

Report

Population Version

The data consists of 1068 simulations from networks from the **bnlearn** repository. In order to determine conditional independence for the population version, we consider d -separation from the true DAG. For the estimation of the skeleton, the maximum number of nodes we consider in a separating set is 3 (our default). For each network, we consider target sets T with $|T| \in \{1, 2, 3, 4, 5\}$. Below is a table of some of the results

Same V-Structures

Comparing only the nodes in the neighborhood, we found that in all 930 cases, the population PC correctly identified all the V-structures

SHD

Also, for all 930 cases, we found that the SHD was 0 in every case.

False Negatives and False Positives

Since we do not implement all of Meek's rules in the local setting, we can view some other statistics concerning false negatives and false positives. Each number in the table below is the number of times that number of false positives/false negatives are observed for a particular network and set of target nodes. These statistics come from comparisons between the estimated CPDAG and the true CPDAG.

False Negatives

##														
##	0	1	2	3	4	5	6	7	8	10	12	14	20	
##	675	155	121	30	30	24	13	7	6	2	3	1	1	

False Positives

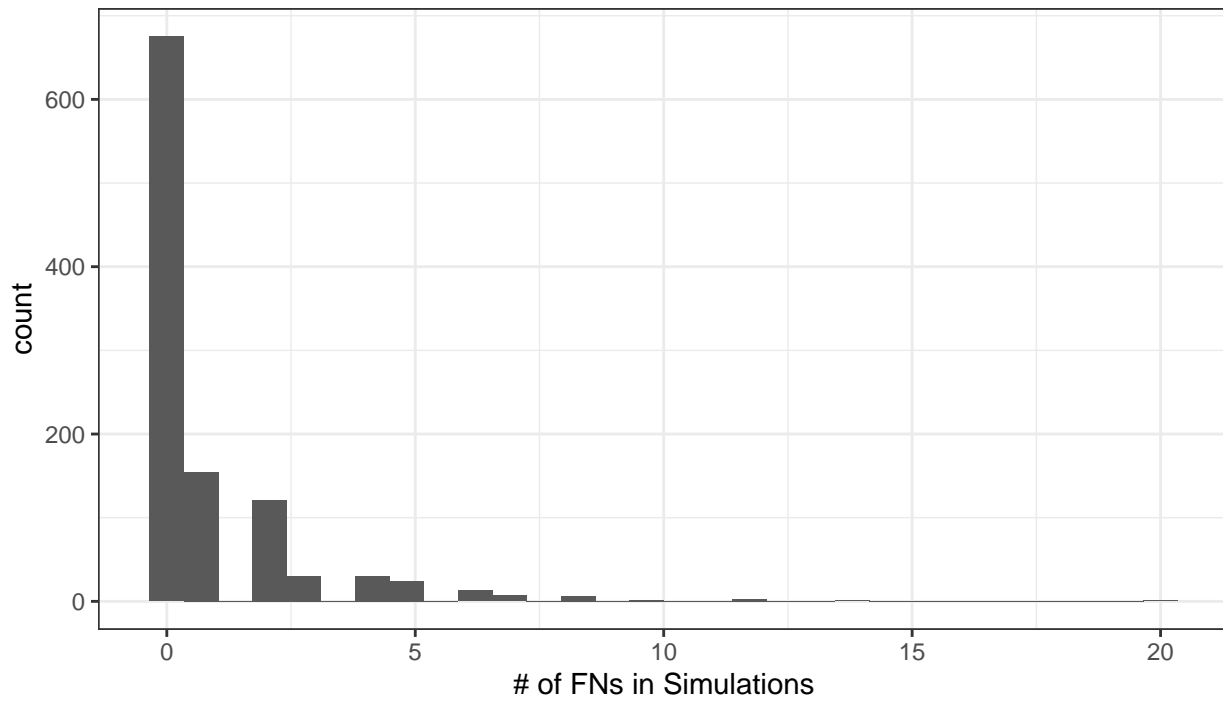
##																		
##	0	1	2	3	4	5	6	7	8	9	10	11	12	14	15	17	20	21
##	650	151	124	25	30	24	19	13	3	1	3	2	2	1	1	1	6	1
##	22	28	29	33	34	35	40											
##	1	2	1	2	2	2	1											

These tables are equivalent because each false negative and false positive represents an undirected edge in the estimated CPDAG that is directed in the true CPDAG.

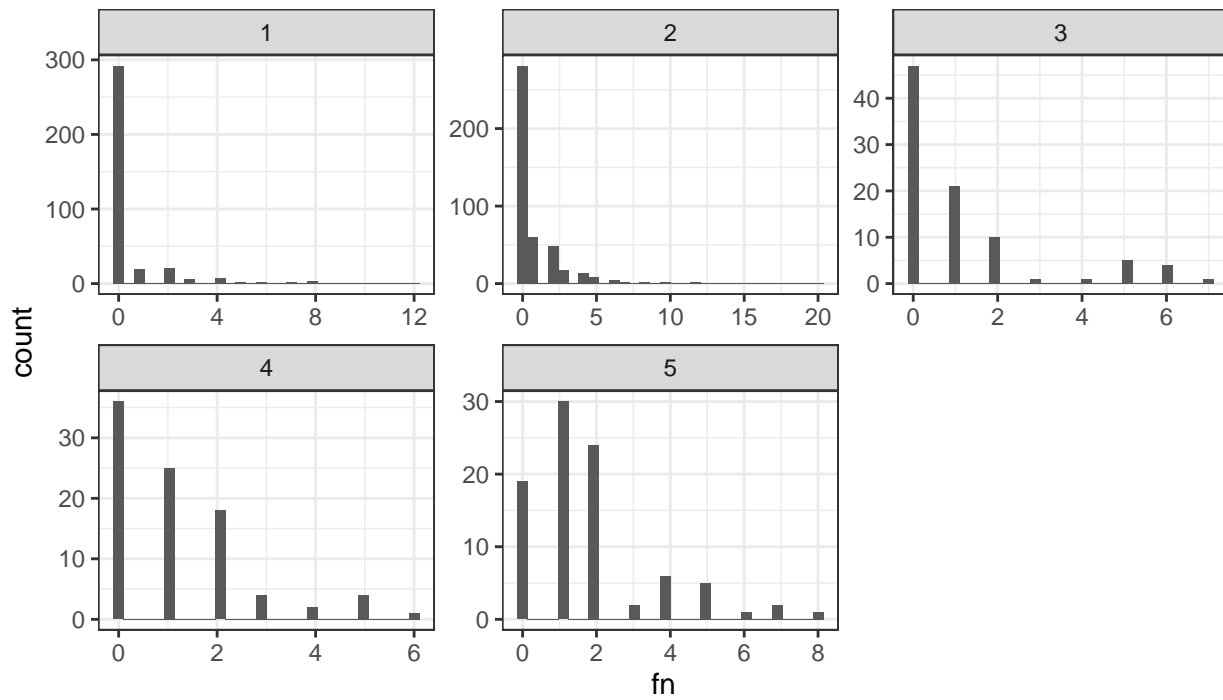
Visualizations

False Negatives

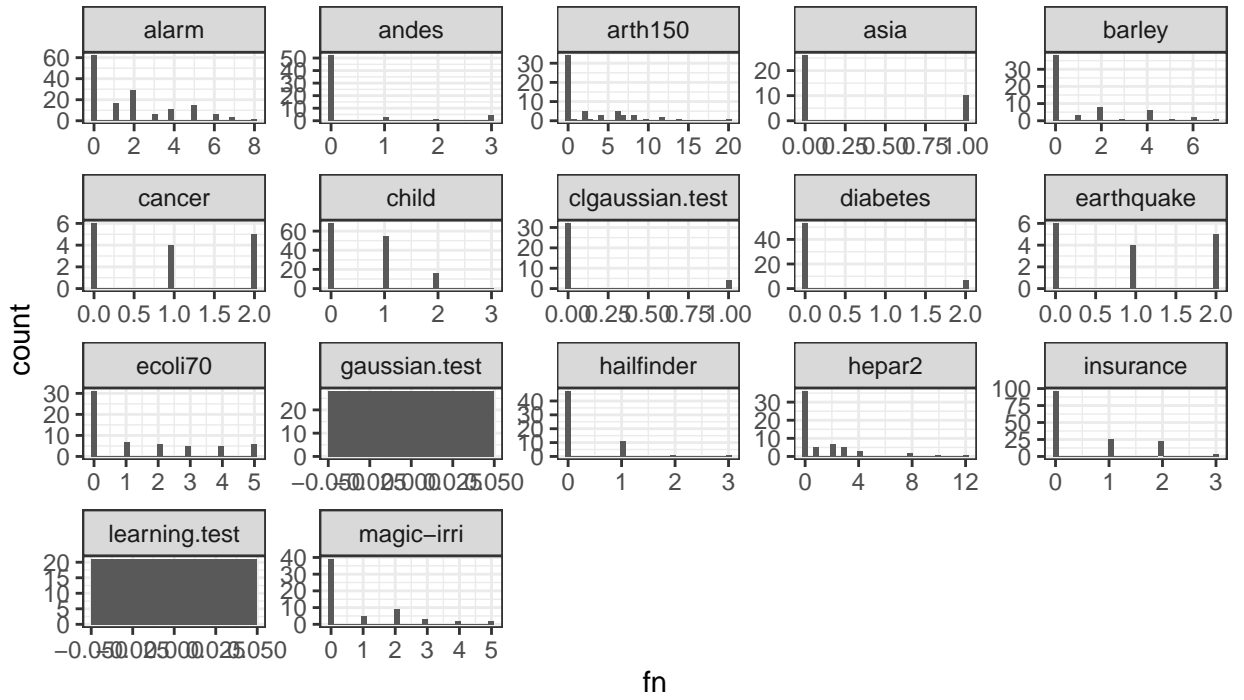
Distribution of Number of False Negatives



Distribution of FNs for Different Number of Targets

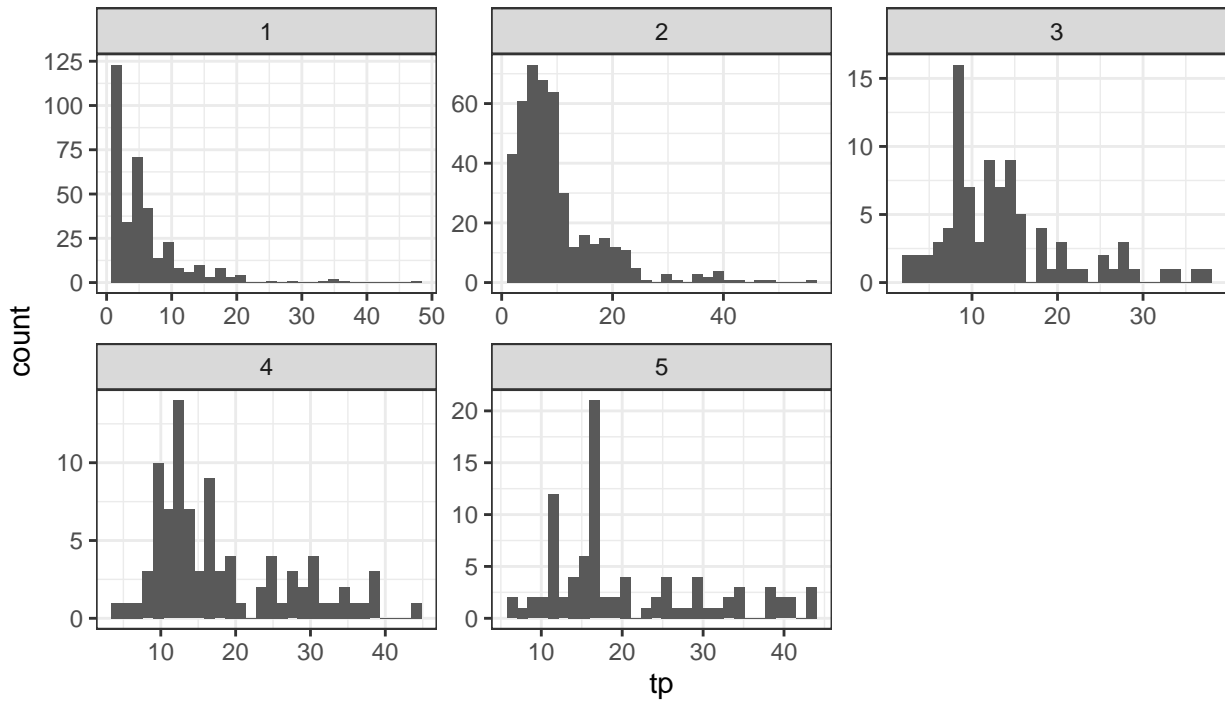


Distribution of FNs for Different Networks

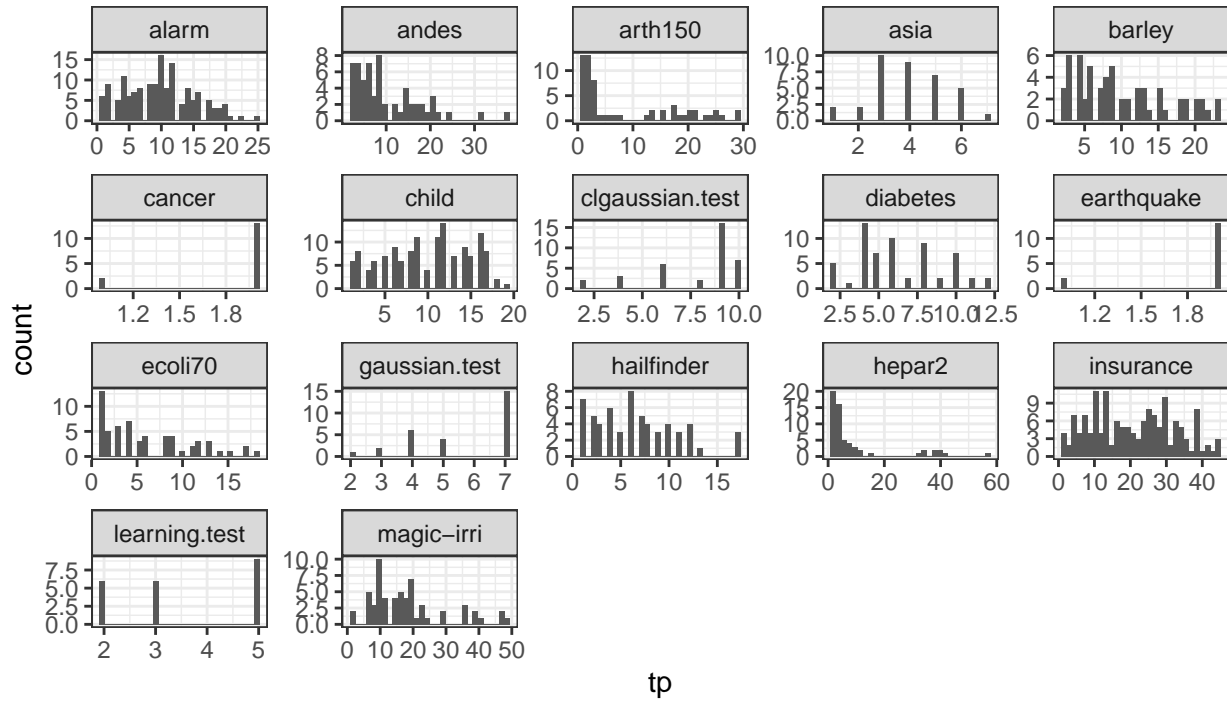


True Positives

Distribution of True Positives for Different Number of Targets

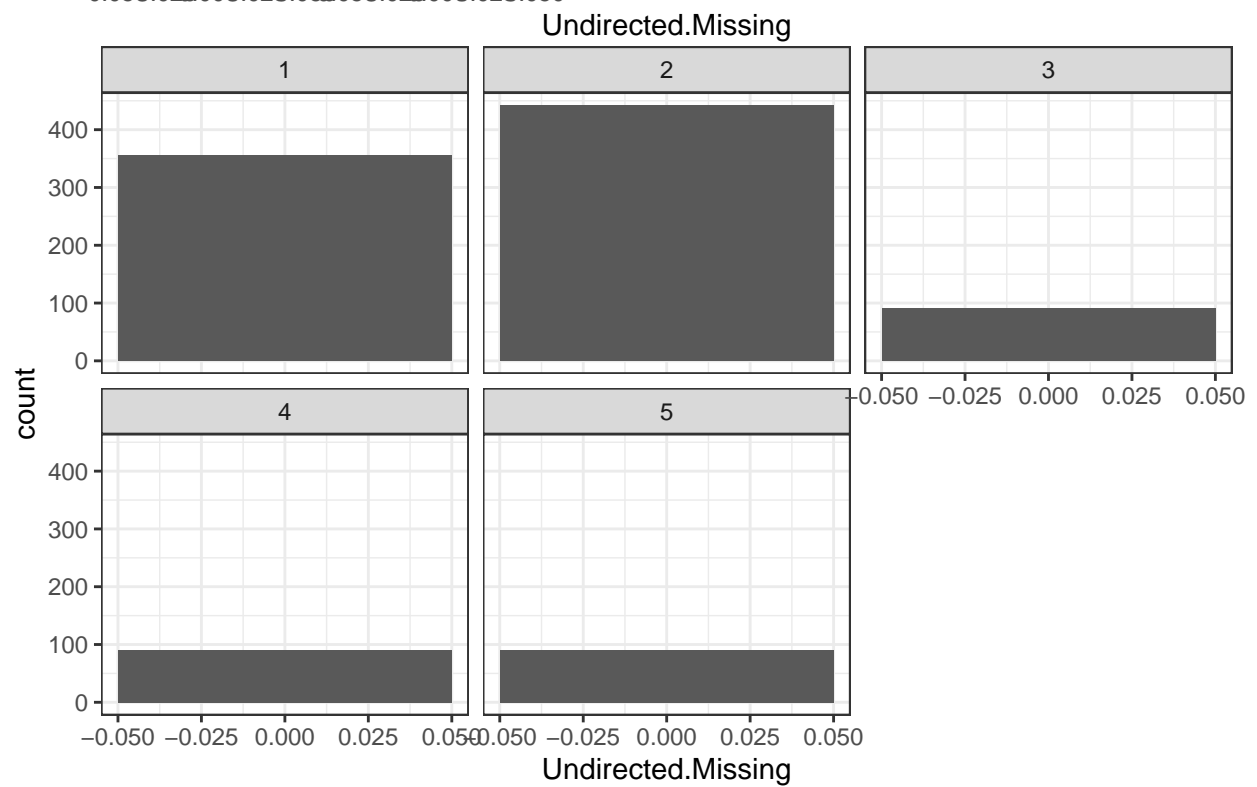
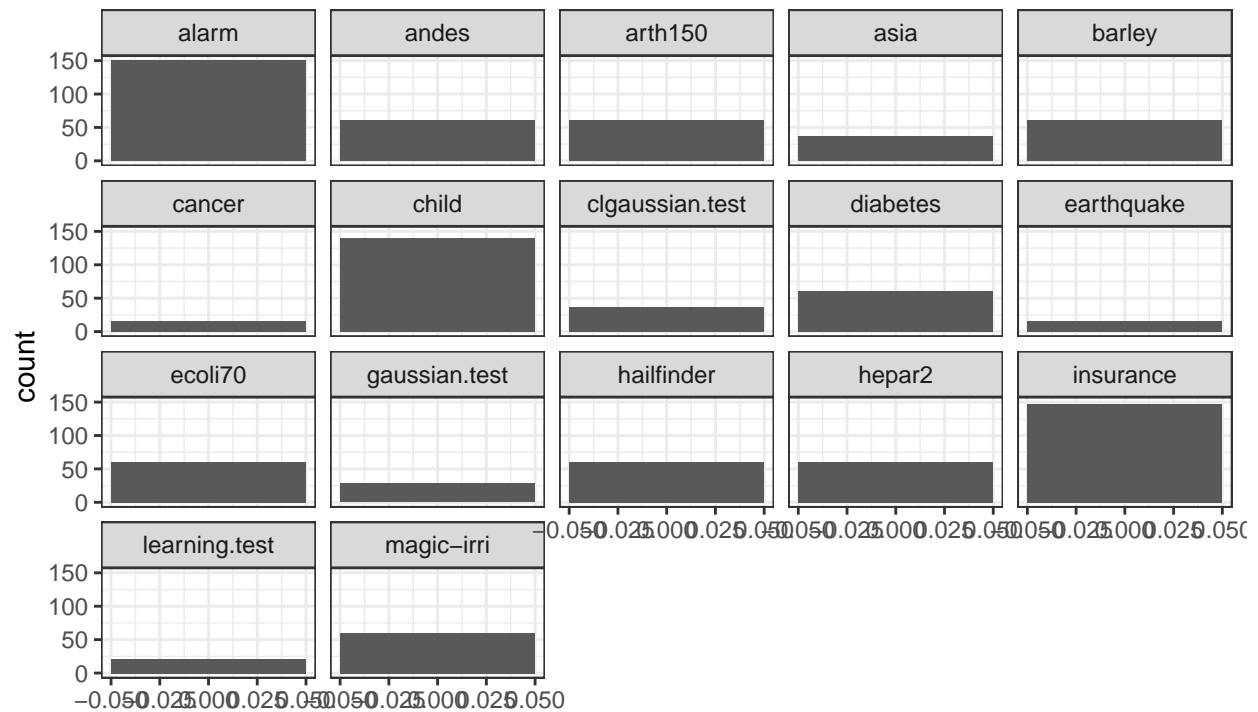


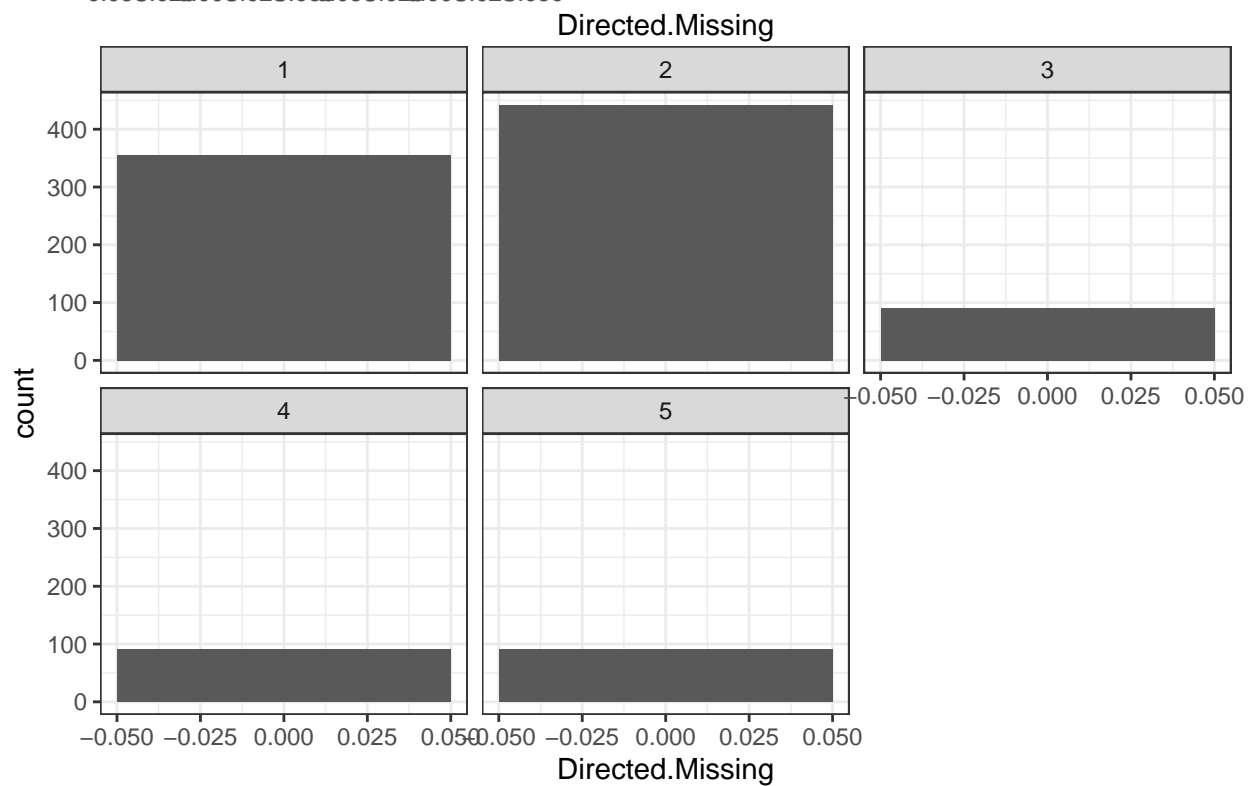
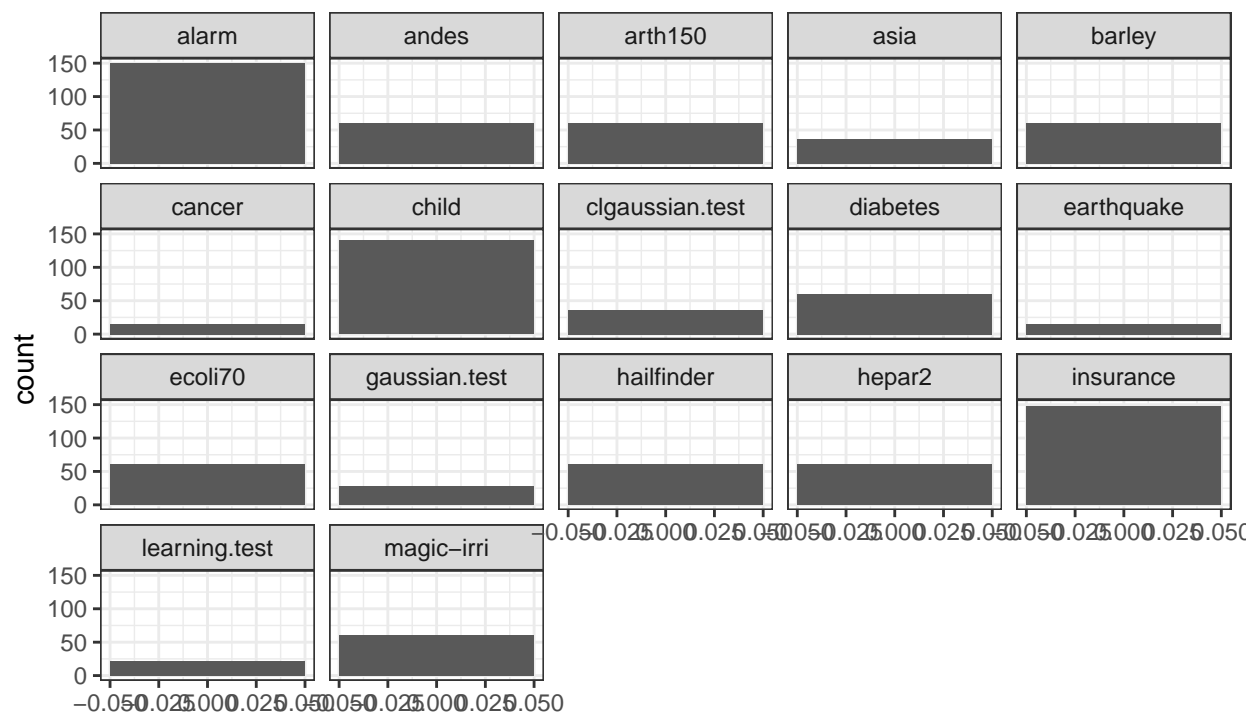
Distribution of TPs for Different Networks

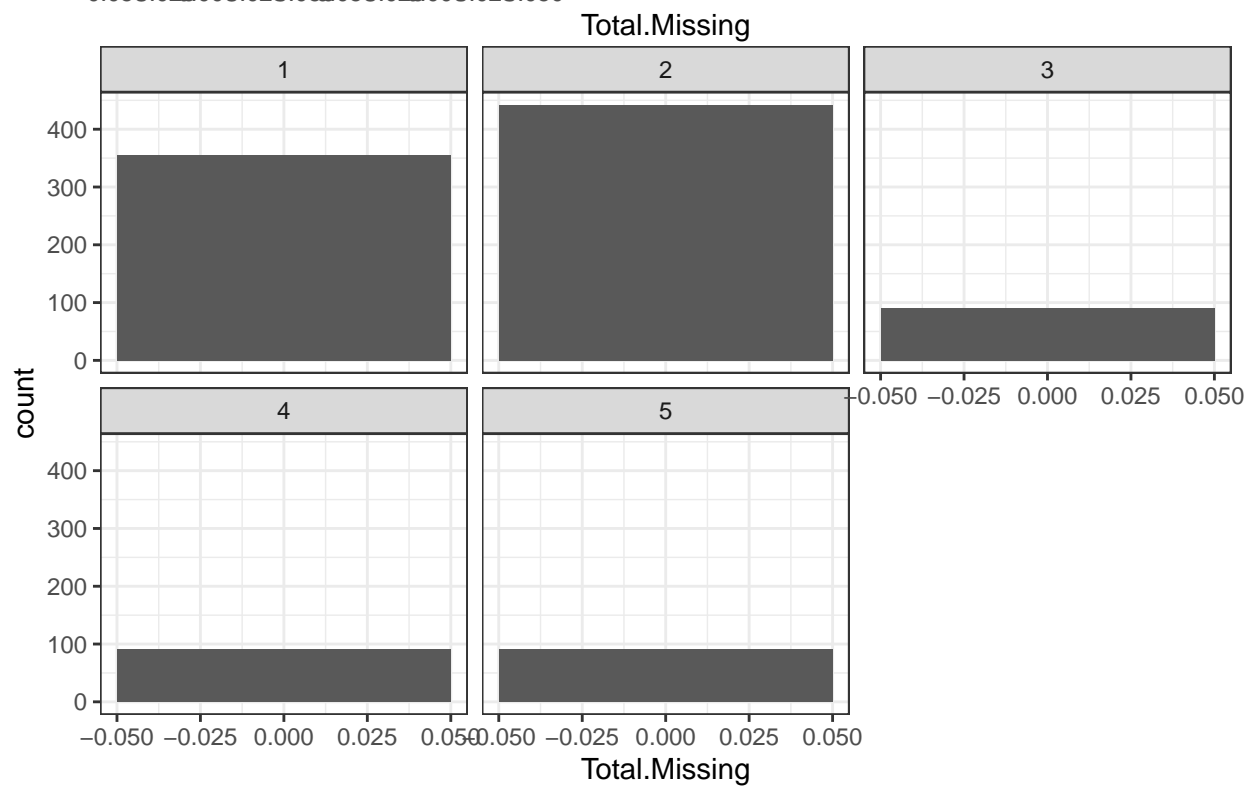
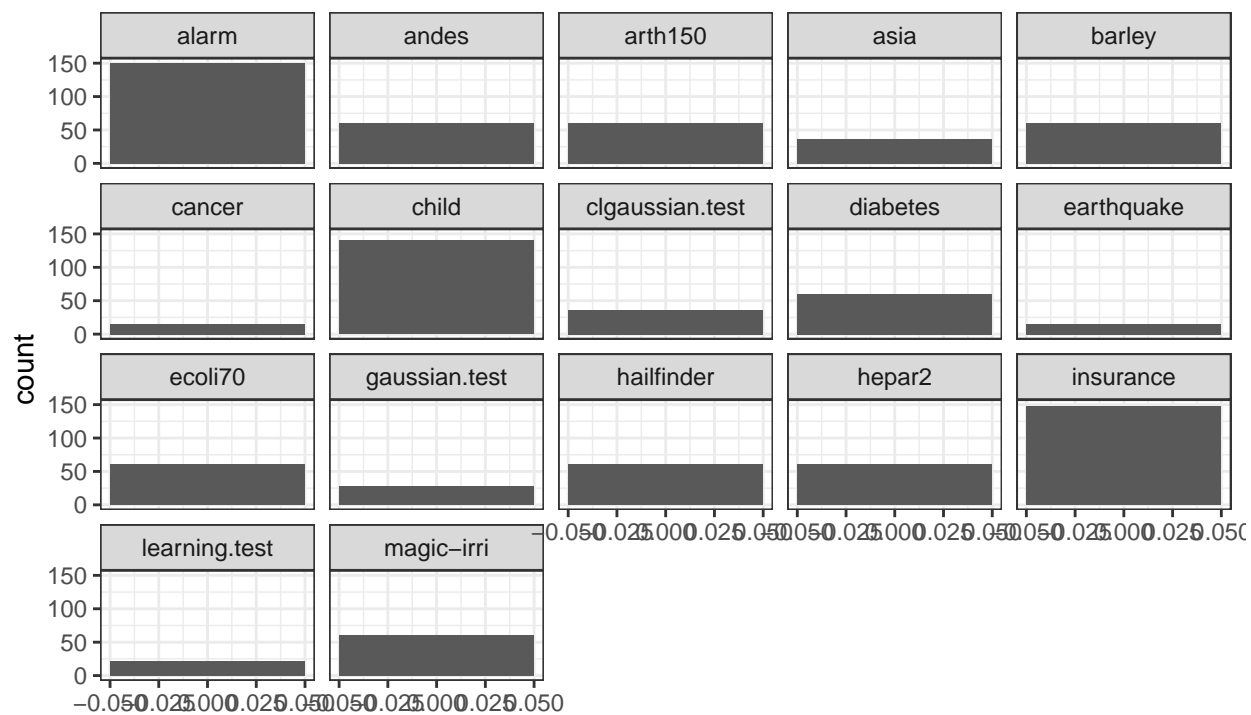


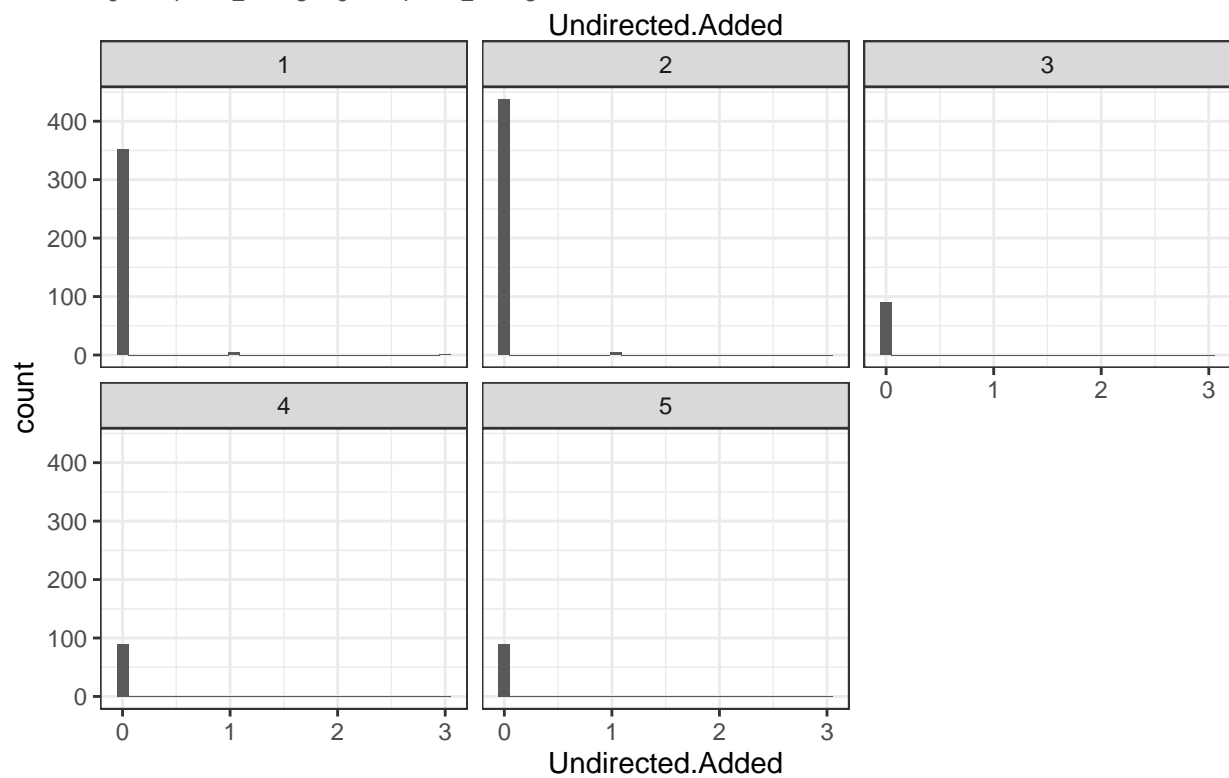
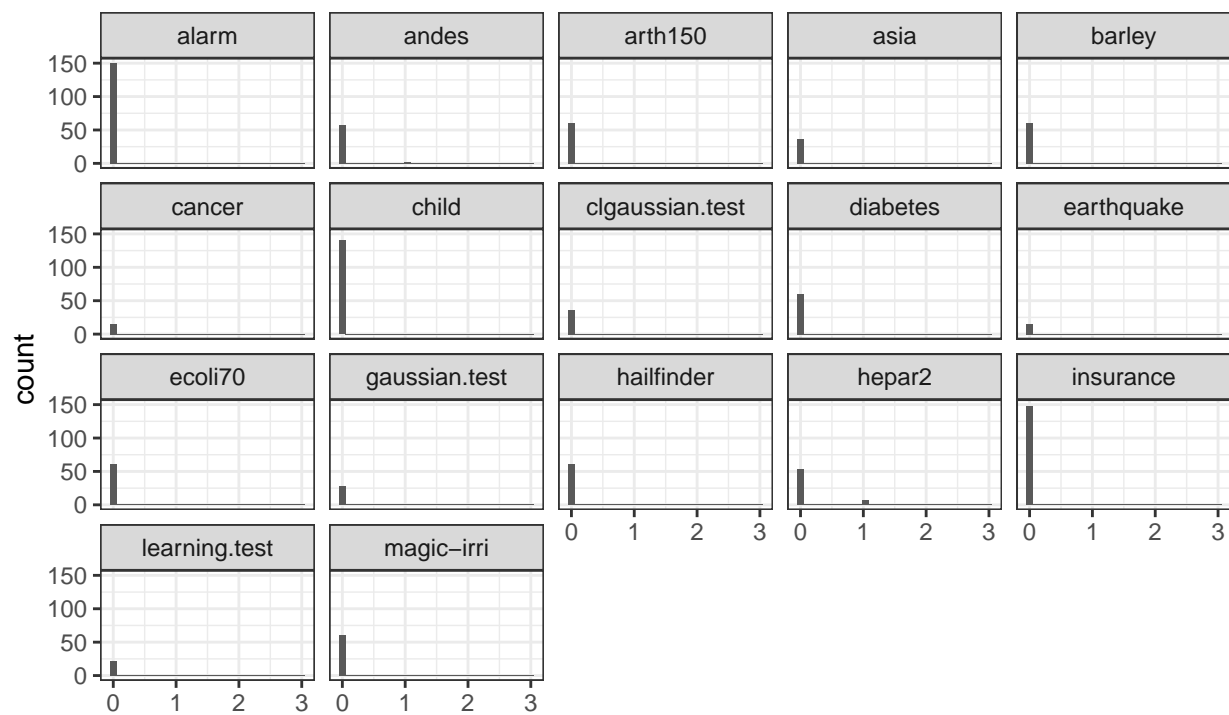
Distribution of Other Statistics

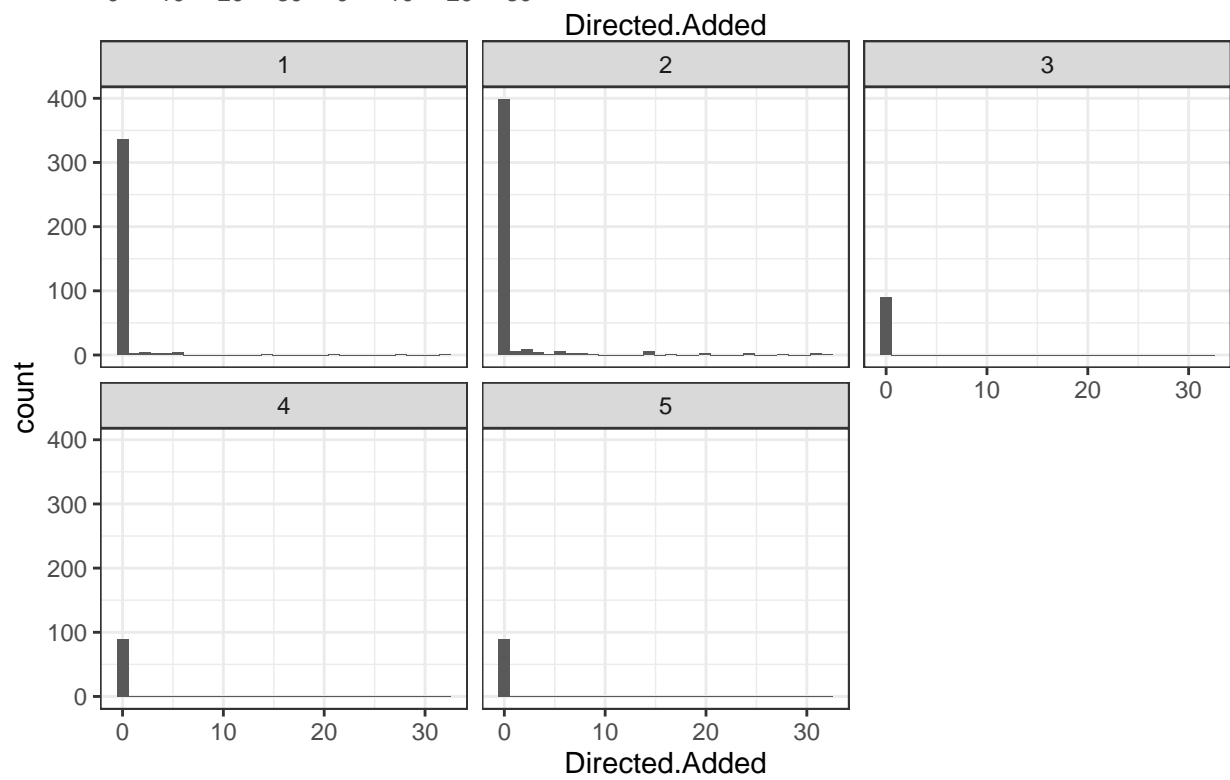
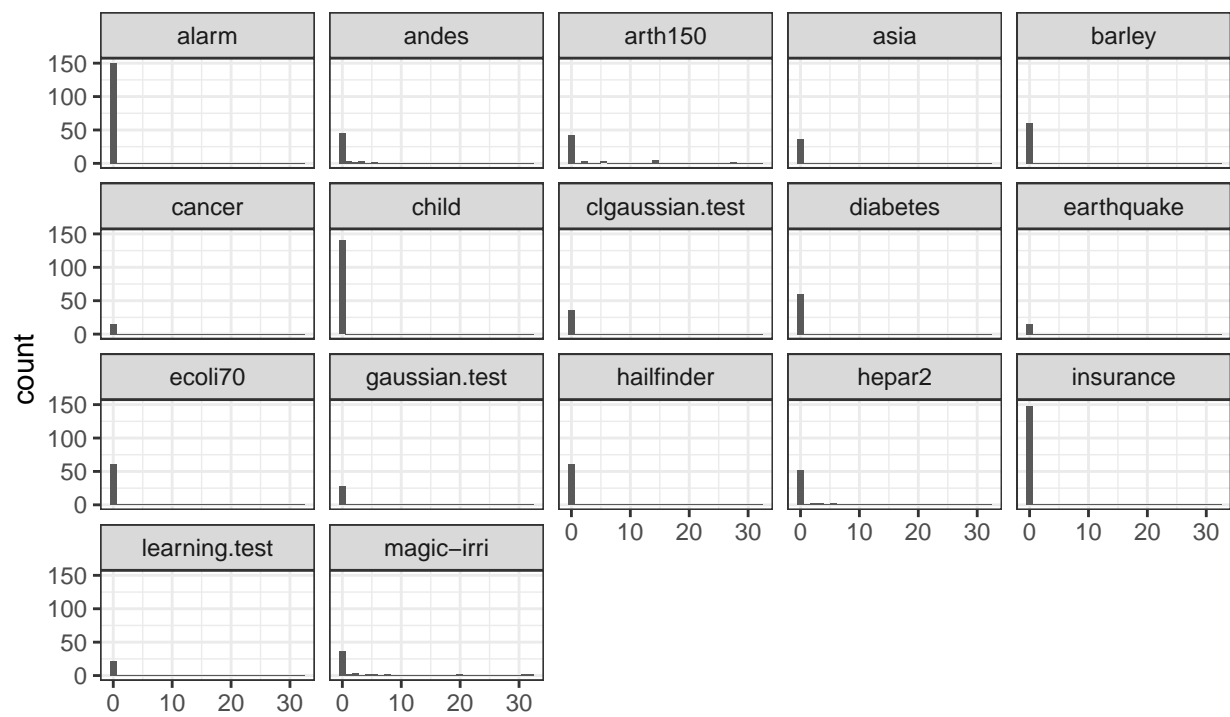
Undirected Edges Missing in Estimated CPDAG

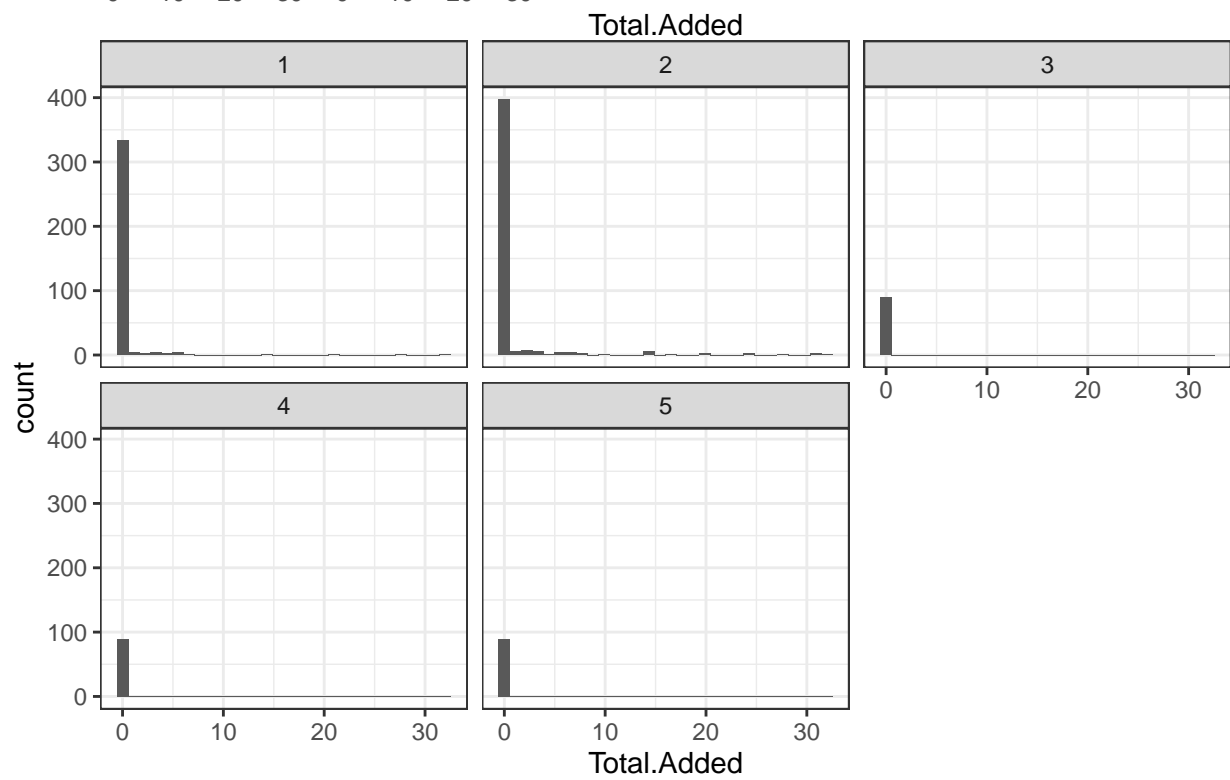
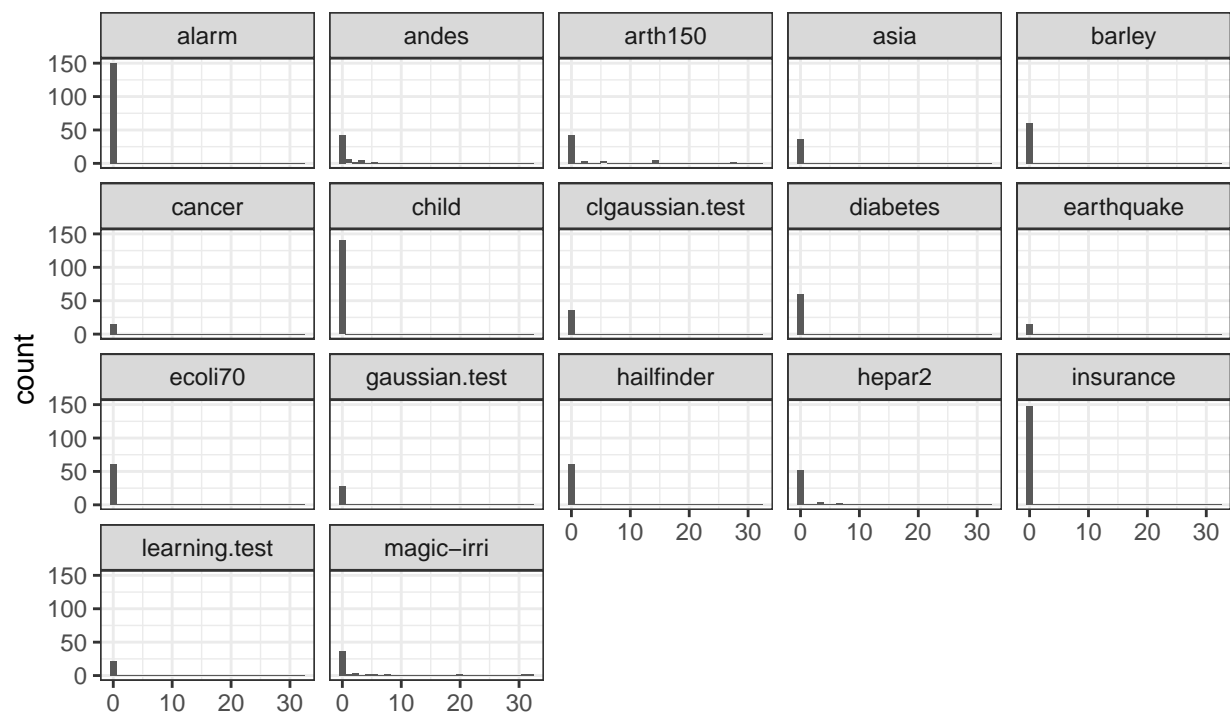


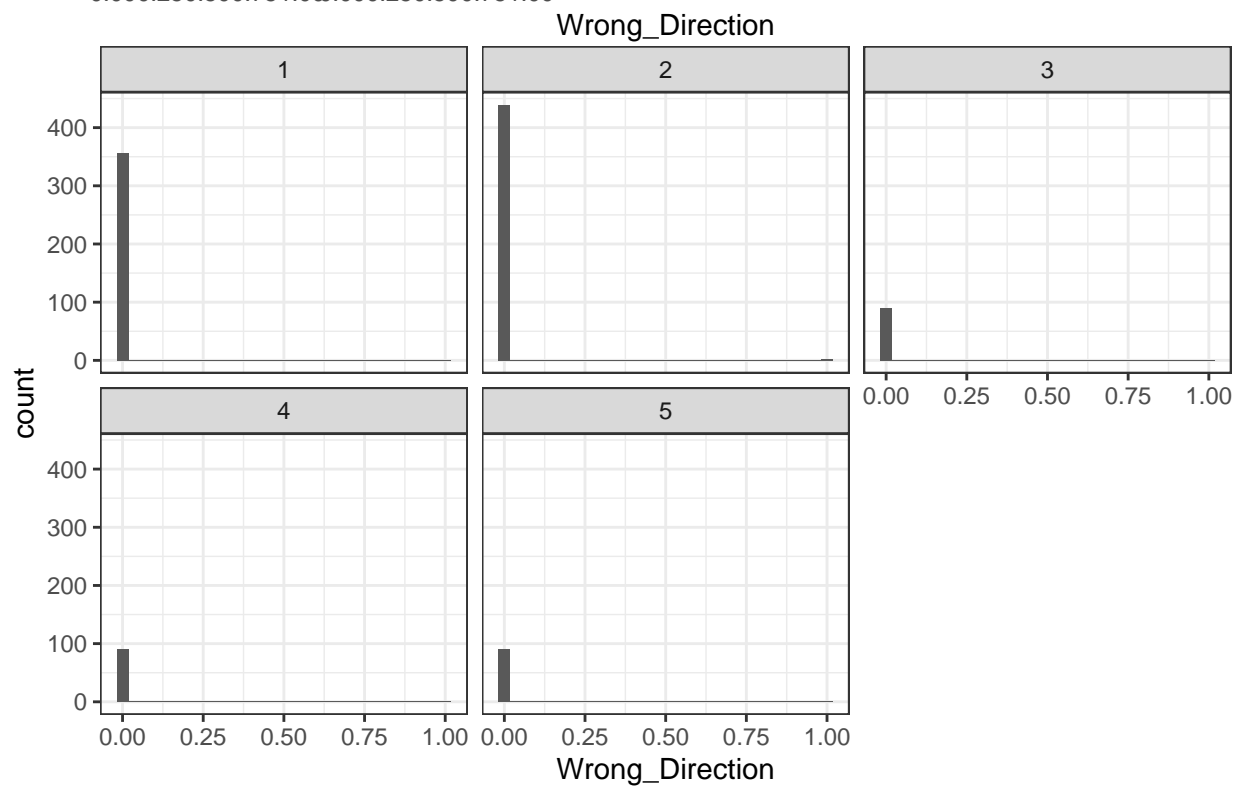
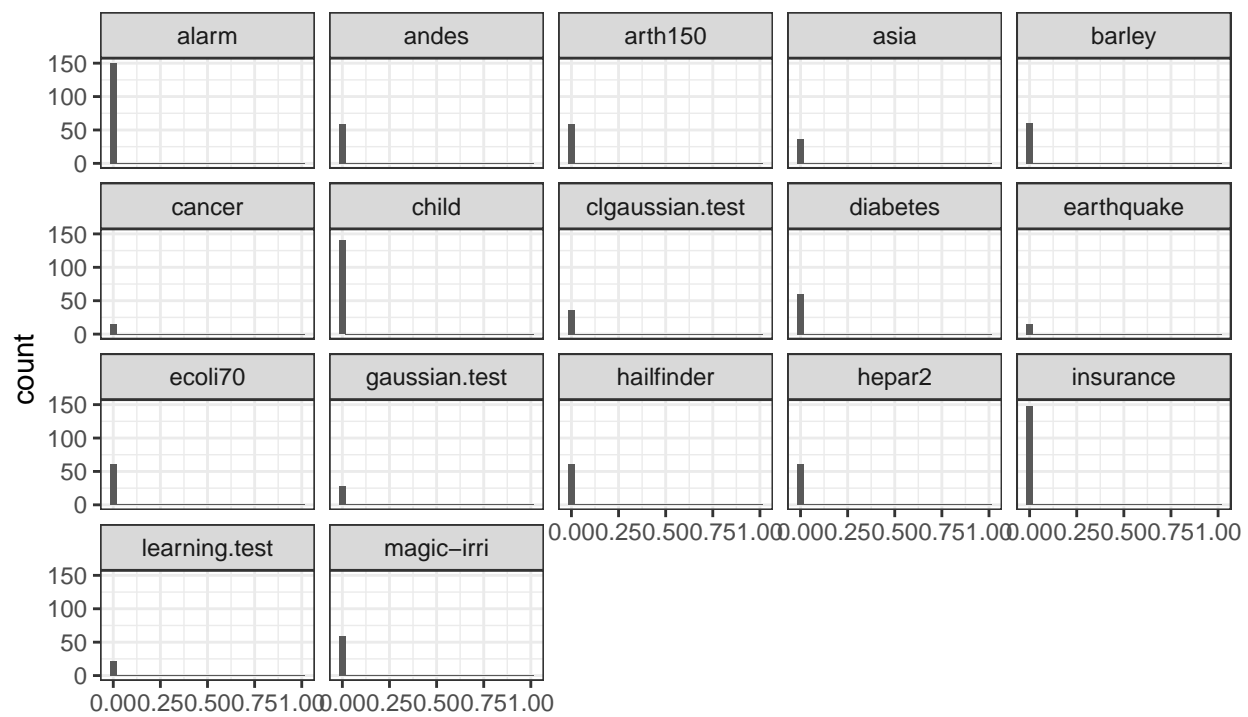


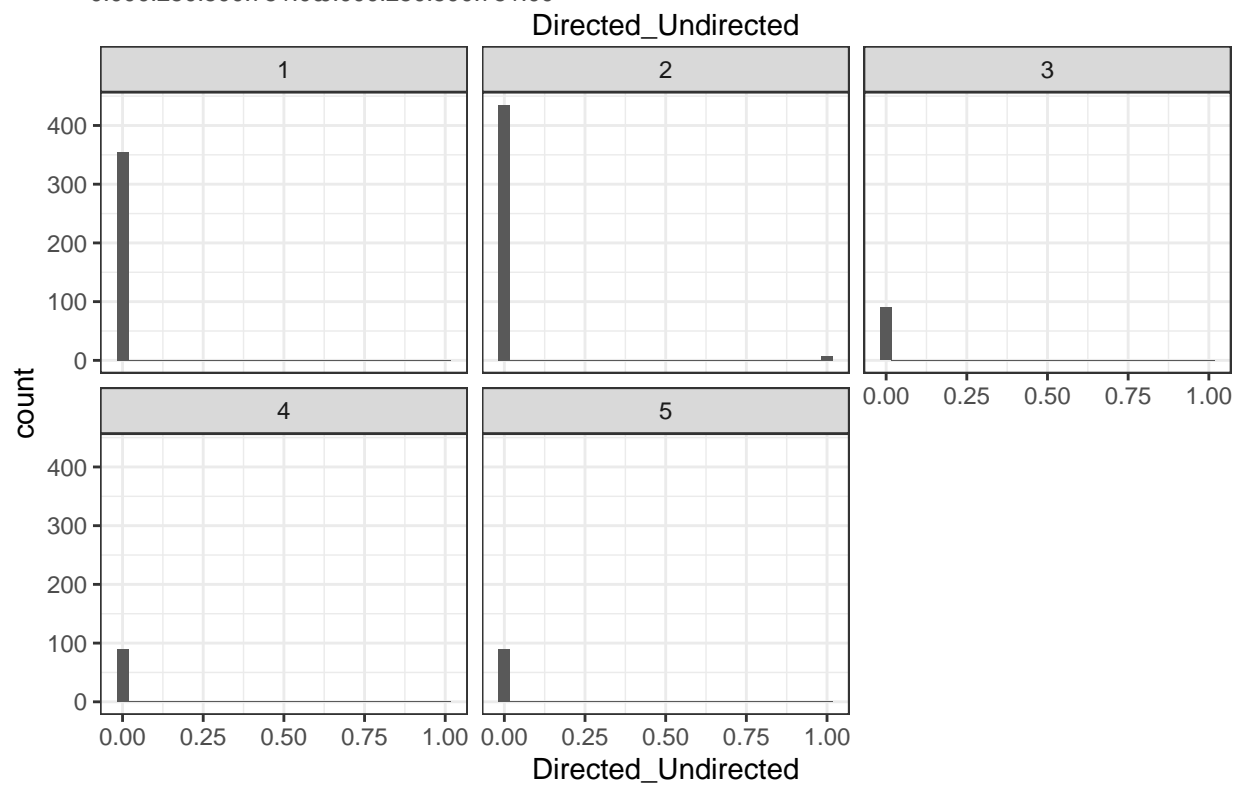
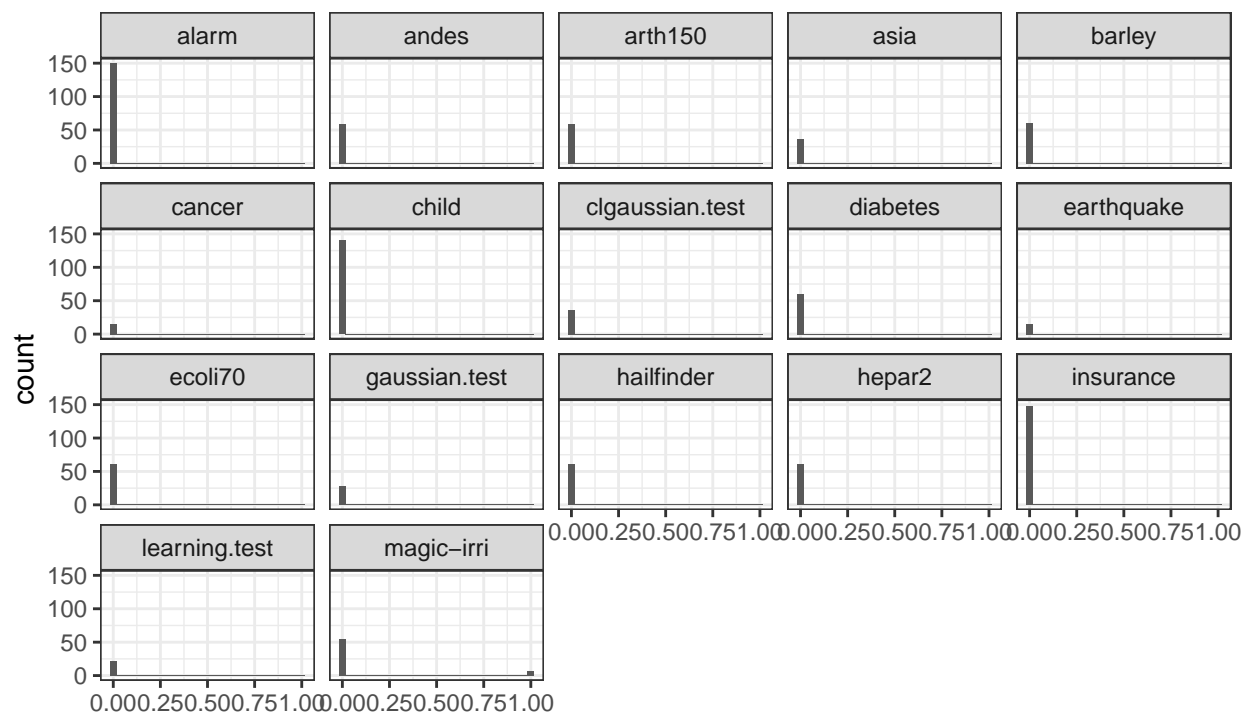


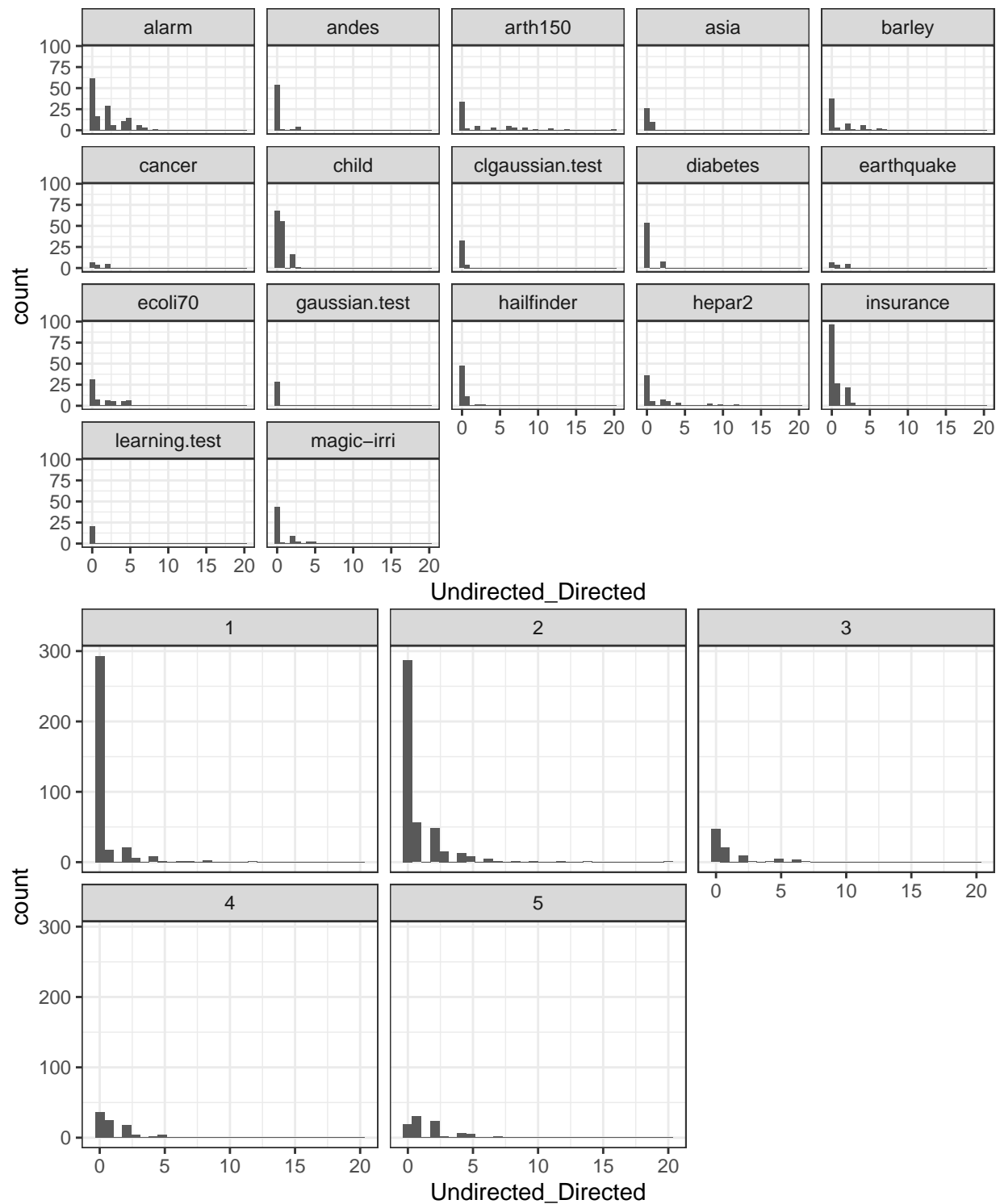












Sample Version

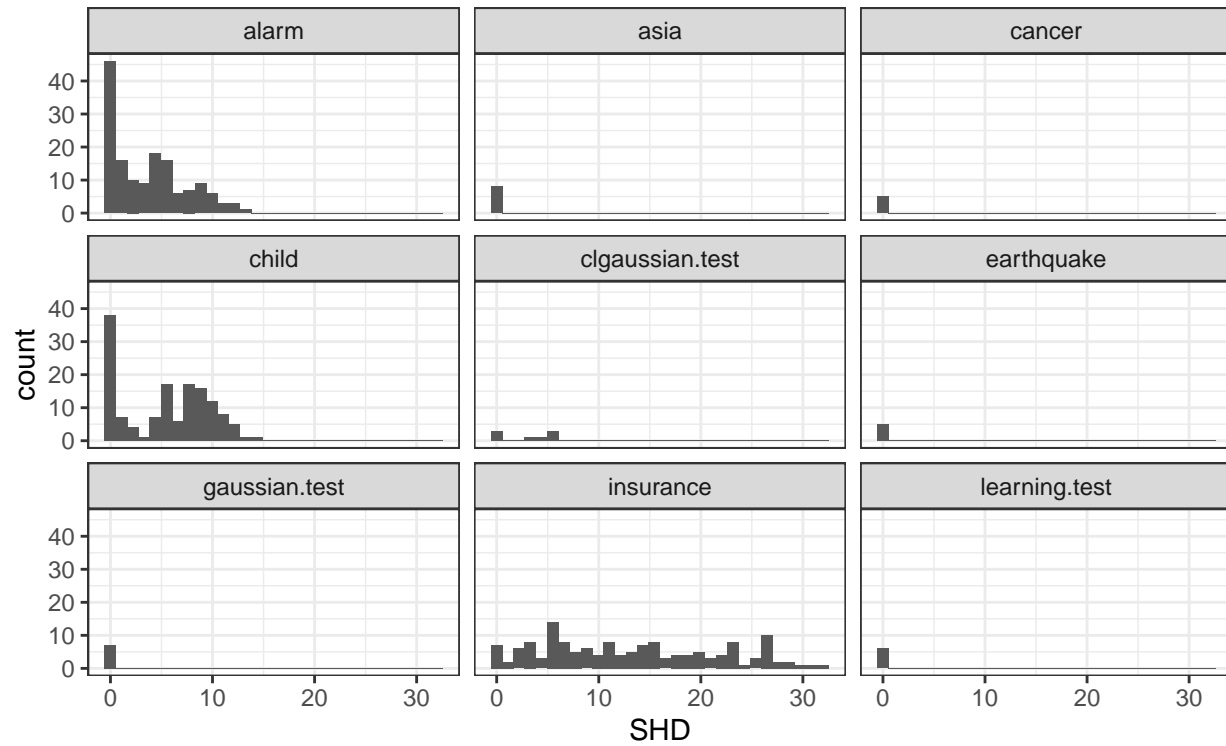
This is a preliminary display of the results. We are using a significance level of 0.05 for our hypothesis tests.

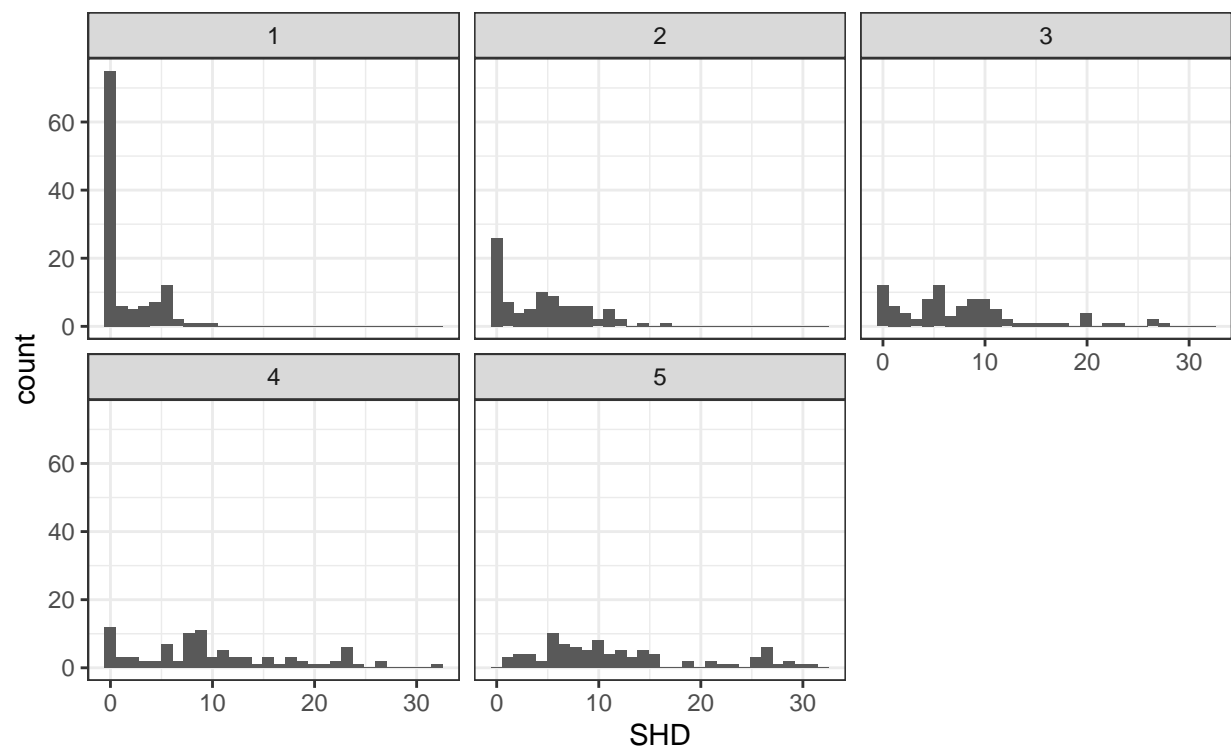
Same V-Structures

```
##
##  0  1
## 335 141
```

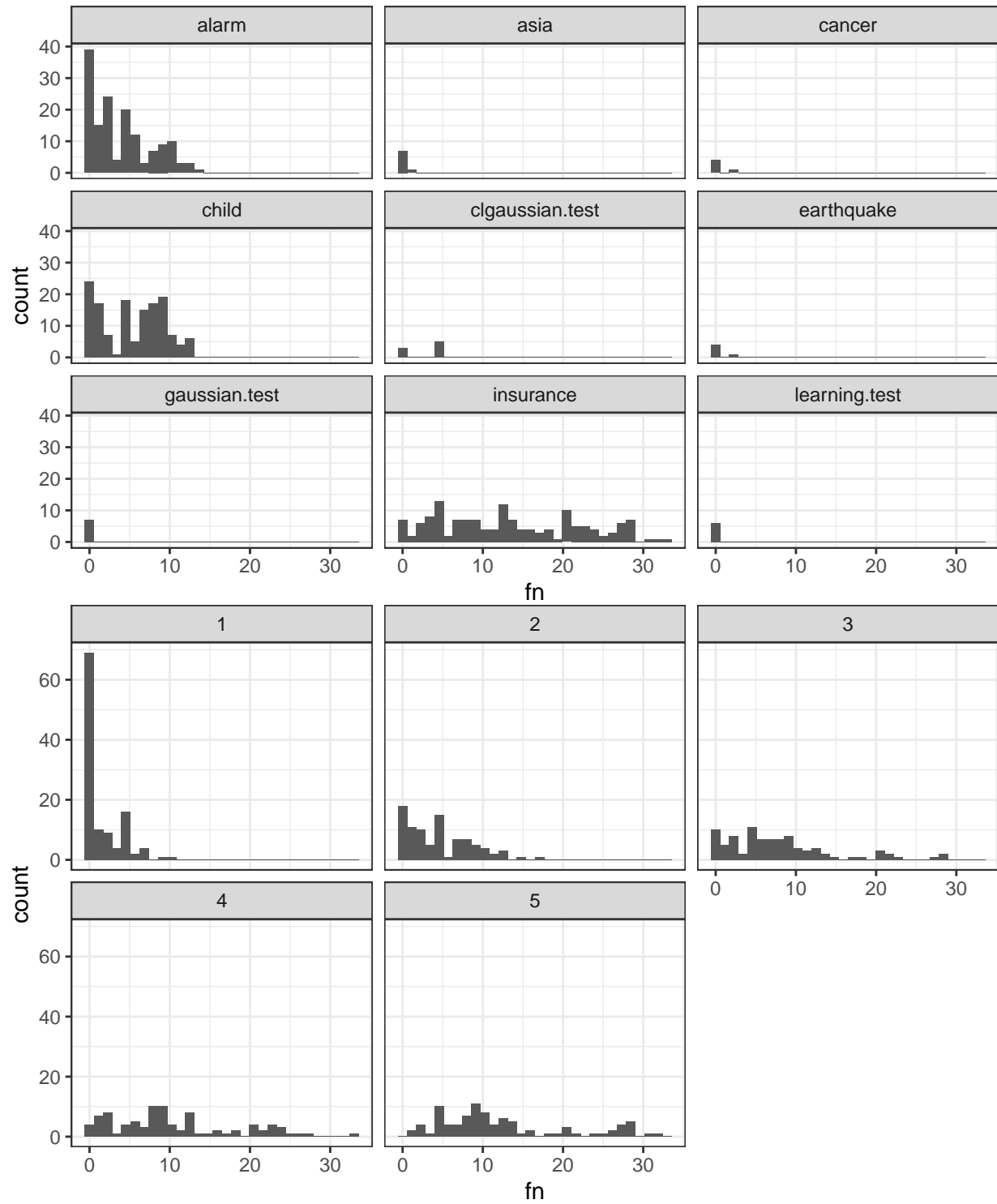
SHD

```
##
##  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## 125 25 20 19 29 29 21 20 29 31 22 19 12 7 8 4 4 3
## 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32
##  4  4  5  3  4  8  1  3  4  6  2  2  1  1  1
```

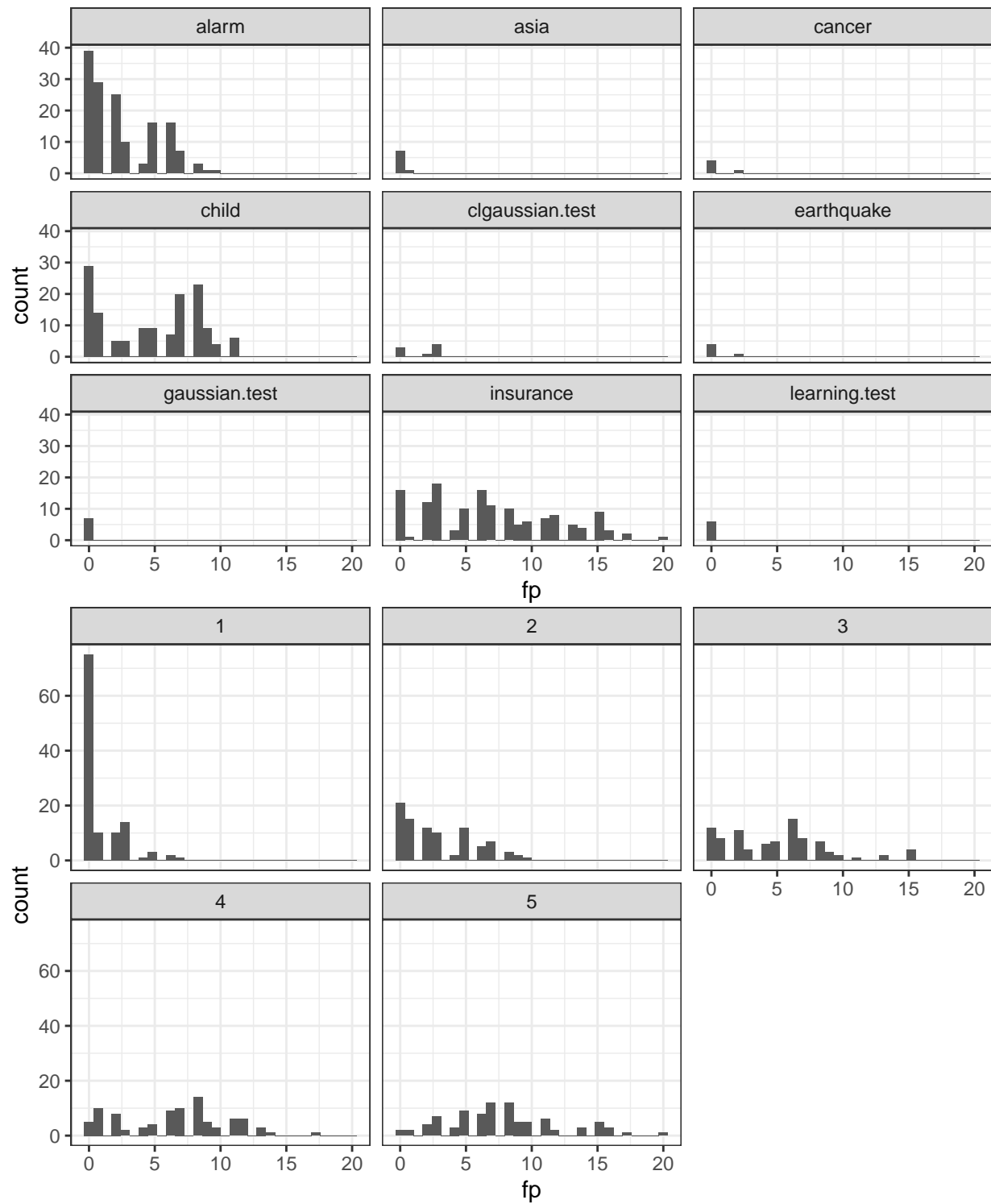




False Negatives

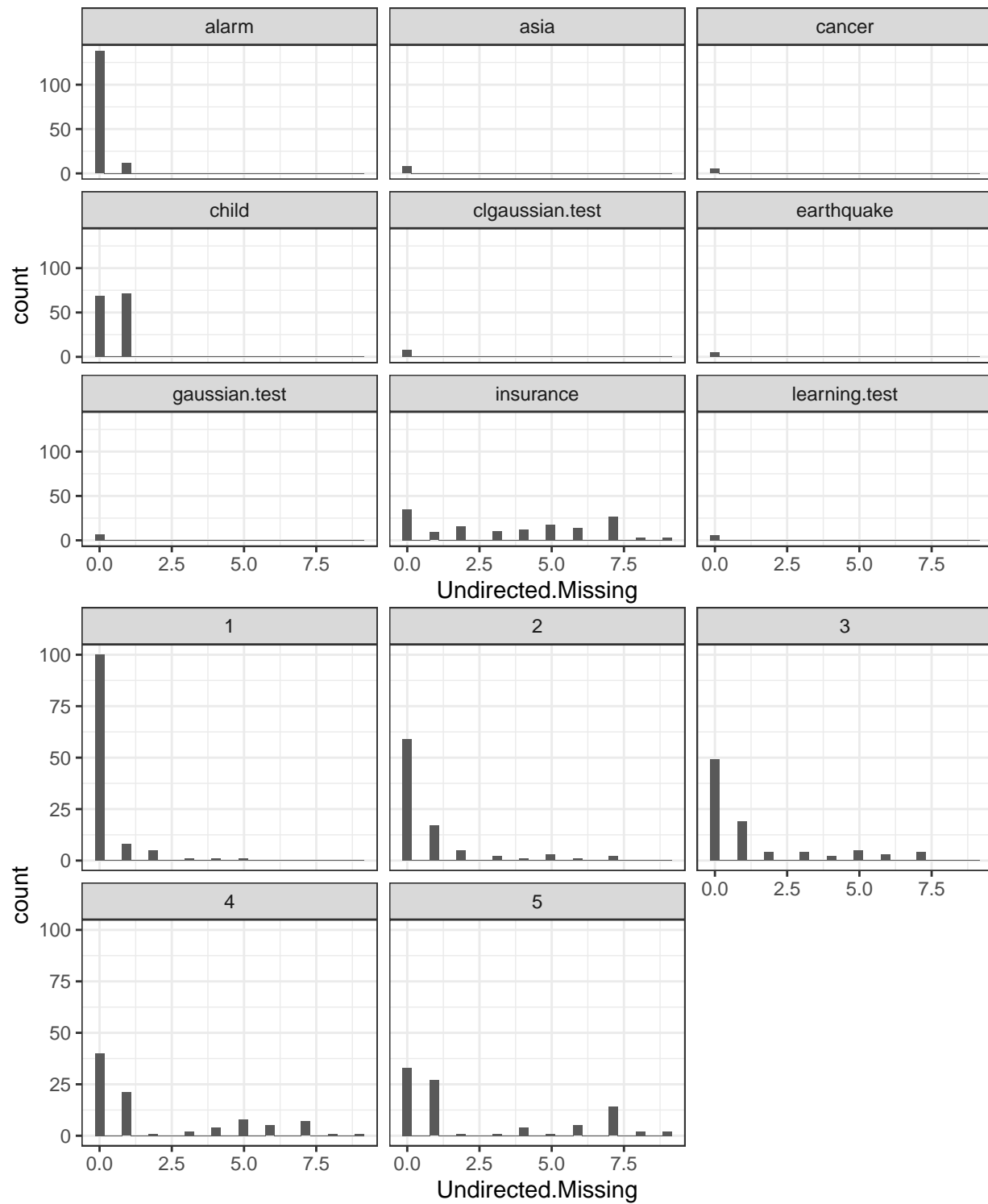


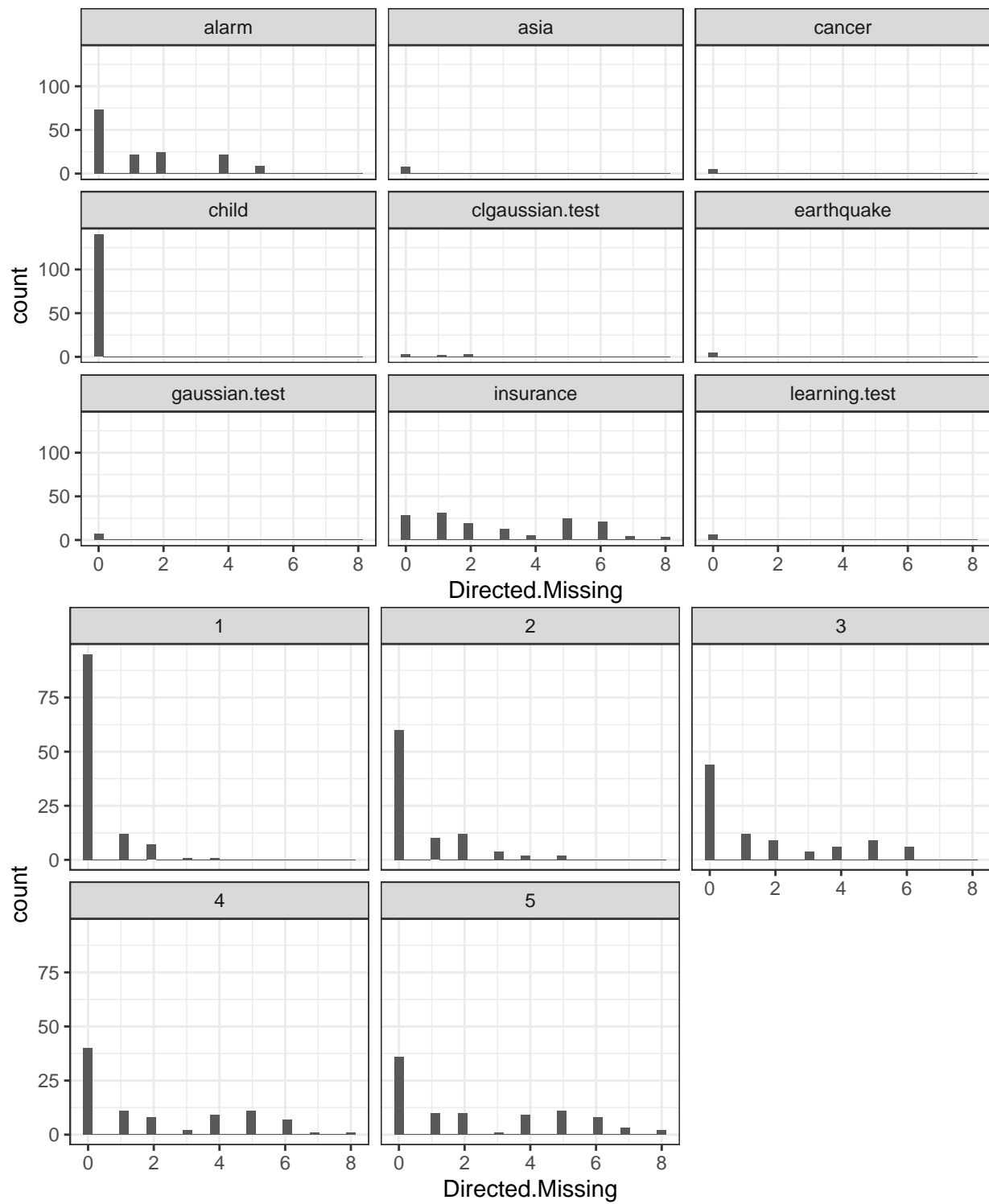
False Positives

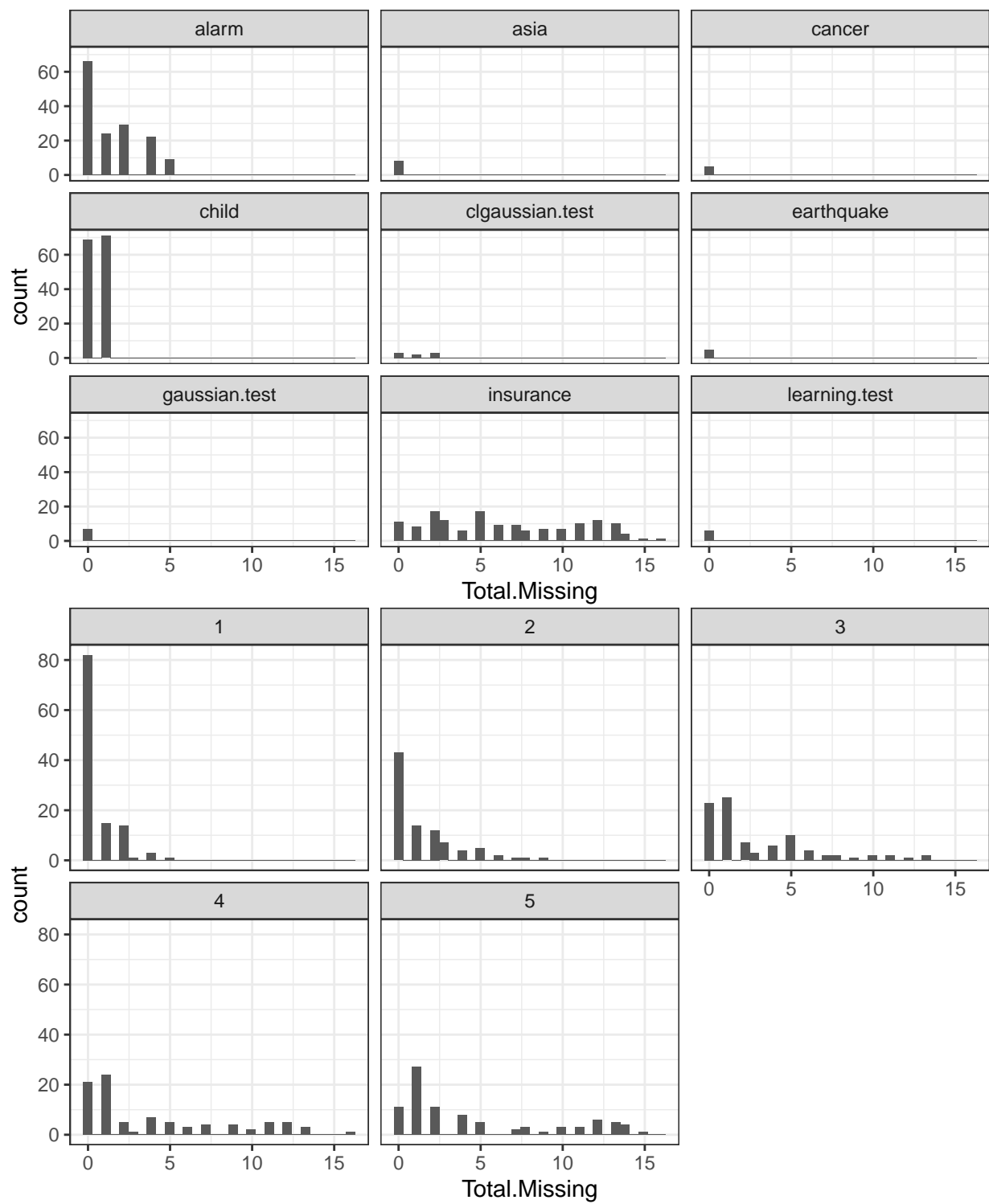


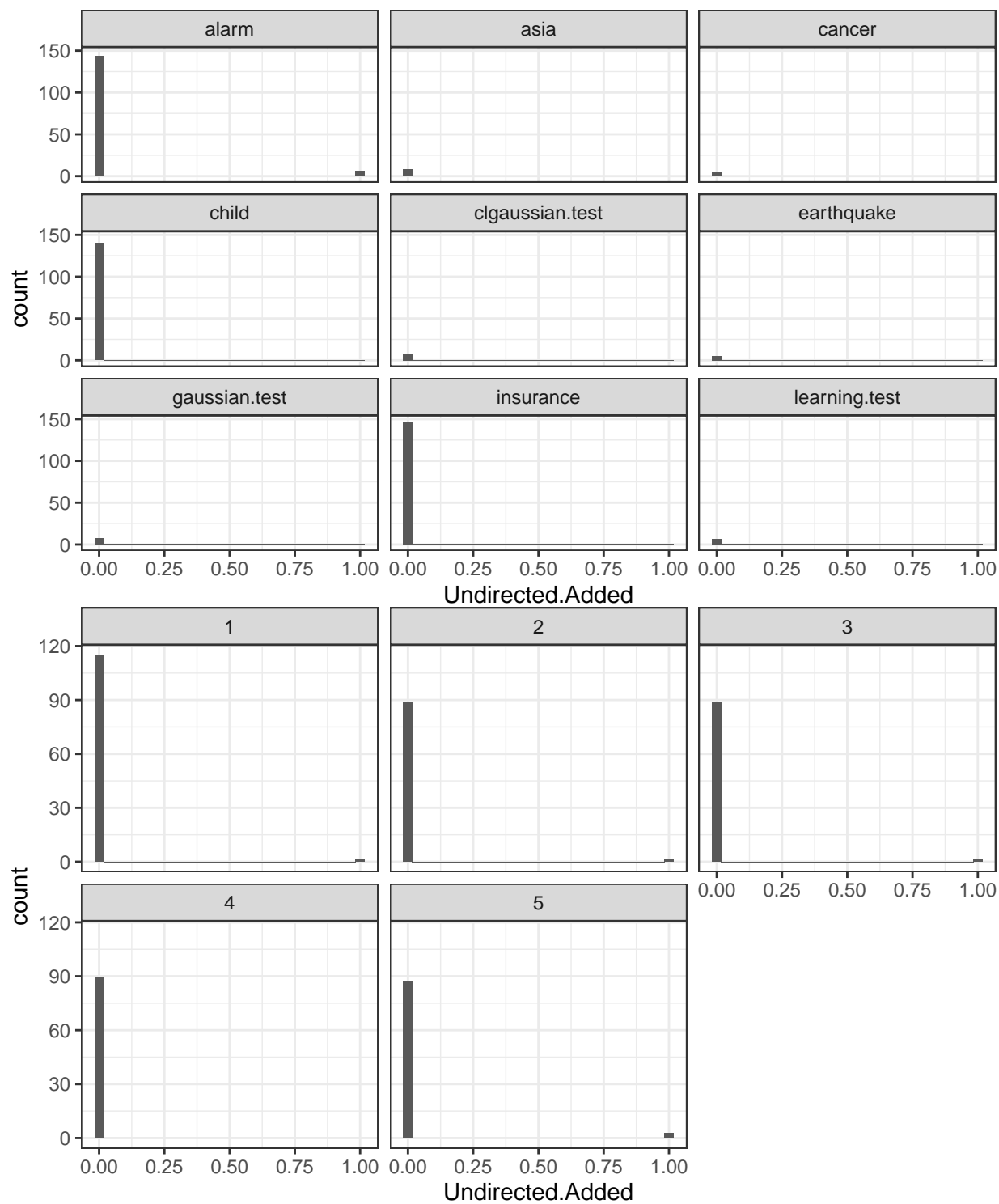
Distribution of Other Statistics

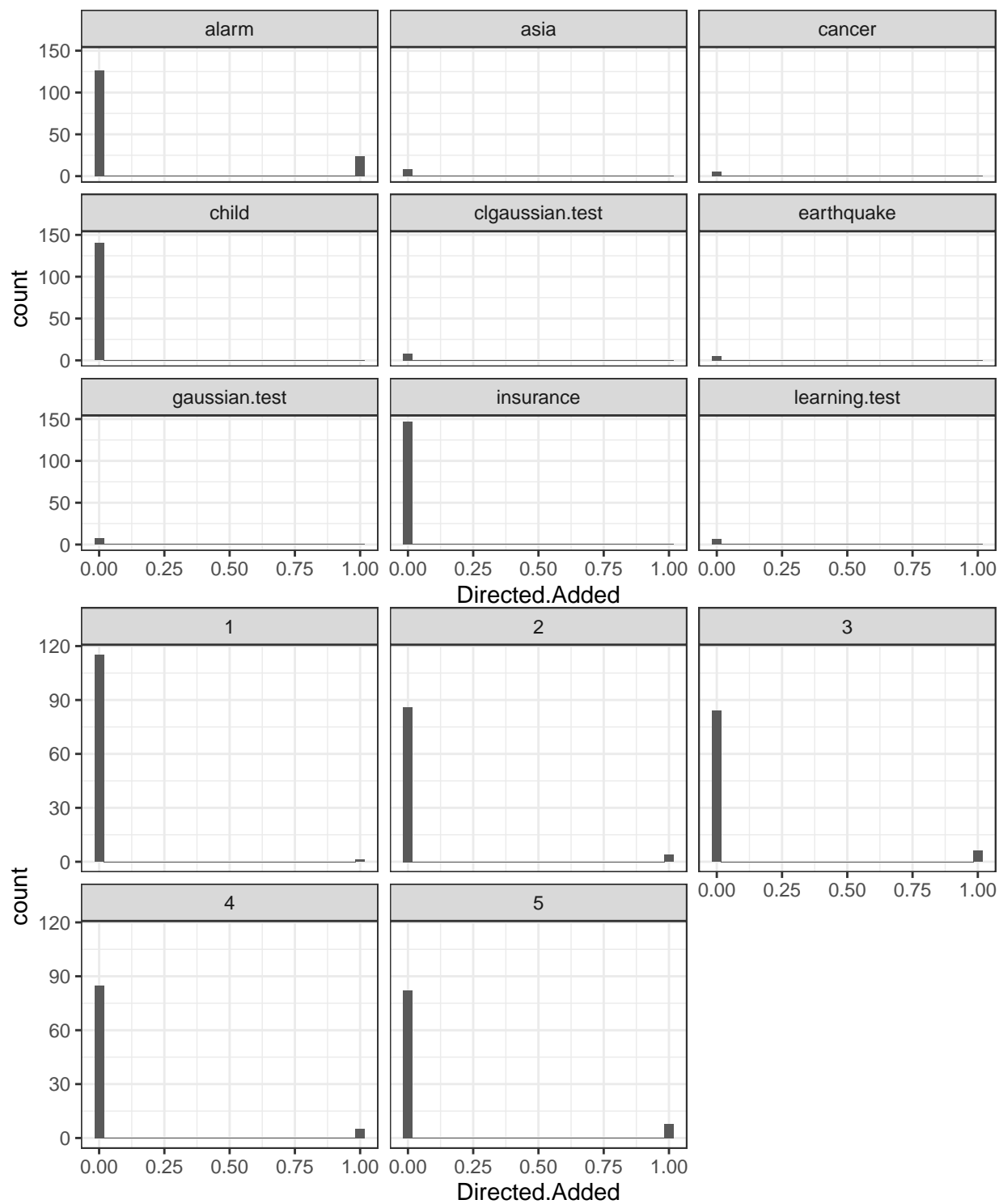
Undirected Edges Missing in Estimated CPDAG

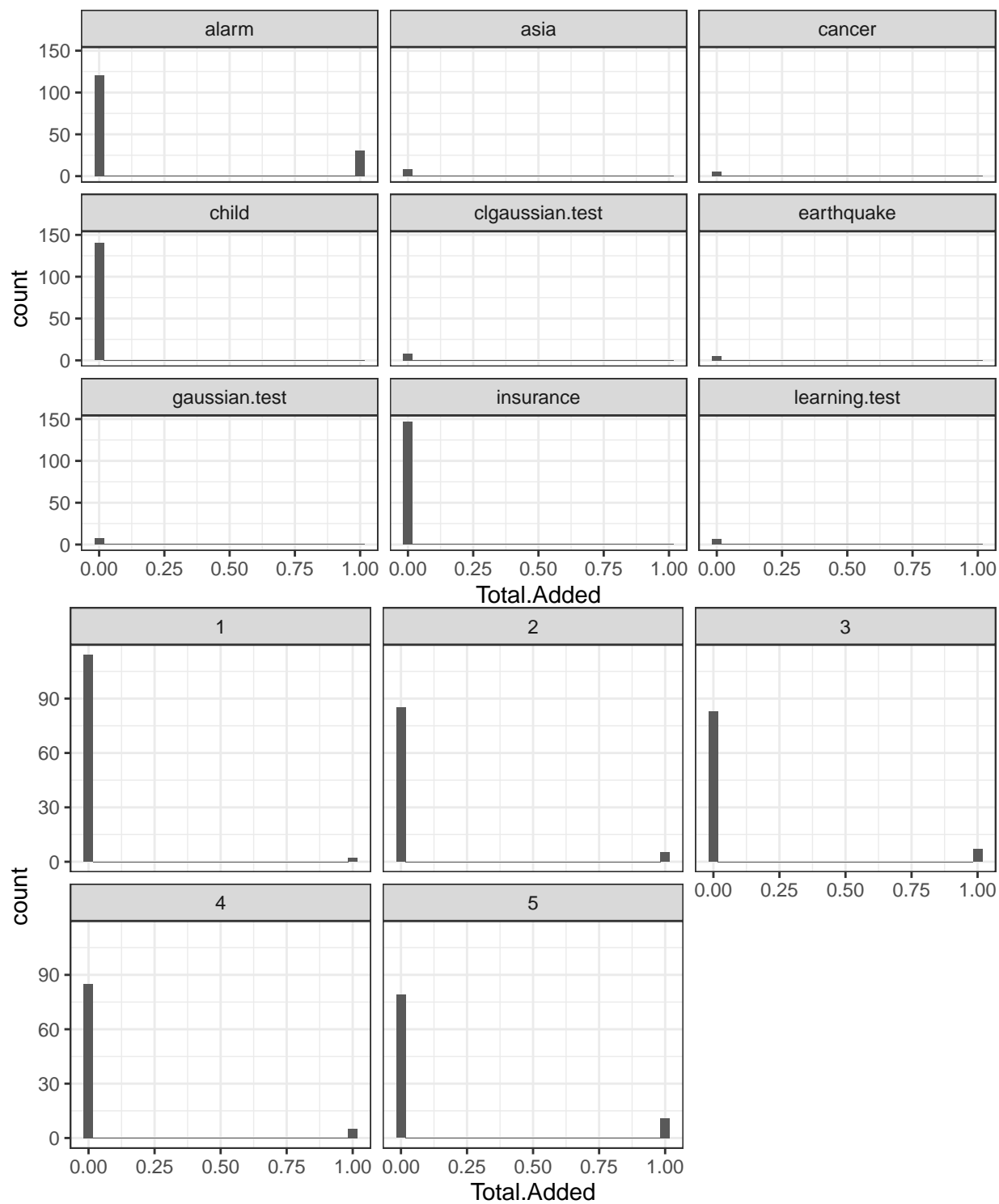


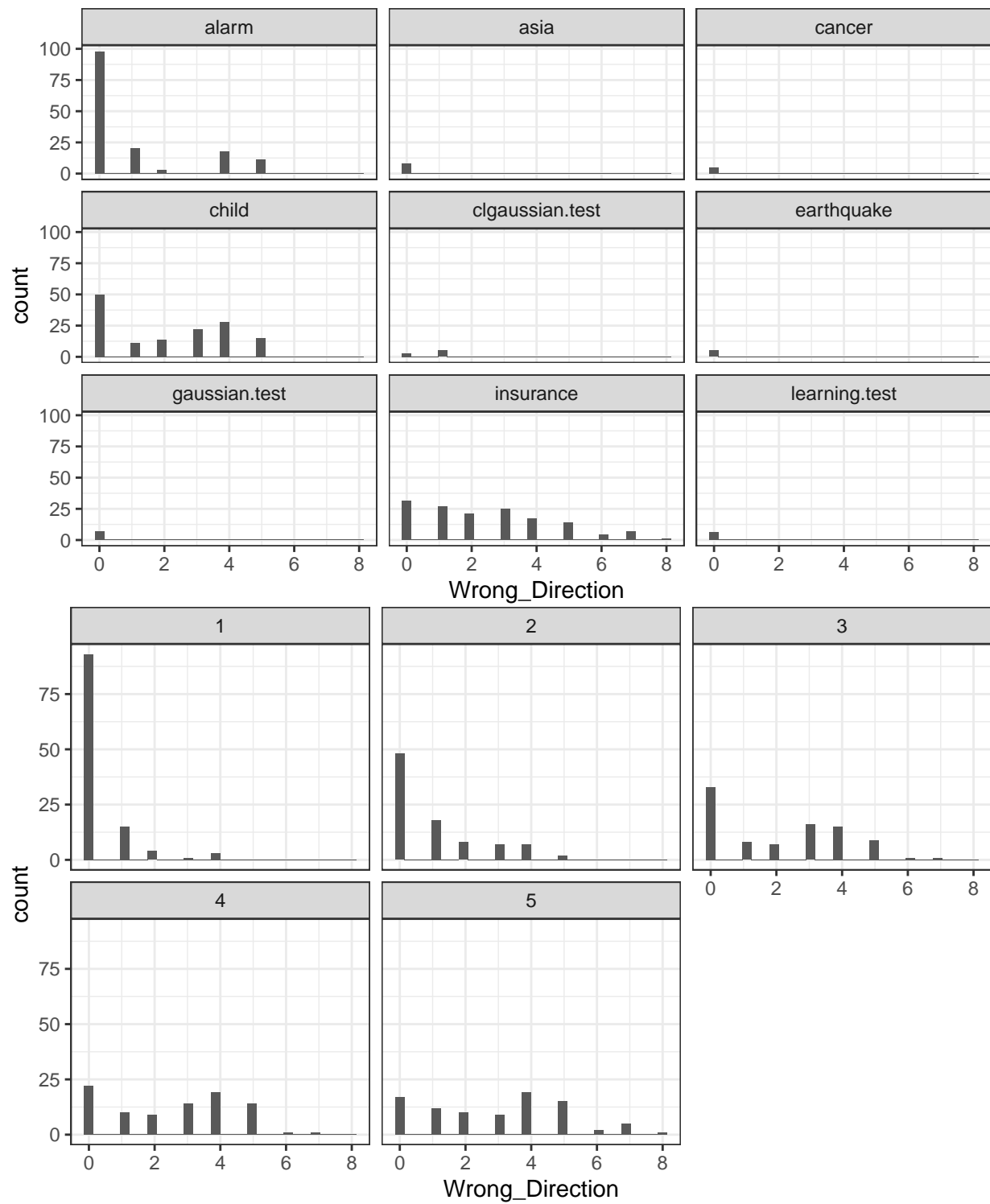


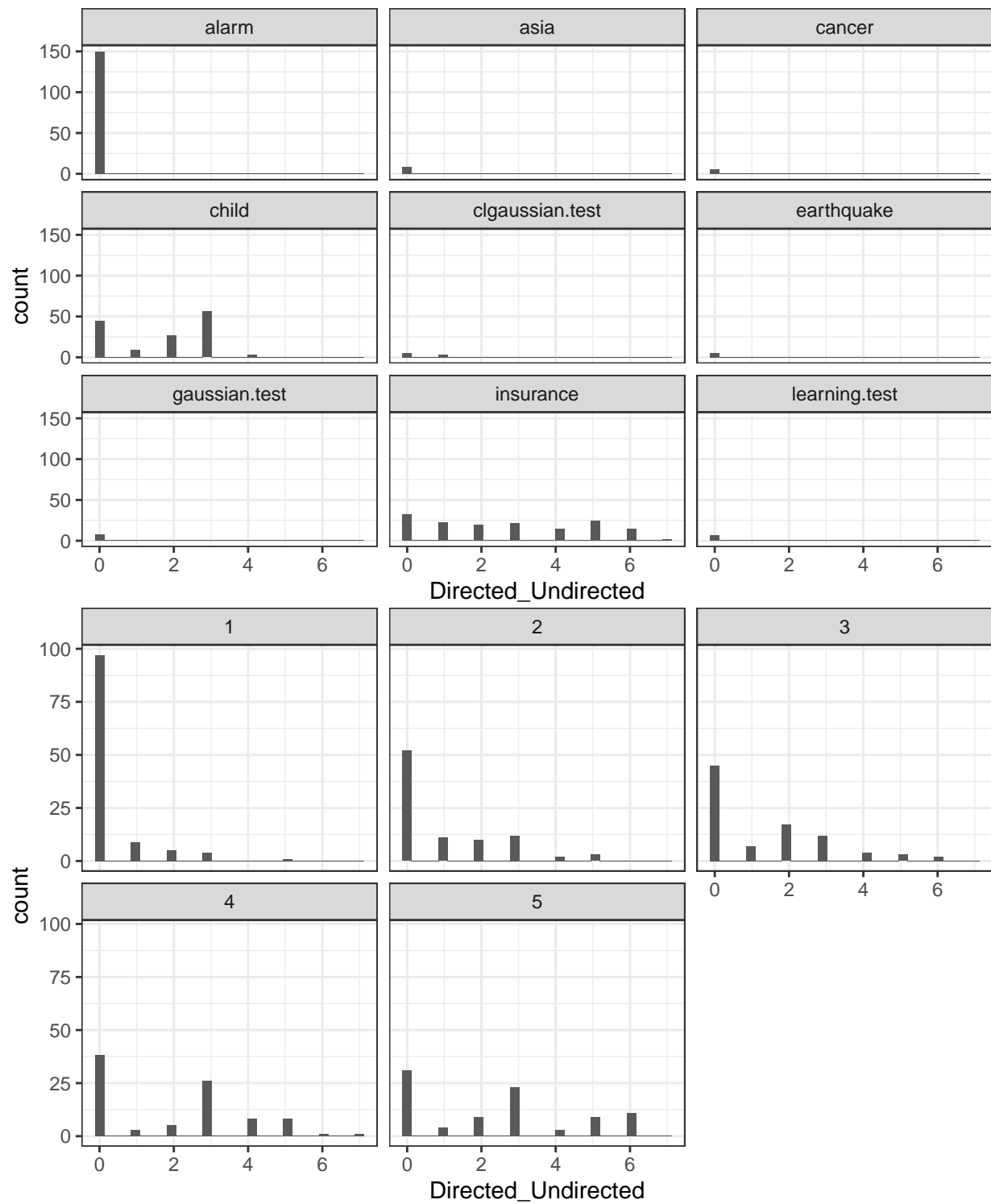


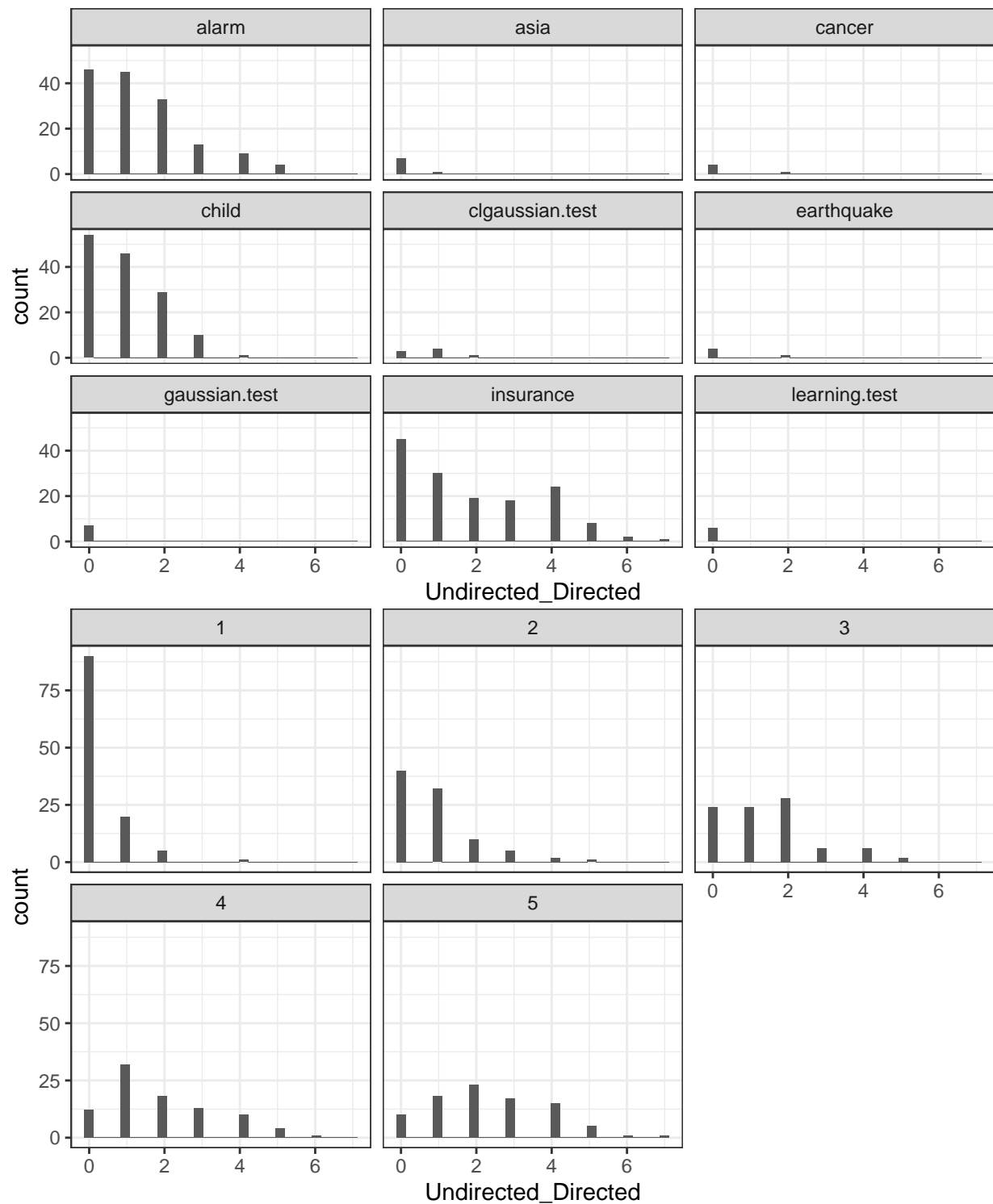












Sample Version Number 2

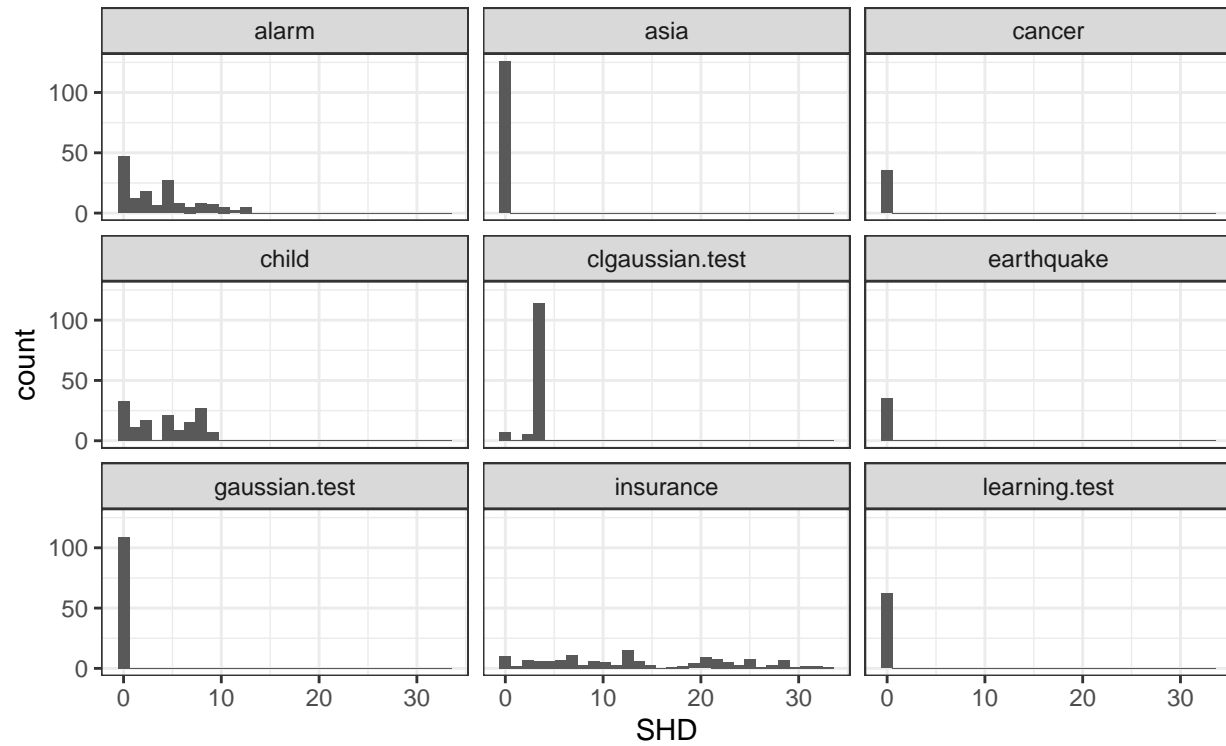
This is a preliminary display of the results. We are using a significance level of 0.005 for our hypothesis tests.

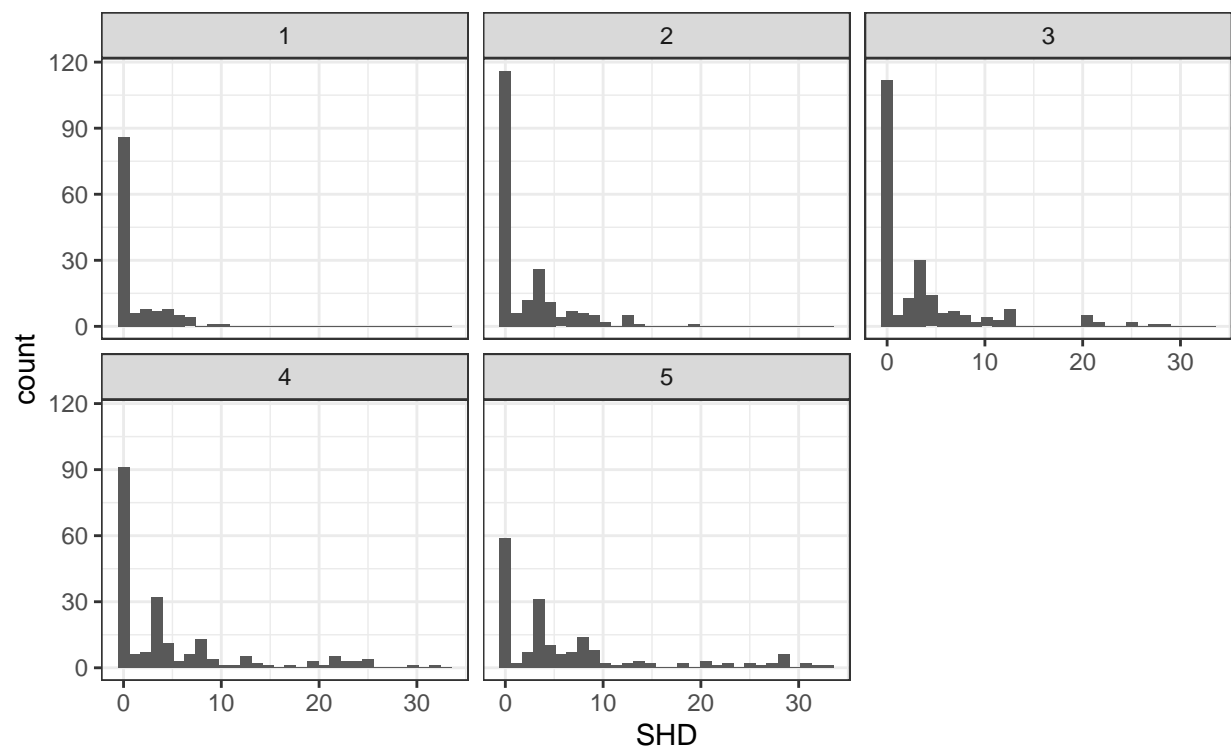
Same V-Structures

```
##
##  0  1
## 432 498
```

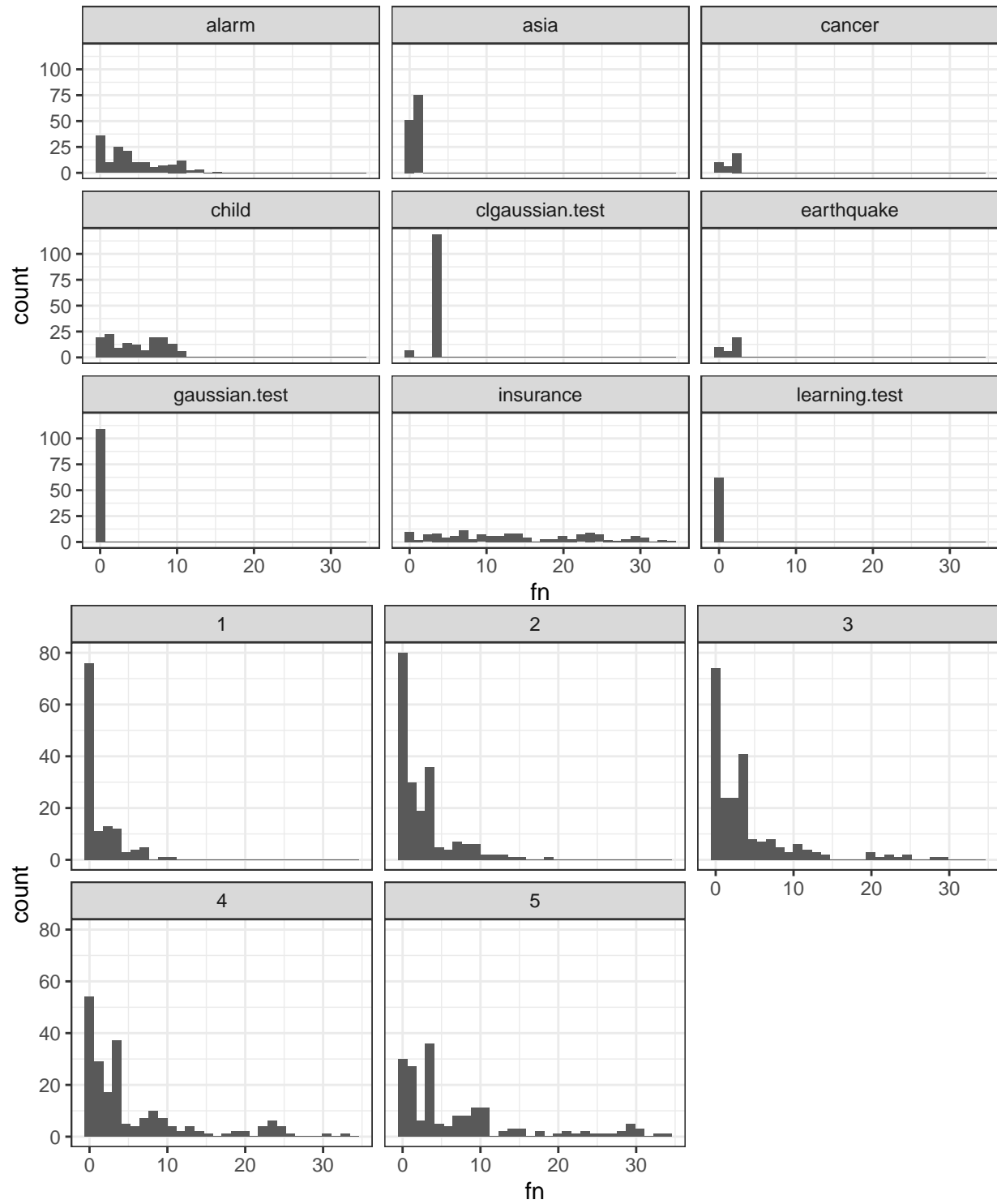
SHD

```
##
##  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 17 18
## 464 25 47 126 25 29 24 31 38 20 10 5 7 13 6 3 1 2
## 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
##  4  5  4  8  5  3  8  1  3  2  5  1  2  2  1
```

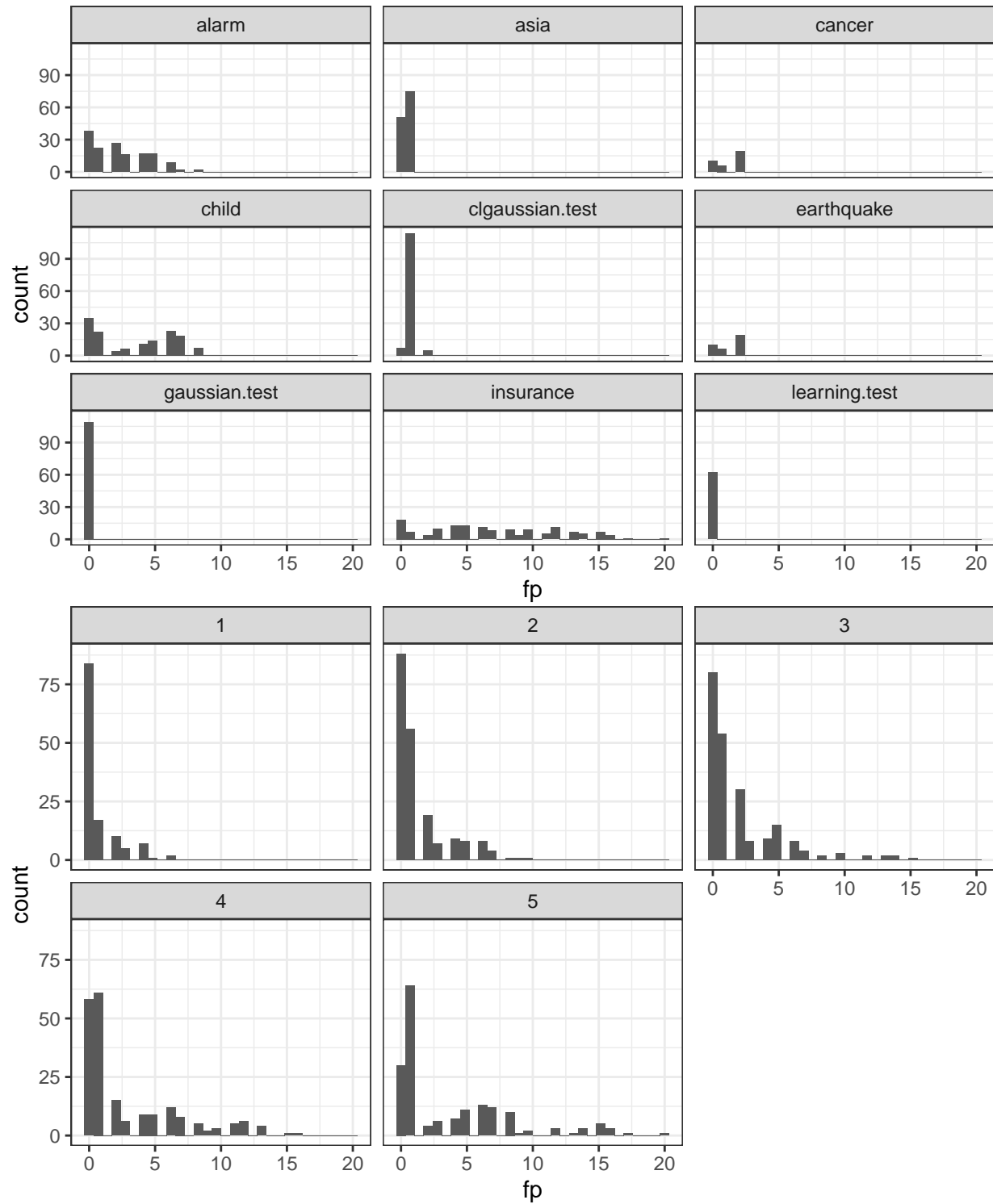




False Negatives



False Positives



Distribution of Other Statistics

Undirected Edges Missing in Estimated CPDAG

