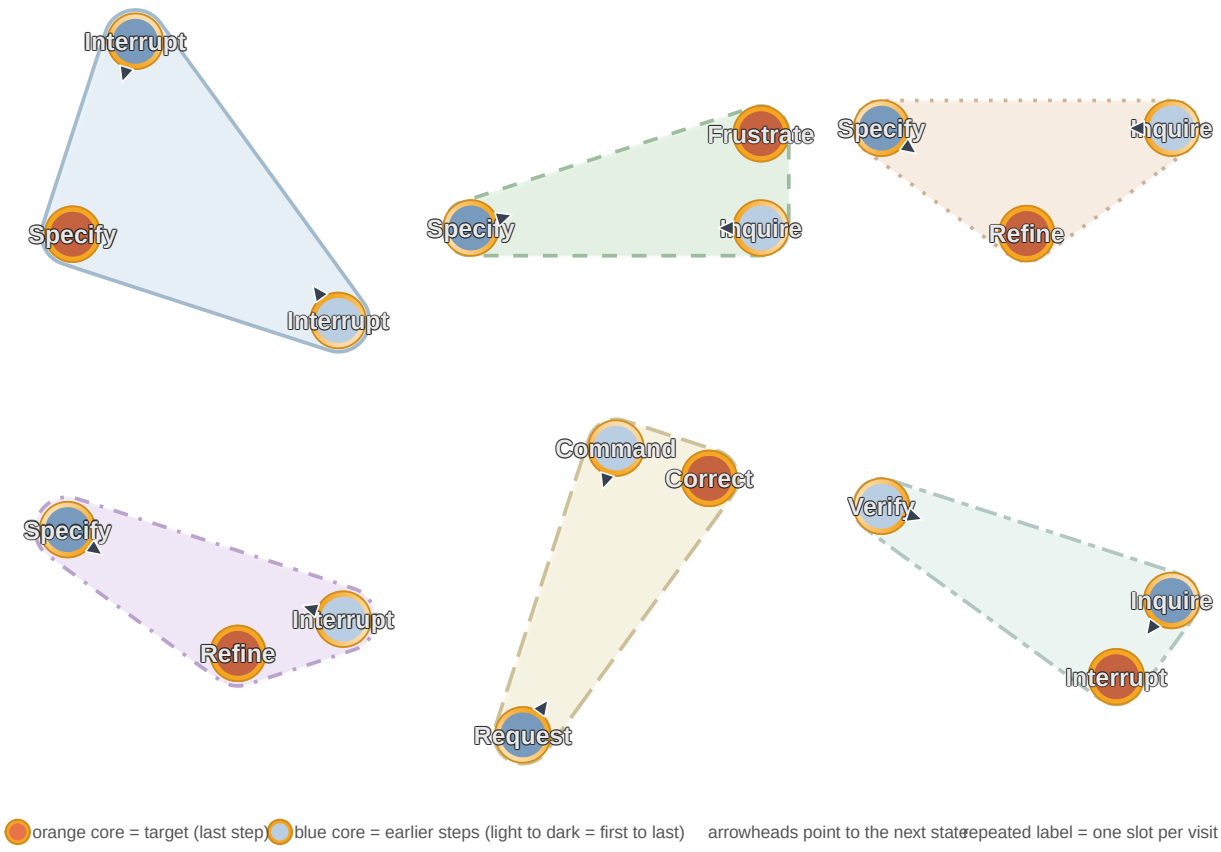

Interrupt
Interrupt
Interrupt
Request
Verify
Request
Frustrate
Interrupt
Interrupt
Correct
Interrupt
Refine
Correct
Frustrate
Request
Refine
Inquire
Refine
Command
Interrupt
Interrupt
Verify
Frustrate
Verify
Interrupt
Verify
Request
orange core = target (last step)
blue core = earlier steps (light to dark = first to last)
arrowheads point to the next state
repeated label = one slot per visit

```r
summary(hypa, type = "under", order_by = "ratio", n = 8)
```

```
## HYPA Summary
##
##   Order(s): 2 | Edges: 729
##   Alpha: 0.05 | p_adjust: none
##   Anomalous: 149 (over: 103, under: 46) | order_by: ratio
##
##   Under-represented (top 8 ):
##                                path observed expected     ratio      p_tail
##  Interrupt -> Interrupt -> Specify        0 5.817073 0.0000000 0.002970473
##    Inquire -> Specify -> Frustrate        1 7.779682 0.1285400 0.003661319
##       Inquire -> Specify -> Refine        1 7.094247 0.1409593 0.006702541
##     Interrupt -> Specify -> Refine        1 6.925337 0.1443973 0.007770947
##      Command -> Request -> Correct        1 5.974283 0.1673841 0.017711857
##     Verify -> Inquire -> Interrupt        1 5.207729 0.1920223 0.033944925
##    Correct -> Frustrate -> Inquire        2 7.907027 0.2529396 0.014756758
##     Verify -> Specify -> Interrupt        2 7.588739 0.2635484 0.018885541
```

`Interrupt -> Interrupt -> Specify` never occurs although 5.8 occurrences are expected: after two interruptions, programmers do not return directly to specifying the task.

```r
plot_simplicial(hypa, anomaly = "under", max_pathways = 6,
                dismantled = TRUE, ncol = 3)
```



The same analysis of `group_regulation_long`, the regulation actions of students working in groups (Tikka, López-Pernas, & Saqr, 2025), finds fewer anomalous paths.

```
regulation_net <- build_network(group_regulation_long, method = "relative",
                                action = "Action", actor = "Actor",
                                time = "Time")
build_hypa(regulation_net)
```

```
## HYPA: Path Anomaly Detection
##   Order(s):     2
##   Edges:        679
##   Anomalous:    29 (alpha=0.05, p_adjust=none)
##     Over-repr:  22
##     Under-repr: 7
```

29 of its 679 paths are anomalous (4%), against 149 of 729 (20%) in the programming sessions: the regulation sequences are closer to what their first-order transitions predict.

Simplicial complexes

A network describes pairs of states (Saqr, López-Pernas, Conde-González, & Hernández-García, 2024). A simplicial complex also describes groups: two connected states form a 1-simplex (an edge), three mutually connected states a 2-simplex (a filled triangle), and $k + 1$ mutually connected states a k-simplex (Battiston et al., 2020). `build_simplicial()` builds the clique complex, in which every group of mutually connected states is a simplex. Two states are connected when the transition between them, in either direction, has a probability of at least `threshold`.

Building the complex

The threshold decides which transitions count. At 0.05 every pair of the nine actions is connected and the complex is a single 8-simplex, which describes nothing; at 0.12 the complex keeps the frequent transitions.

```
complex <- build_simplicial(net, threshold = 0.12)
complex
```

```
## Clique Complex
##   9 nodes, 31 simplices, dimension 2
##   Density: 24.0%  |  Mean dim: 0.90  |  Euler: -1
##   f-vector: (f0=9 f1=16 f2=6)
##   Betti: b0=1 b1=2
##  Nodes: Command, Correct, Frustrate, Inquire, Interrupt, Refine, Request, Specify, Verify
```

The complex has 9 states, 16 edges and 6 filled triangles, and no larger groups. Its Betti numbers count its holes: $\beta_0 = 1$ means it is connected, $\beta_1 = 2$ that it has two loops, cycles of edges that are not filled by triangles. The Euler characteristic, $9 - 16 + 6 = -1$, equals $\beta_0 - \beta_1$.

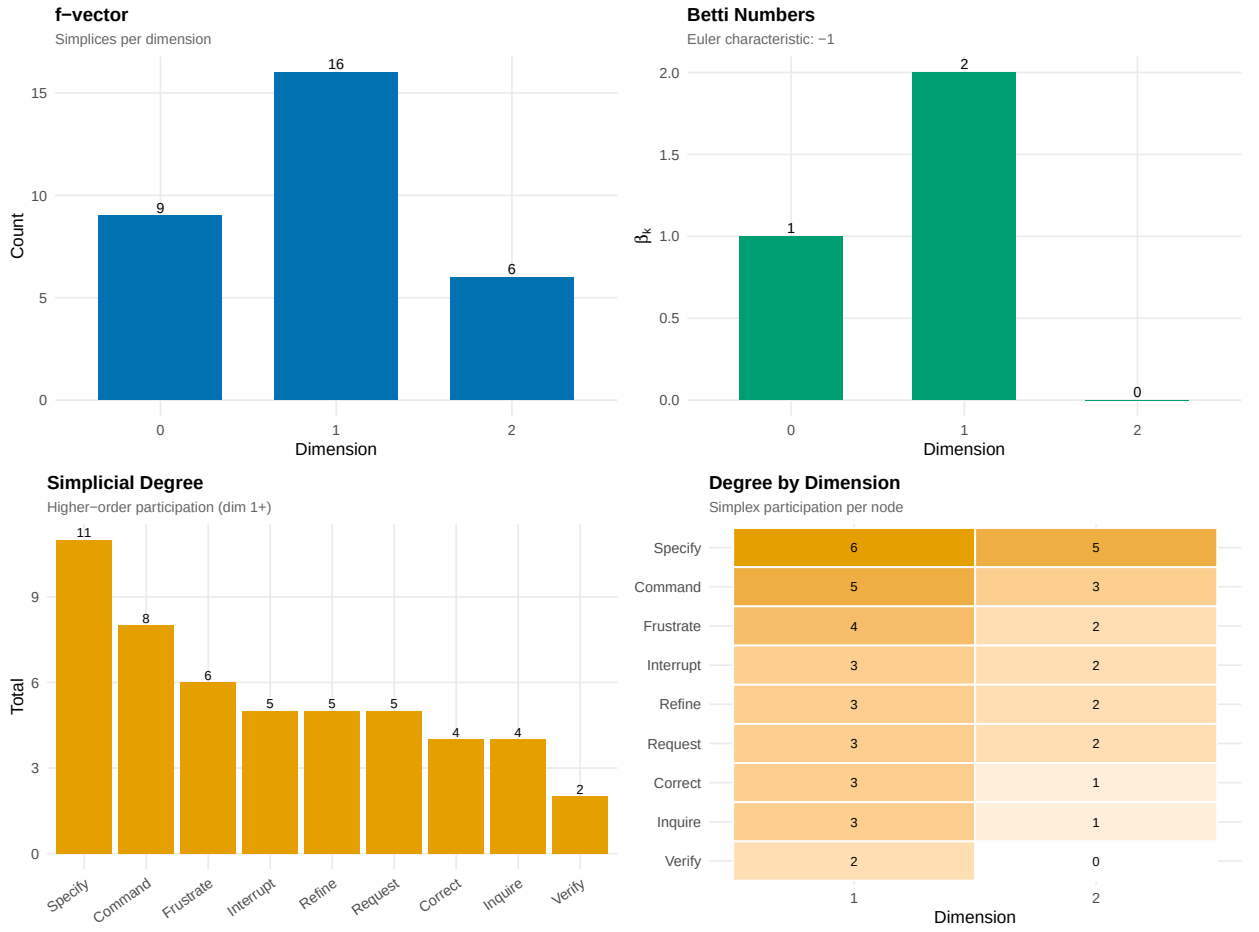
```
simplicial_degree(complex)
```

```
##        node d0 d1 d2 total
## 8   Specify  1  6  5    11
```

```
## 1   Command  1  5  3     8
## 3 Frustrate  1  4  2     6
## 5 Interrupt  1  3  2     5
## 6    Refine  1  3  2     5
## 7   Request  1  3  2     5
## 2   Correct  1  3  1     4
## 4   Inquire  1  3  1     4
## 9    Verify  1  2  0     2
```

`simplicial_degree()` counts, for each state, the simplices of each dimension it belongs to.

```
plot(complex)
```



The four panels show the number of simplices per dimension (the f-vector), the Betti numbers, each state's number of simplices, and that number by dimension.

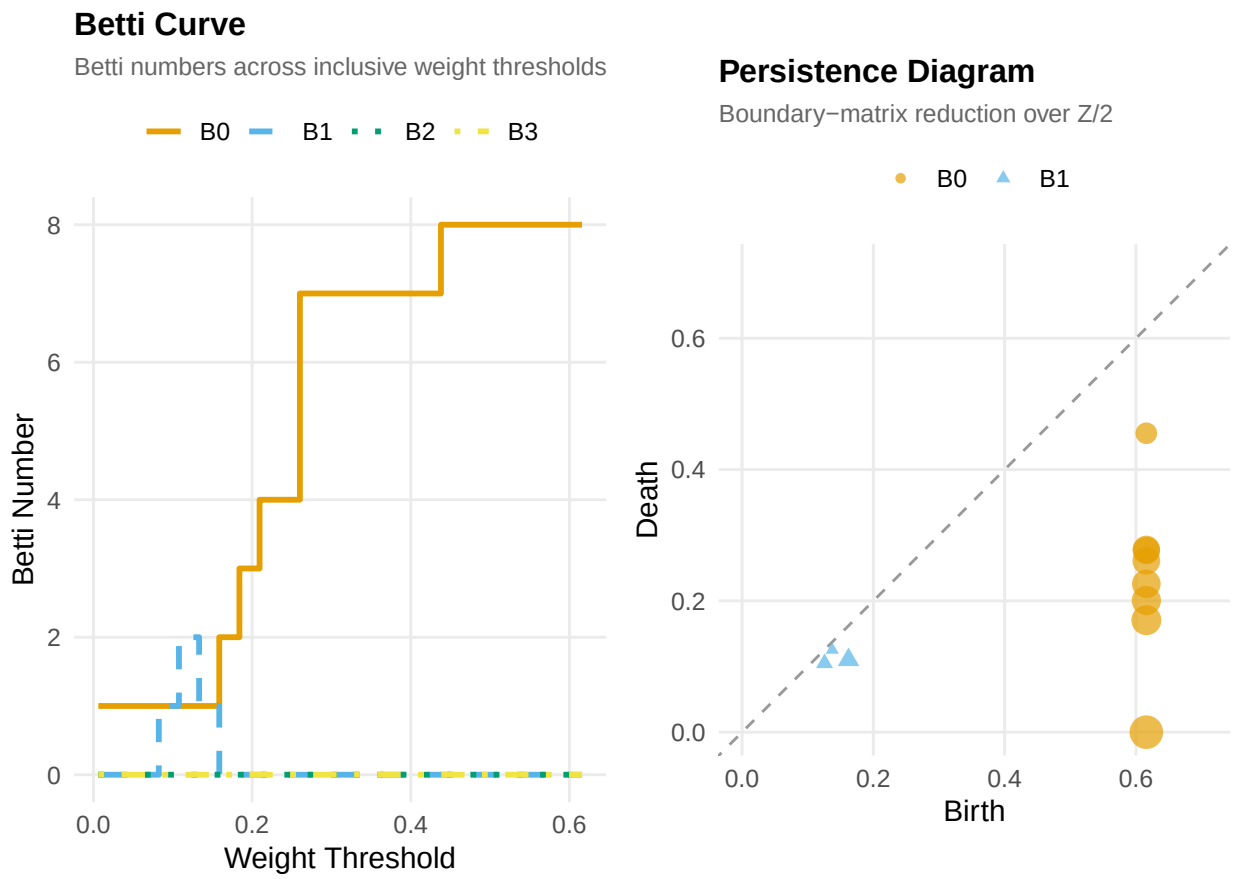
Persistent homology

A complex at one threshold depends on the threshold. Persistent homology builds the complex at a sequence of thresholds, from the strongest edge down, and records when each component and each loop appears and disappears (Edelsbrunner, Letscher, & Zomorodian, 2002). A feature that lasts over a wide range of thresholds does not depend on the choice of one.

```
persistence <- persistent_homology(net, n_steps = 25)
persistence
```

```
## Persistent Homology
##   25 filtration steps [0.6158 → 0.0062]
##   Features: b0: 8 (1 persistent)  |  b1: 3 (0 persistent)
##   Longest-lived:
##     b0: 0.6158 → 0.0000 (life: 0.6158)
##     b0: 0.6158 → 0.1706 (life: 0.4452)
##     b0: 0.6158 → 0.2005 (life: 0.4154)
```

```
plot(persistence)
```



The left panel, the Betti curve, shows the number of components and loops at each threshold. The right panel, the persistence diagram, places each feature at the threshold where it appears and the one where it disappears; points far from the diagonal last longest. The states join into one component as the threshold falls below 0.17. Three loops appear at some threshold and all are filled by triangles before the lowest one.

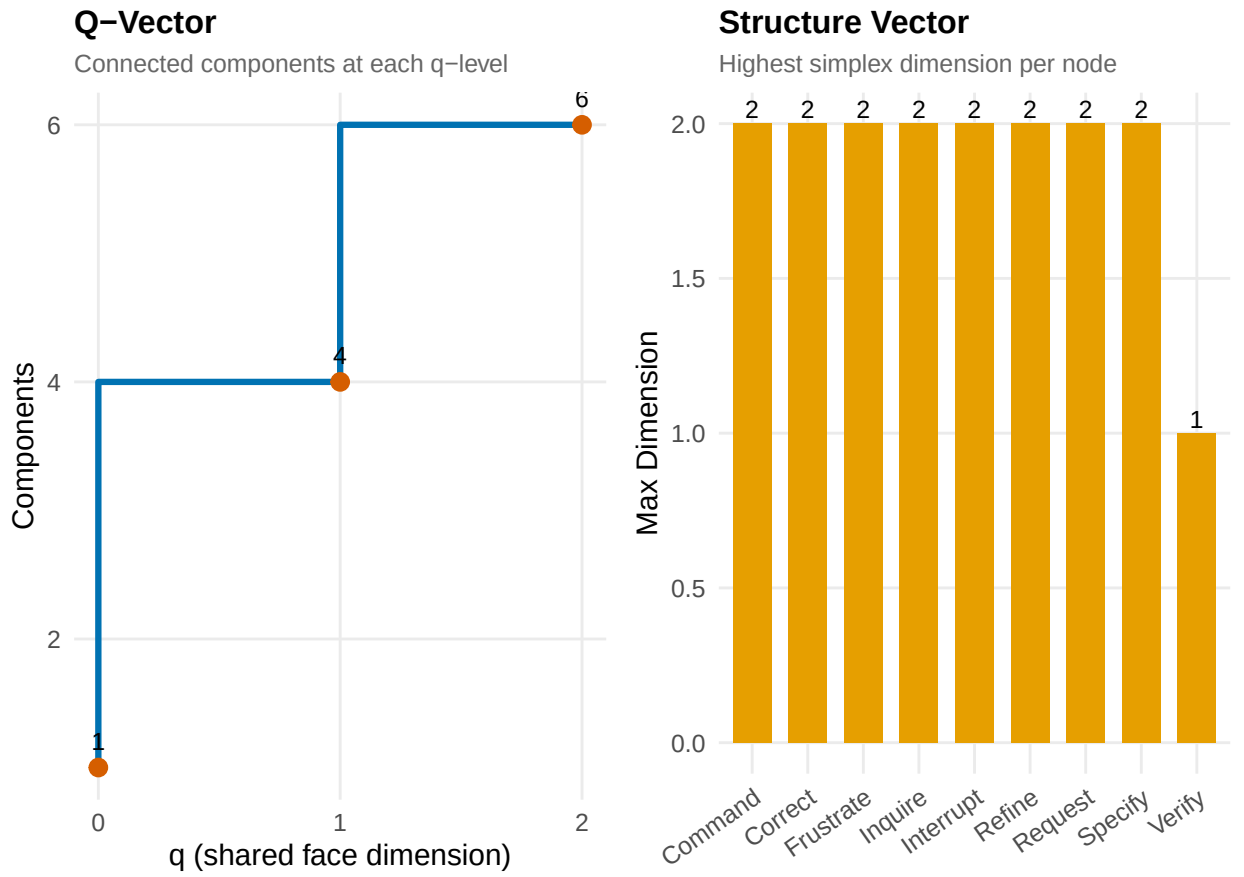
Q-analysis

Q-analysis describes how the largest simplices are connected to each other (Atkin, 1974). Two simplices are q-connected when they share a face of dimension q or higher: a state for $q = 0$, an edge for $q = 1$, a triangle for $q = 2$.

```
q_structure <- q_analysis(complex)
q_structure
```

```
## Q-Analysis (max q = 2)
##   Components: q2:6 q1:4 q0:1
##   Fragments at q = 1 (1 → 4 components)
##  Structure: Command:2 Correct:2 Frustrate:2 Inquire:2 Interrupt:2 Refine:2 Request:2 Specify:2 Verify:1
```

```
plot(q_structure)
```



At $q = 0$ the complex is one component: every group of states shares at least one state with another. At $q = 1$ it splits into four components, so the triangles are joined through single states rather than through shared edges. The structure vector gives, for each state, the dimension of the largest simplex it belongs to: every state except `Verify` belongs to a triangle.

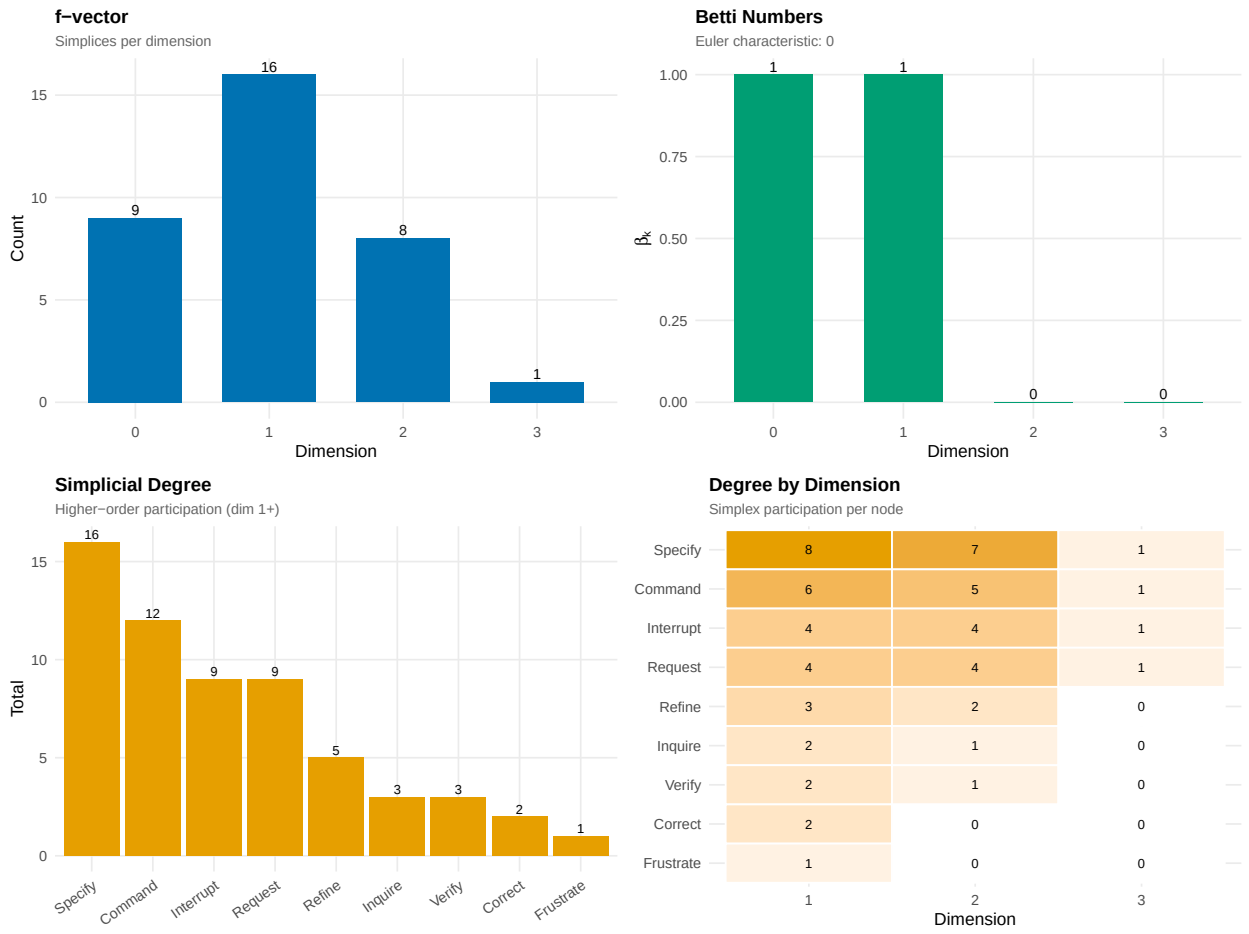
A complex from the higher-order paths

`type = "pathway"` builds the complex from the paths of the higher-order network instead of the cliques: each frequent path is a simplex of the states it passes through.

```
pathway_complex <- build_simplicial(hon, type = "pathway", max_pathways = 30)
pathway_complex
```

```
## Pathway Complex
##   9 nodes, 34 simplices, dimension 3
##   Density: 13.3%  |  Mean dim: 1.03  |  Euler: 0
##   f-vector: (f0=9 f1=16 f2=8 f3=1)
##   Betti: b0=1 b1=1
##  Nodes: Command, Correct, Frustrate, Inquire, Interrupt, Refine, Request, Specify, Verify
```

```
plot(pathway_complex)
```



The 30 most frequent paths form a connected complex ($\beta_0 = 1$) with one loop ($\beta_1 = 1$), of 16 edges, 8 triangles and one 3-simplex.

Checking the computation

`verify_simplicial()` recomputes the cliques with igraph and checks the Euler-Poincaré relation between the simplex counts and the Betti numbers.

```
verify_simplicial(net, threshold = 0.12)
```

```
##   Cliques:  MATCH (31 simplices)
##   Betti:    b0=1 b1=2 b2=0
##   Euler:    -1 (Euler-Poincare: VERIFIED)
```

How to cite this article

Saqr, M., López-Pernas, S., & Misiejuk, K. (2026). *Higher-order network analysis with simplicial complexes: From transition networks to topological analysis*. Nestimate. https://doi.org/10.5281/zenodo.24528514 · HTML · PDF

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