

Supplementary Materials for Comparison of Methods for Imputing Social Network Data

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1 Results on Network Statistics

We analyzed NRMSEs on network statistics in networks with 100 nodes corresponding to Figures 1 to 6 of this document.

- **Density:** For missing data conditions other than the MNAR1 tie and mix non-response conditions, multiple methods worked well including BERGMs, RE, DP, and RF, where RE had the best performances. However, under the MNAR1 tie and mix non-response conditions, NRMSEs were much larger for all methods except MICE and BERGMs, possibly due to the larger proportion of missing present edges compared to other conditions. Different from other methods, MICE and BERGMs had slightly higher NRMSEs of density in Simulations 2 and 3 than in 1 and 4. Overall, MICE and BERGMs performed best on recovering density under the MNAR1 tie and mix non-response conditions.
- **Reciprocity:** A similar pattern as for density held for the MNAR1 tie and mix non-response conditions. Reciprocity NRMSE patterns were also similar across the 4 simulations. While DP and KNN worked best when the missing data condition was not MNAR1 tie or mix non-response, BERGMs performed better under the MNAR1 tie or mix non-response condition.
- **Gwesp:** BERGMs again had good performance under the MNAR1 tie or mix non-response condition. RE and DP had better performance in other conditions. NRMSEs of gwesp were higher than that of density or reciprocity.
- **HomophilyA:** KNN and RF had the worst performance on recovering the homophily statistics of covariate A, whereas DP had the best overall performances across all conditions. In Simulations 3 and 4, the MNAR conditions had slightly worse NRMSEs than those in Simulations 1 and 2. The NRMSEs of homophilyA were relatively high compared to other statistics, suggesting that Moran's I on covariate A was difficult to recover.
- **HomophilyB:** For this statistics, simpler methods such as RE, DP, and null-tie imputation had better performances than the others, and the simpler networks in Simulation 1 had the best NRMSEs. BERGMs' performances were worse in the MNAR1 tie or mix non-response condition than in other conditions, whereas other methods did not differ much by missing data mechanisms. MICE had worse performances under tie non-response conditions, and PA had worse performances under actor non-response conditions. Overall, the NRMSEs of homophilyB were quite small compared to the other statistics.

- HomophilyC: The results for the homophily statistics of covariate C did not differ much across sample sizes, missing data mechanisms, types, and imputation methods. NRMSEs of homophilyC mainly differed across the 4 simulations. The NRMSEs were much larger in Simulation 1 where the networks were simpler than in the rest of the simulations.

2 Results on ERGM Coefficients

We analyzed NRMSEs of ERGM coefficients for networks with 100 nodes. In some simulations, the coefficients for some ERGM terms were set to be 0, so they were not interpretable compared to those of the non-zero ones. Here, for each term, we only compared simulations with the corresponding coefficients set to be non-zero. As we expected, estimating ERGM coefficients directly gave closest values to those of the complete networks in most conditions. The analysis below focused more on the imputation methods. The detailed results corresponding to the analysis can be found in Figures 7 to 14.

- Edges: All methods performed similarly in Simulations 2 to 4 whereas performances on Simulation 1 was noticeably worse. Differences in missing data conditions were negligible except in the MNAR1 tie and mix non-response conditions where the NRMSEs tended to be larger.
- Mutual: The NRMSE patterns for the mutual term were similar across simulations but different across missing data conditions. In particular, the MNAR1 tie and mix non-response conditions should be differentiated from the other missing data conditions, and performance on actor non-response conditions were also worse than others in specific methods such as MICE. DP had the best performance out of all imputation methods followed by the BERGMs. RE had the worst mutual NRMSEs.
- NodematchB: We only compared the nodematchB coefficients in Simulations 2 to 4 because they were set to be 0 in Simulation 1. Although the NRMSEs were relatively low, performances of different methods differed. BERGMs worked well in conditions other than MNAR1 tie or mix non-response ones. Further, the BERGMs worked almost as well as directly estimating the ERGM coefficients in Simulation 4. MICE and RE had higher NRMSEs than others, and the rest had similar performances.
- NodematchC: The MNAR1 tie and mix non-response conditions were again recovered worse than others. Not counting these conditions, the more complex BERGM2 algorithm had NRMSEs closest to directly estimating the ERGM coefficients, especially under the MAR and MCAR mechanisms in actor and mix non-responses. In this case, MICE and KNN had some of the worst performances, however, overall NRMSEs were quite small.
- NodecovA: When not counting the MNAR1 tie and mix non-response conditions, DP and the two BERGMs had the best performances just below directly estimated ERGM coefficients. The trends were similar between Simulation 3 and 4, but were different across missing data conditions. Overall, the NRMSEs for nodecovA were also quite low.
- NodefactorB: The MNAR1 tie and mix non-response conditions again had higher NRMSEs than other conditions. Overall, the nodefactorB coefficients were low except in the MNAR1 tie and mix non-response conditions. RE had the best performance out of all imputation methods for this term.

- NodecovC: Although the NRMSE patterns differed across missing data conditions, they were similar across simulations. The overall performances of the imputation methods were similar, but the best method in each condition differed.
- Gwesp: We investigated the gwesp coefficients in Simulation 4 only. Different methods worked similarly well in the tie non-response conditions, whereas null-tie imputation, KNN, and the more complex BERGM2 algorithm had more bias in the actor non-response and mix non-response conditions. While other missing data mechanisms had similar trends, NRMSEs in MNAR1 under tie and mix non-response conditions were again different. NRMSEs for gwesp were higher than other coefficients with more conditions having larger NRMSEs.

3 Tables

Table 1: Average ERGM Coefficients of Simulated Complete Networks

simulation	size	edges	mutual	gwesp	nodematchB	nodematchC	nodecovA	nodefactorB	nodecovC
1	50.00	-2.09	1.99	-0.01	-0.01	-0.02	0.00	-0.00	0.00
1	100.00	-2.05	1.99	0.00	0.00	-0.00	0.00	-0.01	0.00
2	50.00	-2.90	1.97	-0.02	0.83	0.81	-0.00	-0.01	-0.00
2	100.00	-2.98	1.98	-0.00	0.81	0.80	-0.00	0.00	-0.00
3	50.00	-8.17	1.98	-0.03	0.80	0.82	0.10	0.09	0.10
3	100.00	-8.00	1.99	-0.00	0.80	0.80	0.10	0.10	0.10
4	50.00	-8.12	1.99	0.13	0.80	0.80	0.10	0.10	0.11
4	100.00	-7.95	2.00	0.14	0.80	0.79	0.10	0.10	0.10

Table 2: Average Network Statistics of Simulated Complete Networks

simulation	size	density	gwesp	reciprocity	homophilyA	homophilyB	homophilyC
1	50.00	0.19	0.04	0.50	-0.01	0.52	-0.02
1	100.00	0.19	0.04	0.50	-0.01	0.50	-0.01
2	50.00	0.15	0.02	0.48	-0.03	0.75	0.16
2	100.00	0.14	0.02	0.48	-0.01	0.74	0.18
3	50.00	0.12	0.02	0.47	-0.03	0.72	0.14
3	100.00	0.12	0.02	0.47	-0.03	0.71	0.15
4	50.00	0.18	0.05	0.56	-0.06	0.70	0.15
4	100.00	0.14	0.03	0.50	-0.03	0.70	0.14

Table 3: NRMSEs of Network Statistics by Sample Size

	method	size	density	reciprocity	gwesp	homophilyA	homophilyB	homophilyC
1	null	100	0.27	0.26	0.38	1.60	0.01	0.20
2	null	50	0.26	0.26	0.38	1.52	0.02	0.41
3	RE	100	0.13	0.29	0.22	1.46	0.02	0.21
4	RE	50	0.13	0.28	0.22	1.48	0.02	0.41
5	DP	100	0.16	0.17	0.24	1.14	0.02	0.31
6	DP	50	0.15	0.10	0.23	1.43	0.03	0.49
7	PA	100	0.23	0.28	0.36	2.25	0.04	0.29
8	PA	50	0.22	0.28	0.37	1.94	0.04	0.49
9	KNN	100	0.21	0.18	0.40	3.34	0.02	0.36
10	KNN	50	0.20	0.19	0.41	2.72	0.04	0.56
11	RF	100	0.13	0.24	0.20	1.98	0.02	0.22
12	RF	50	0.12	0.19	0.21	1.82	0.03	0.45
13	MICE	100	0.16	0.18	0.36	1.52	0.06	0.30
14	MICE	50	0.15	0.17	0.35	1.48	0.05	0.48
15	BERGM1	100	0.10	0.14	0.21	1.54	0.04	0.26
16	BERGM1	50	0.11	0.14	0.26	1.34	0.05	0.46
17	BERGM2	100	0.11	0.12	0.23	1.37	0.04	0.31
18	BERGM2	50	0.11	0.13	0.29	1.33	0.04	0.50

Table 4: Best Method for Each Network Statistics

	mechanism	type	simulation	density	reciprocity	gwesp	homophilyA	homophilyB	homophilyC
1	mcar	actor	1	RE	DP	RE	null	RE	null
2	mcar	tie	1	RE	KNN	RE	RE	RE	null
3	mcar	mix	1	RE	DP	RE	RE	RE	RE
4	mar	actor	1	RE	DP	RE	null	RE	null
5	mar	tie	1	RE	KNN	RE	RE	RE	null
6	mar	mix	1	RE	DP	RE	null	RE	null
7	mnar1	actor	1	DP	DP	MICE	null	RE	null
8	mnar1	tie	1	MICE	BERGM2	MICE	MICE	MICE	BERGM1
9	mnar1	mix	1	MICE	BERGM1	MICE	BERGM1	MICE	BERGM1
10	mnar2	actor	1	RE	DP	DP	null	RE	null
11	mnar2	tie	1	BERGM1	KNN	BERGM1	null	null	null
12	mnar2	mix	1	DP	DP	BERGM1	null	null	null
13	mcar	actor	2	RE	DP	RE	null	null	null
14	mcar	tie	2	RE	MICE	RE	RE	null	RE
15	mcar	mix	2	RE	DP	RE	null	null	RE
16	mar	actor	2	RE	DP	RE	null	MICE	null
17	mar	tie	2	RE	MICE	RE	RE	RF	RE
18	mar	mix	2	RE	DP	RE	BERGM2	RF	null
19	mnar1	actor	2	DP	DP	null	null	null	null
20	mnar1	tie	2	BERGM1	BERGM2	BERGM1	BERGM1	null	RE
21	mnar1	mix	2	BERGM1	BERGM2	BERGM2	BERGM2	RE	RE
22	mnar2	actor	2	RE	DP	DP	null	RE	null
23	mnar2	tie	2	DP	KNN	RE	null	null	null
24	mnar2	mix	2	DP	DP	RE	null	null	null
25	mcar	actor	3	RE	DP	RE	BERGM2	null	null
26	mcar	tie	3	RE	MICE	RE	null	null	null
27	mcar	mix	3	RE	DP	RE	null	null	null
28	mar	actor	3	RE	DP	RE	BERGM2	RE	null
29	mar	tie	3	RE	MICE	RE	null	RF	null
30	mar	mix	3	RE	MICE	RE	null	RE	null
31	mnar1	actor	3	DP	DP	null	DP	null	null
32	mnar1	tie	3	BERGM2	BERGM2	BERGM2	BERGM2	RE	RE
33	mnar1	mix	3	MICE	BERGM2	MICE	BERGM2	RE	BERGM1
34	mnar2	actor	3	RE	null	null	DP	null	null
35	mnar2	tie	3	DP	MICE	RE	null	null	null
36	mnar2	mix	3	DP	DP	RE	DP	null	null
37	mcar	actor	4	RE	DP	RE	RE	null	RE
38	mcar	tie	4	RE	MICE	RE	RE	null	null
39	mcar	mix	4	RE	BERGM2	RF	BERGM2	null	RE
40	mar	actor	4	RE	DP	RE	RE	null	RE
41	mar	tie	4	RE	MICE	RE	BERGM2	null	RE
42	mar	mix	4	RE	DP	RF	RE	null	null
43	mnar1	actor	4	DP	DP	null	DP	null	null
44	mnar1	tie	4	MICE	BERGM2	BERGM2	BERGM2	RE	RE
45	mnar1	mix	4	MICE	BERGM2	BERGM2	BERGM1	RE	BERGM1
46	mnar2	actor	4	RE	null	DP	DP	null	BERGM1
47	mnar2	tie	4	DP	KNN	RE	null	null	null
48	mnar2	mix	4	DP	DP	RE	DP	null	null

Table 5: NRMSEs of ERGM Coefficients by Sample Size

	imp_method	ssize	edges	mutual	gwesp	nodematchB	nodematchC	nodecovA	nodefactorB	nodecovC
1	null	50	0.13	0.23	10.32	0.13	0.12	0.25	1.79	0.49
2	null	100	0.14	0.22	8.14	0.11	0.09	0.24	1.30	0.34
3	RE	50	0.13	0.56	3.82	0.22	0.21	0.30	0.92	0.41
4	RE	100	0.11	0.56	1.62	0.20	0.19	0.26	0.44	0.30
5	DP	50	0.10	0.10	5.60	0.19	0.17	0.21	1.38	0.41
6	DP	100	0.06	0.16	2.58	0.12	0.12	0.13	0.88	0.25
7	PA	50	0.15	0.29	7.03	0.18	0.15	0.30	1.52	0.50
8	PA	100	0.15	0.27	4.07	0.15	0.12	0.30	1.05	0.38
9	KNN	50	0.18	0.29	10.32	0.18	0.23	0.36	1.44	0.56
10	KNN	100	0.18	0.26	10.96	0.13	0.21	0.28	1.00	0.37
11	RF	50	0.14	0.36	4.89	0.18	0.22	0.30	1.11	0.47
12	RF	100	0.10	0.45	1.94	0.15	0.19	0.22	0.62	0.29
13	MICE	50	0.14	0.32	7.68	0.30	0.26	0.29	1.23	0.44
14	MICE	100	0.11	0.31	4.54	0.29	0.23	0.19	0.82	0.27
15	BERGM1	50	0.11	0.22	4.15	0.26	0.22	0.25	1.50	0.52
16	BERGM1	100	0.09	0.21	1.76	0.20	0.19	0.22	0.88	0.37
17	BERGM2	50	0.14	0.19	6.66	0.26	0.23	0.28	1.49	0.49
18	BERGM2	100	0.14	0.16	5.49	0.19	0.17	0.23	0.88	0.31
19	none	50	0.09	0.08	4.23	0.11	0.10	0.17	0.97	0.34
20	none	100	0.06	0.04	1.62	0.07	0.06	0.10	0.41	0.18

Table 6: Best Method for Each ERGM Coefficient

mech	type	sim	edges	mutual	gwesp	nodematchB	nodematchC	nodecovA	nodefactorB	nodecovC
mcar	actor	1	DP	DP	RE	RE	RF	RE	RE	RE
mcar	tie	1	PA	MICE	null	RE	RE	RE	RE	RE
mcar	mix	1	DP	DP	RE	RE	RE	RE	RE	RE
mar	actor	1	DP	DP	RE	RE	RE	RE	RE	RE
mar	tie	1	PA	MICE	RE	RE	RE	RE	RE	RE
mar	mix	1	DP	DP	RE	RE	RE	RE	RE	RE
mnar1	actor	1	DP	DP	RE	null	null	MICE	MICE	MICE
mnar1	tie	1	MICE	DP	RE	MICE	BERGM1	RE	BERGM1	RE
mnar1	mix	1	PA	DP	RE	RE	MICE	RE	RE	RE
mnar2	actor	1	RE	DP	RE	MICE	MICE	RE	RE	RE
mnar2	tie	1	null	null	null	null	null	null	null	null
mnar2	mix	1	DP	null	RE	null	null	RE	RE	RE
mcar	actor	2	DP	DP	RE	null	null	RE	RE	RE
mcar	tie	2	PA	MICE	RE	PA	PA	RE	RE	RE
mcar	mix	2	DP	BERGM2	RE	null	null	RE	RE	RE
mar	actor	2	DP	DP	RE	null	null	RE	RE	RE
mar	tie	2	PA	MICE	RE	PA	null	RE	RE	RE
mar	mix	2	DP	DP	RE	null	null	RE	RE	RE
mnar1	actor	2	DP	DP	RE	BERGM2	BERGM2	MICE	RE	MICE
mnar1	tie	2	MICE	DP	RE	KNN	PA	RE	RE	BERGM1
mnar1	mix	2	MICE	DP	RE	null	null	RE	RE	MICE
mnar2	actor	2	RE	null	RE	BERGM2	BERGM2	RE	RE	RE
mnar2	tie	2	null	MICE	RE	null	null	null	RE	null
mnar2	mix	2	DP	null	RE	null	null	RE	RE	RE
mcar	actor	3	DP	BERGM2	RE	null	null	DP	RE	DP
mcar	tie	3	null	BERGM2	RE	PA	null	null	RE	null
mcar	mix	3	BERGM1	BERGM2	RE	null	null	DP	RE	DP
mar	actor	3	BERGM1	BERGM2	RE	null	null	BERGM2	RE	DP
mar	tie	3	BERGM1	BERGM2	RE	null	null	null	RE	null
mar	mix	3	BERGM1	BERGM2	RE	null	null	DP	RE	DP
mnar1	actor	3	null	DP	RE	null	null	null	null	null
mnar1	tie	3	RE	DP	BERGM1	PA	PA	DP	RE	RE
mnar1	mix	3	DP	DP	RE	KNN	null	DP	RE	DP
mnar2	actor	3	DP	null	RE	null	null	DP	RE	DP
mnar2	tie	3	null	BERGM2	RE	null	null	null	null	null
mnar2	mix	3	DP	null	RE	null	null	null	RE	DP
mcar	actor	4	DP	DP	BERGM1	DP	BERGM2	DP	RE	BERGM2
mcar	tie	4	RF	MICE	RF	PA	null	null	null	null
mcar	mix	4	RF	BERGM2	RF	null	null	DP	RE	DP
mar	actor	4	DP	DP	BERGM1	BERGM2	BERGM2	BERGM2	RE	DP
mar	tie	4	DP	DP	RF	null	null	null	RE	null
mar	mix	4	DP	DP	RF	null	null	BERGM2	RE	DP
mnar1	actor	4	null	DP	BERGM1	BERGM2	BERGM2	BERGM2	MICE	BERGM2
mnar1	tie	4	RE	BERGM1	RF	RF	PA	RF	BERGM1	MICE
mnar1	mix	4	MICE	BERGM2	MICE	PA	null	DP	MICE	MICE
mnar2	actor	4	DP	DP	BERGM1	BERGM2	BERGM2	BERGM2	RE	MICE
mnar2	tie	4	null	MICE	null	null	null	null	null	null
mnar2	mix	4	DP	null	BERGM1	null	null	null	RE	null

4 Figures

Figure 1: NRMSEs of the Density Statistics in Networks with 100 Actors

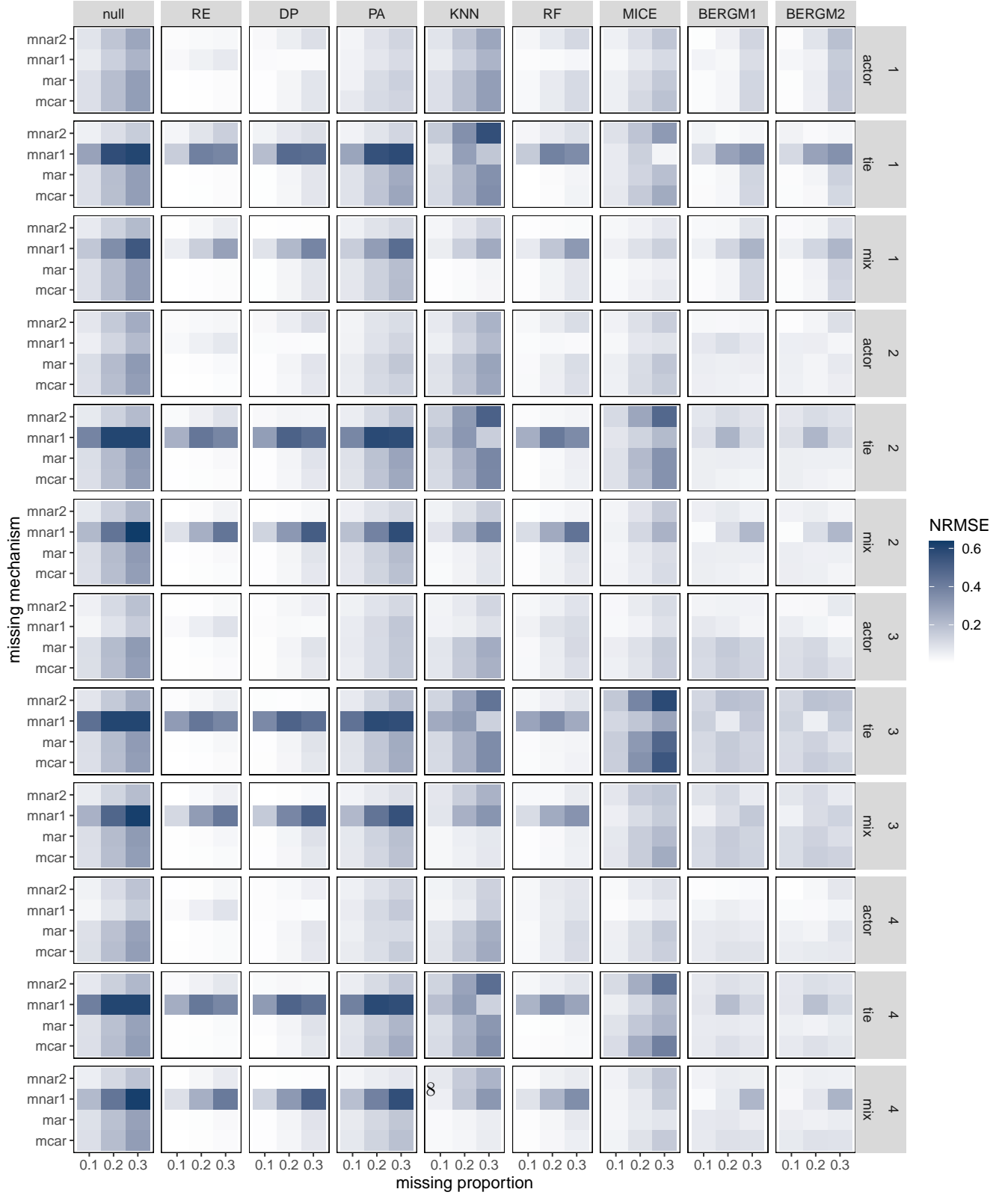


Figure 2: NRMSEs of the Reciprocity Statistics in Networks with 100 Actors

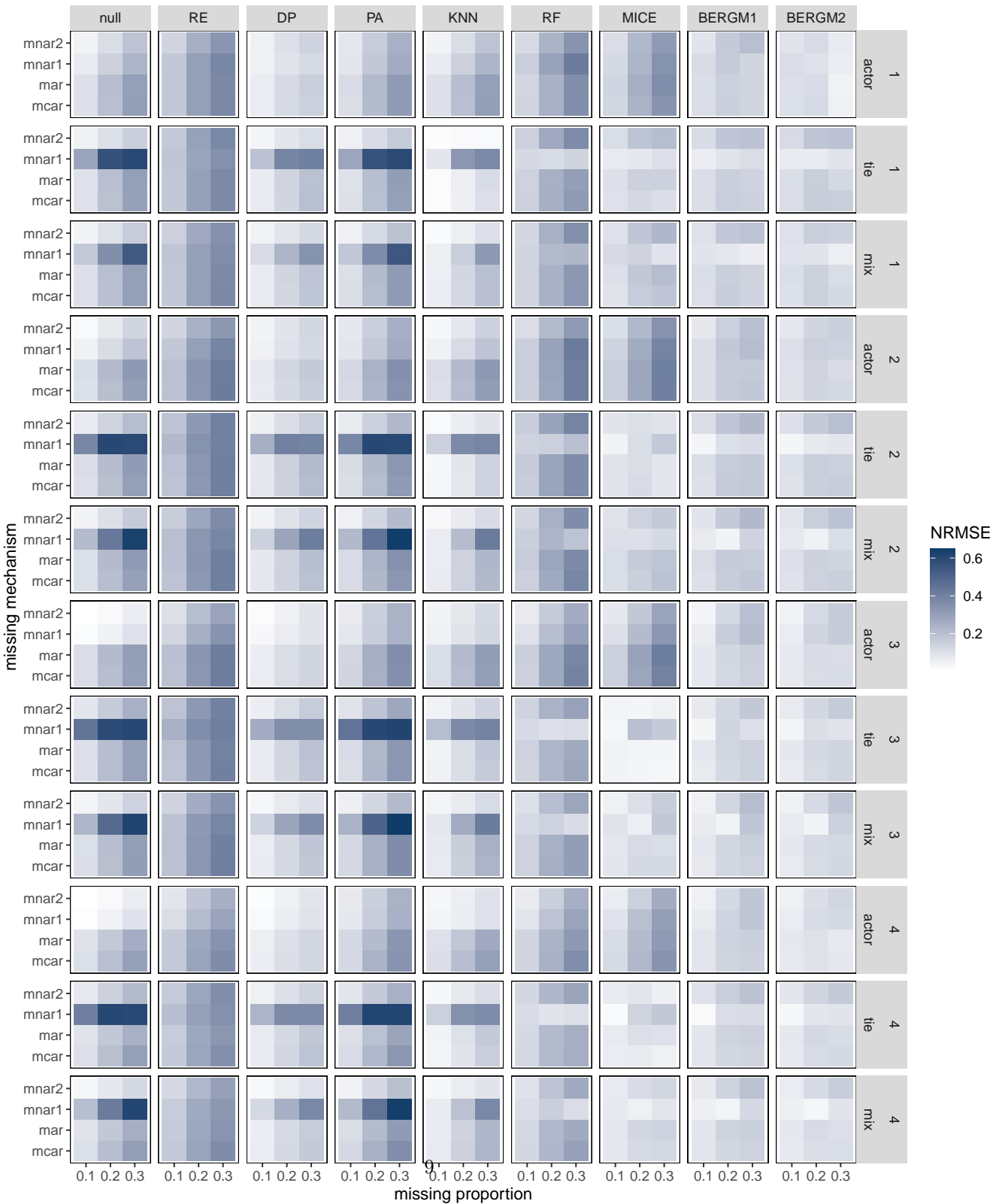


Figure 1 is a heatmap grid showing the Normalized Root Mean Square Error (NRMSE) for various missing data mechanisms, methods, and missing proportions. The grid is organized as follows:

- Rows (Missing Mechanism):** The rows are grouped by missing mechanism: actor, tie, and mix. Each mechanism has four rows corresponding to sample sizes 1, 2, 3, and 4. The labels 'mnar2', 'mnar1', 'mar', and 'mcar' are used for the four rows of each mechanism.
- Columns (Method):** The columns represent different methods: null, RE, DP, PA, KNN, RF, MICE, BERGM1, and BERGM2.
- X-axis (Missing Proportion):** The x-axis for each heatmap shows missing proportions of 0.1, 0.2, and 0.3.
- Color Scale (NRMSE):** A color bar on the right indicates the NRMSE values, ranging from 0.5 (light blue) to 1.5 (dark blue).

The heatmaps illustrate how NRMSE varies across different methods and missing proportions for each mechanism and sample size. For example, in the 'actor' mechanism, NRMSE is generally low (light blue) across all methods and proportions. In contrast, for the 'tie' and 'mix' mechanisms, NRMSE is higher (darker blue) for methods like KNN and MICE, especially at higher missing proportions and smaller sample sizes.

Figure 4: NRMSEs of the HomophilyA Statistics in Networks with 100 Actors

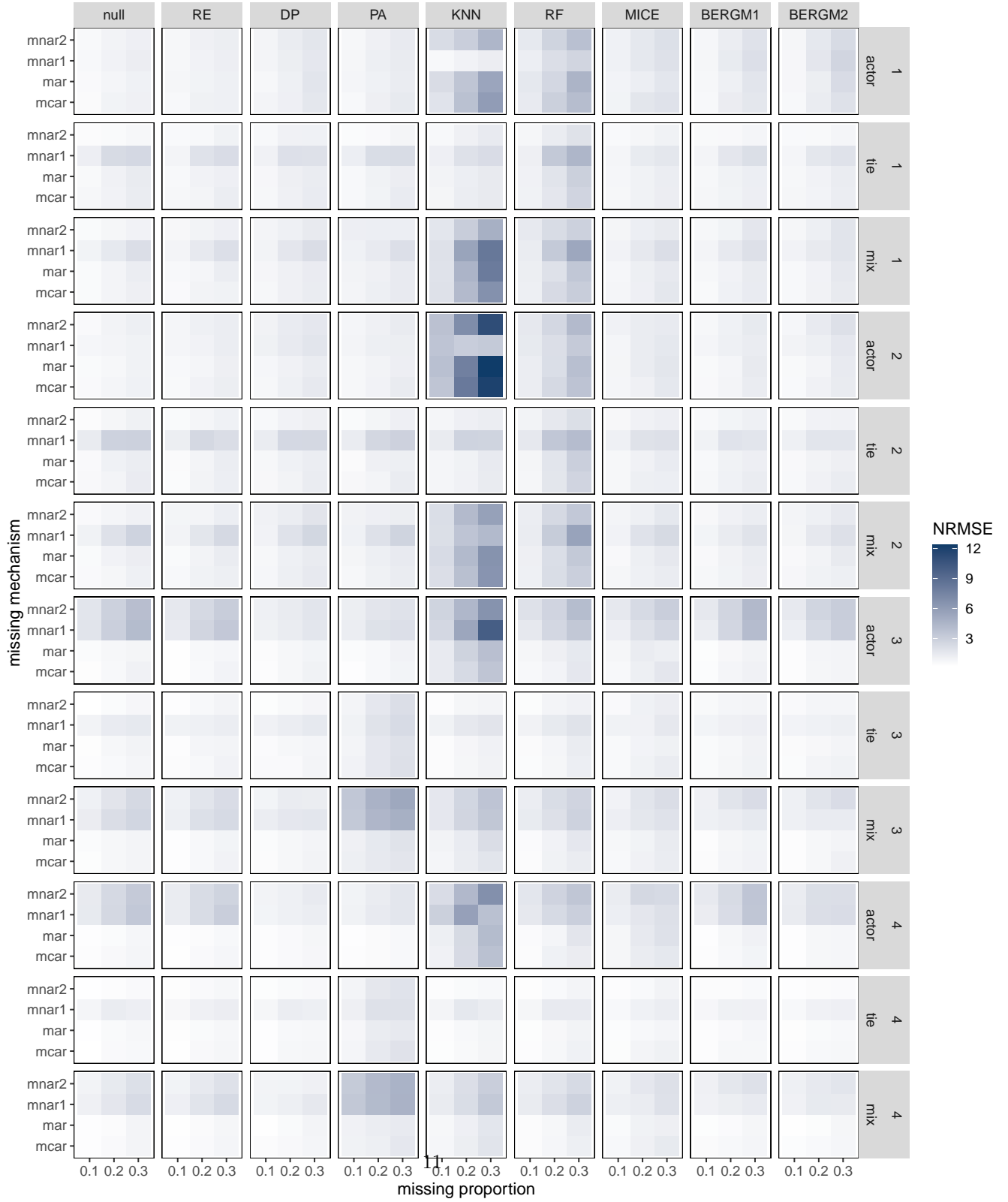


Figure 5: NRMSEs of the HomophilyB Statistics in Networks with 100 Actors

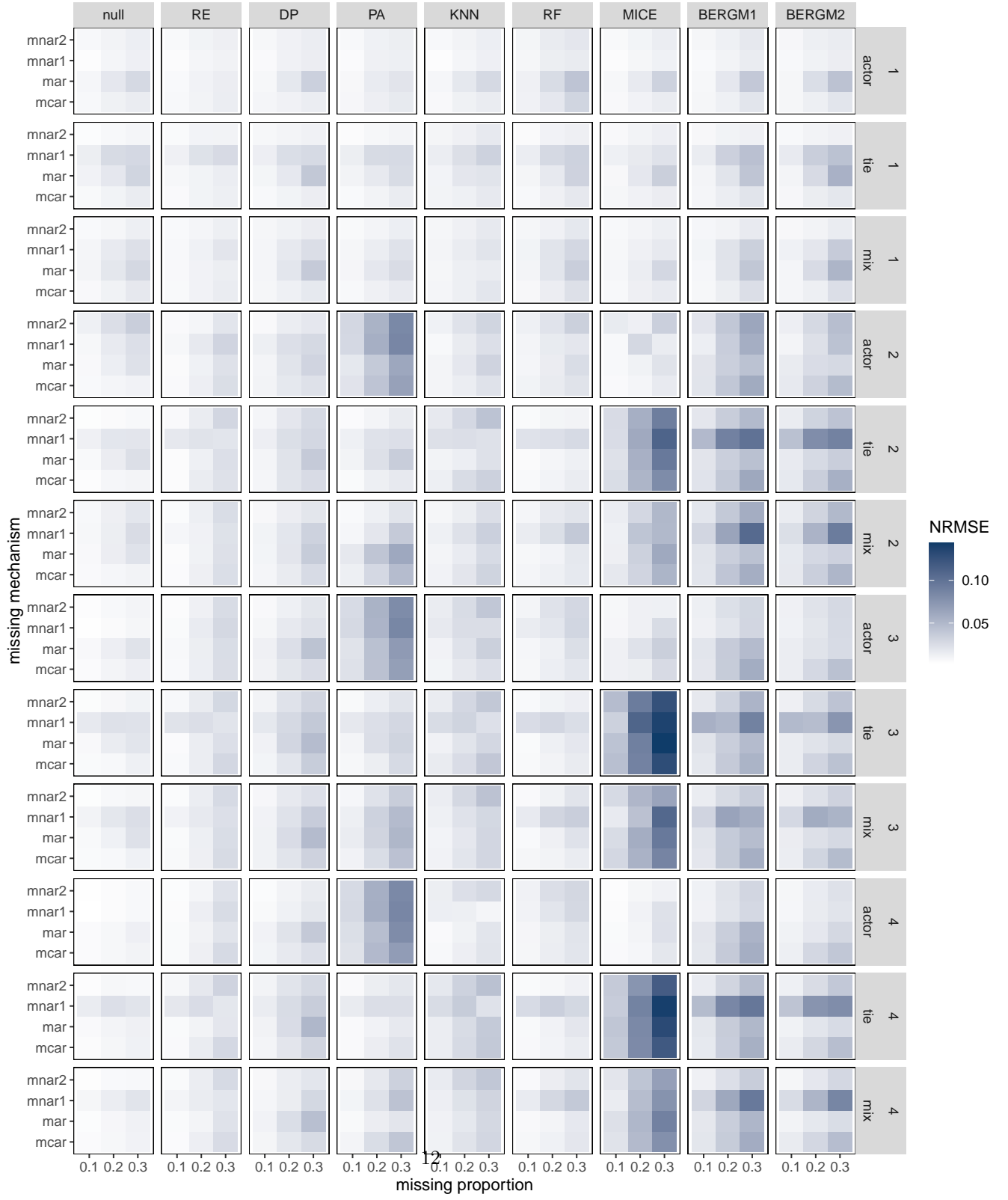


Figure 6: NRMSEs of the HomophilyC Statistics in Networks with 100 Actors

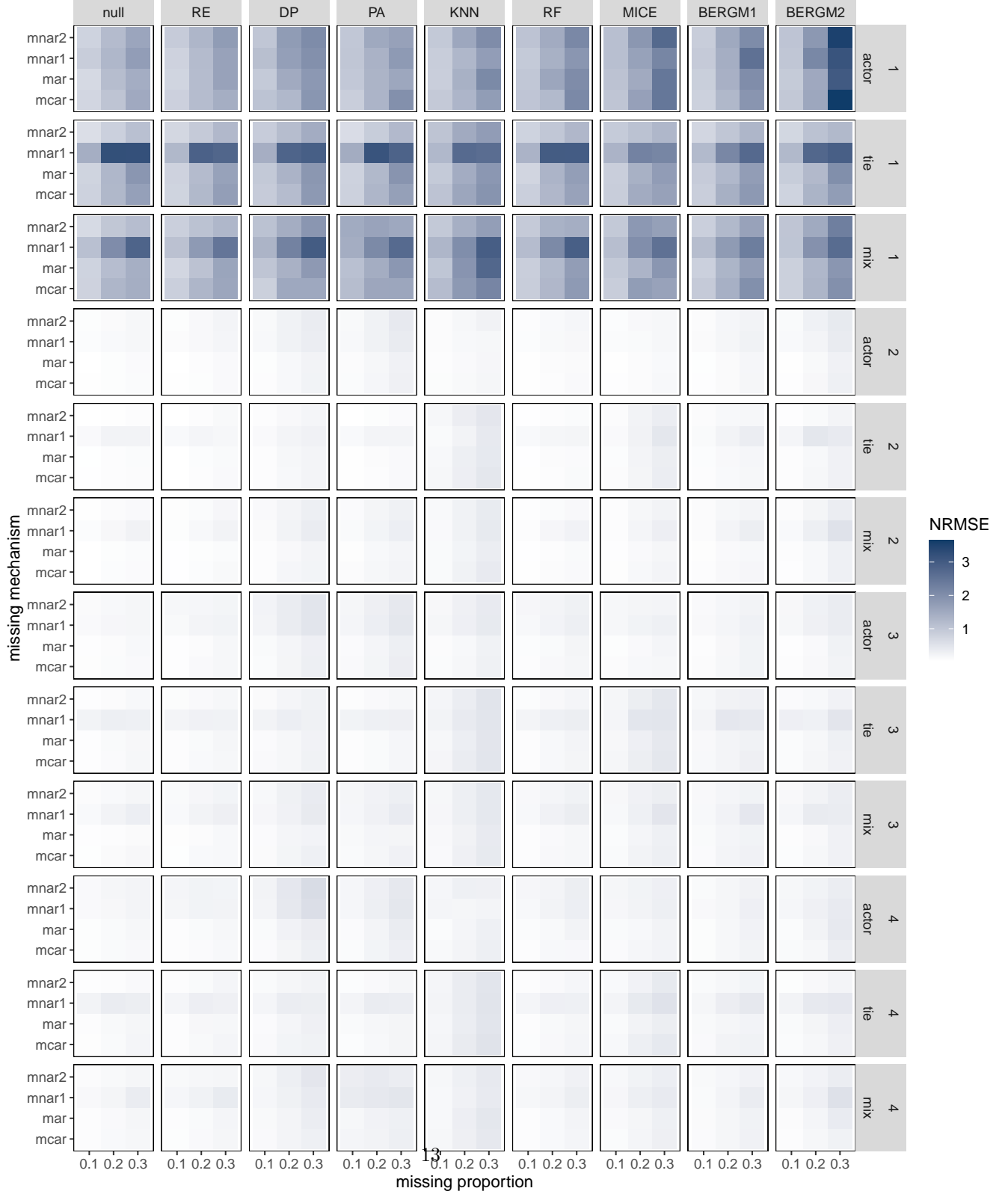


Figure 7: NRMSEs of the Edges Coefficient in Networks with 100 Actors

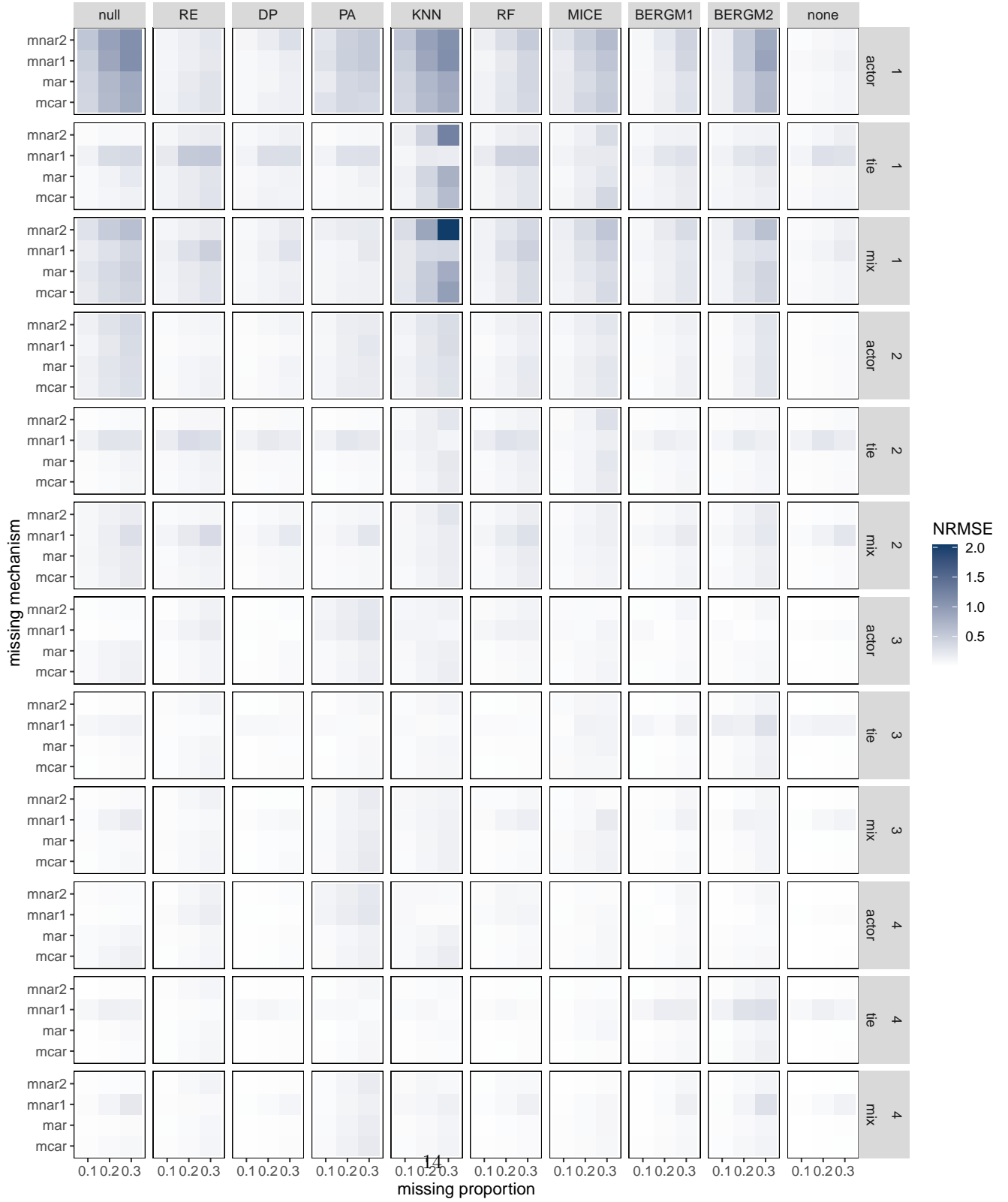


Figure 8: NRMSEs of the Mutual Coefficient in Networks with 100 Actors

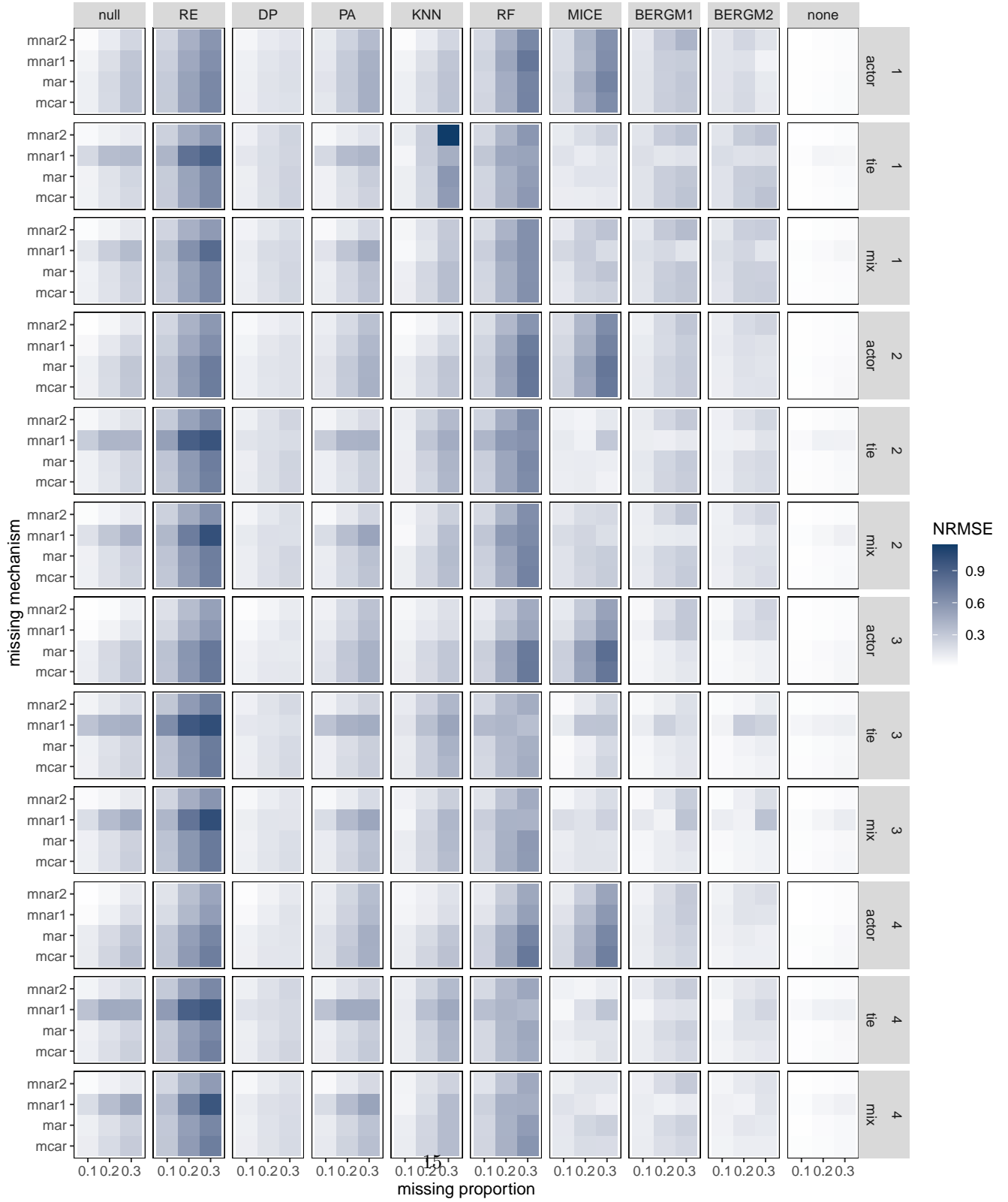


Figure 9: NRMSEs of the NodematchB Coefficient in Networks with 100 Actors

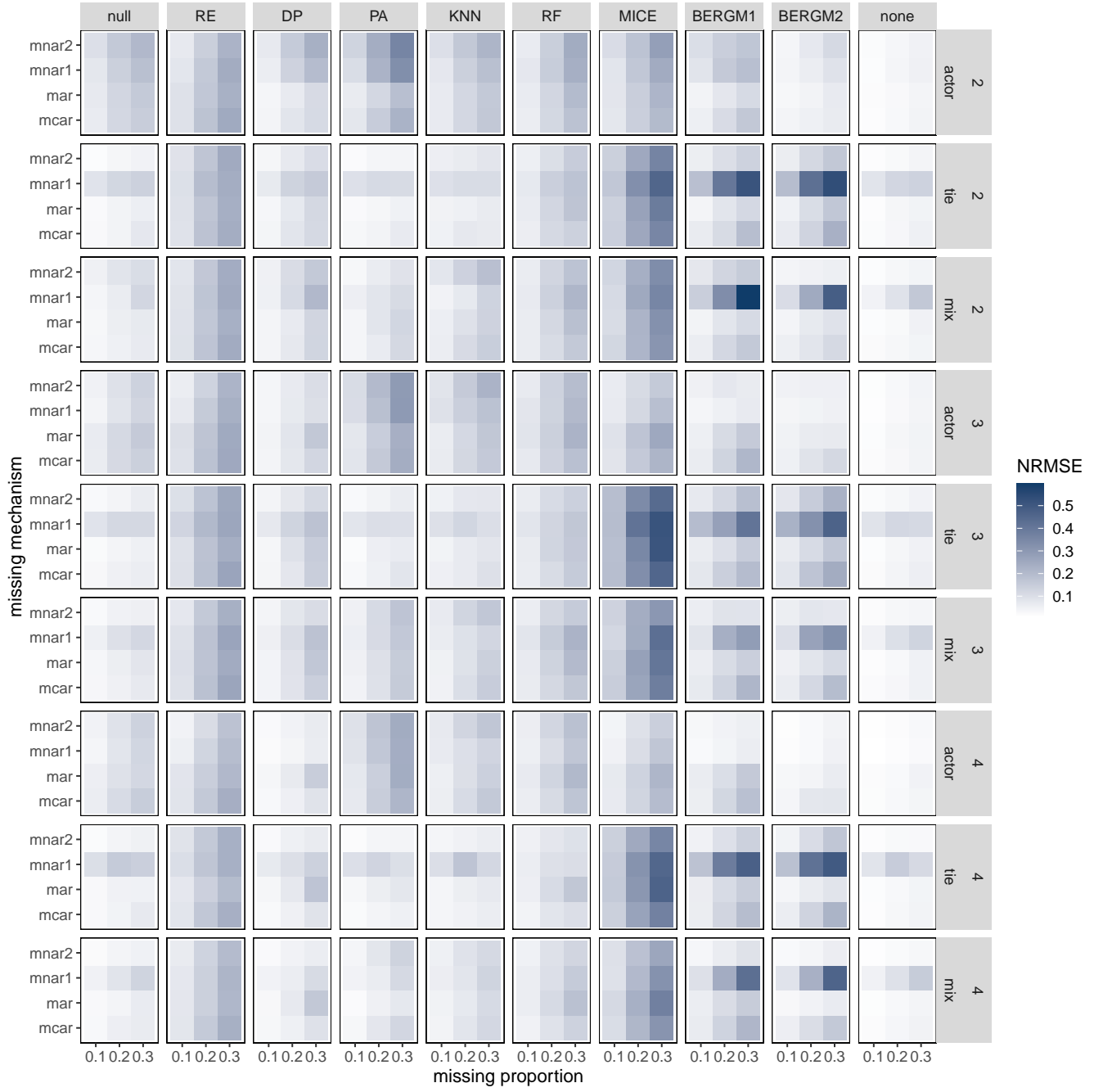


Figure 10: NRMSEs of the NodematchC Coefficient in Networks with 100 Actors

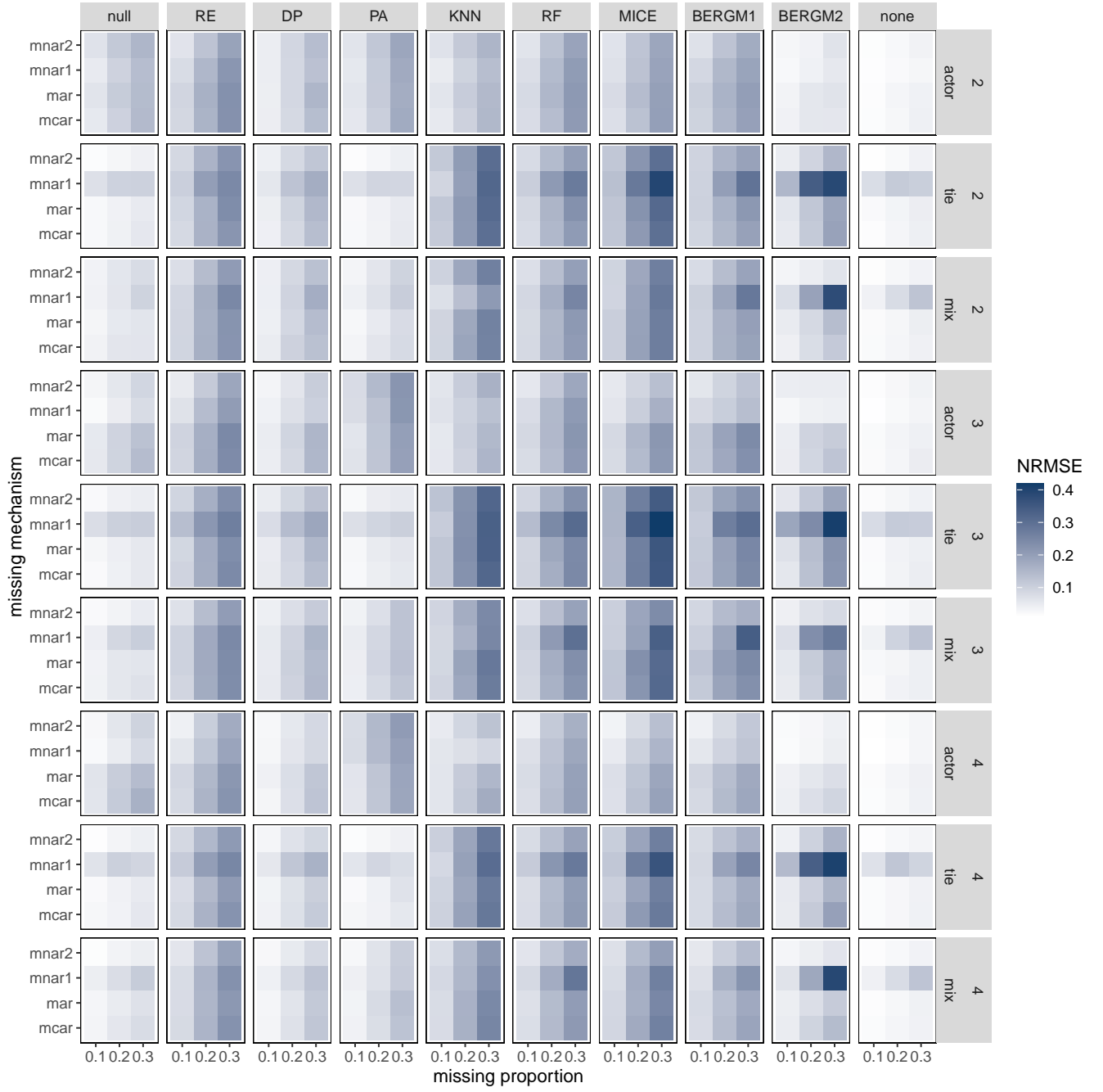


Figure 11: NRMSEs of the NodecovA Coefficient in Networks with 100 Actors

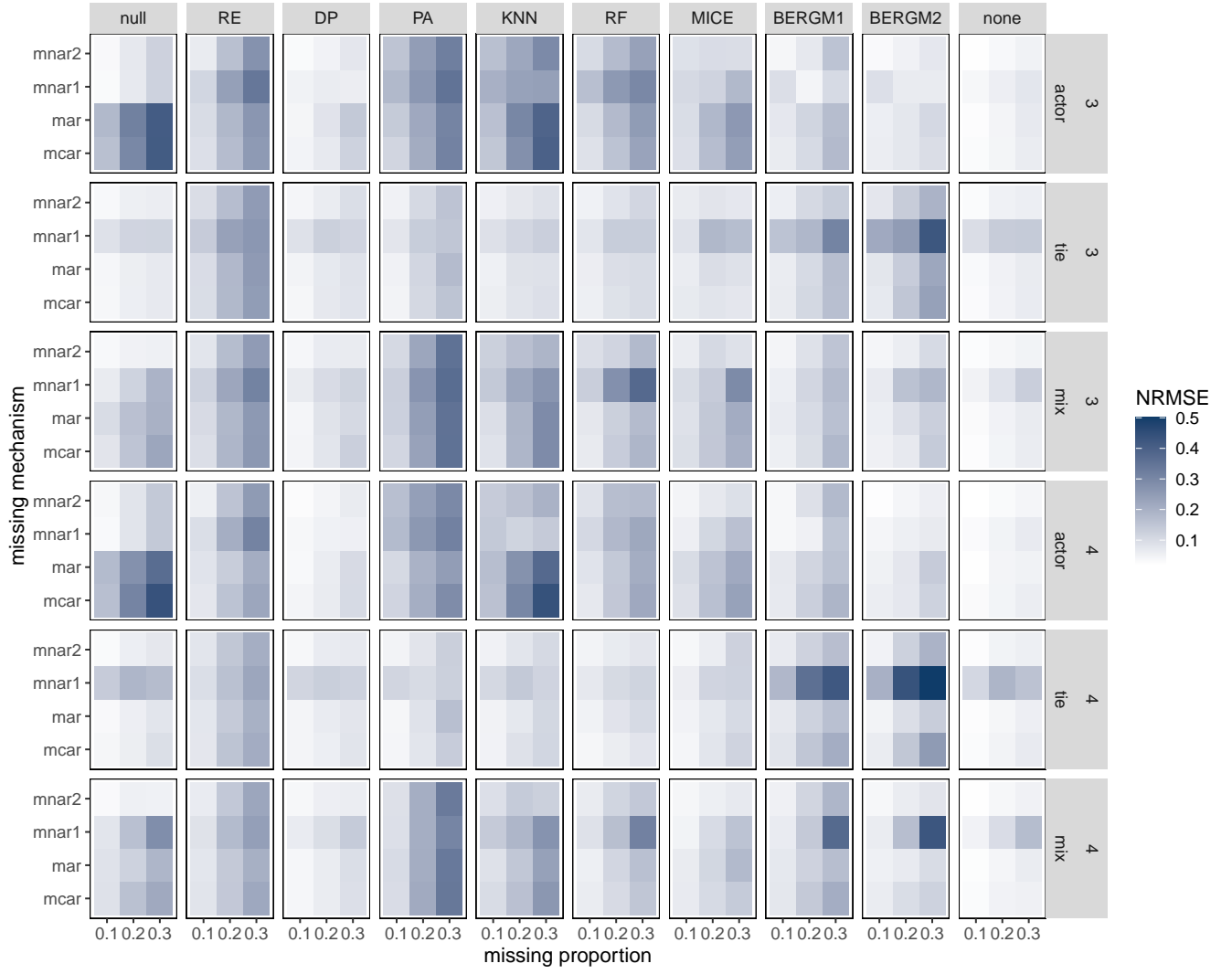


Figure 12: NRMSEs of the NodefactorB Coefficient in Networks with 100 Actors



Figure 13: NRMSEs of the NodecovC Coefficient in Networks with 100 Actors

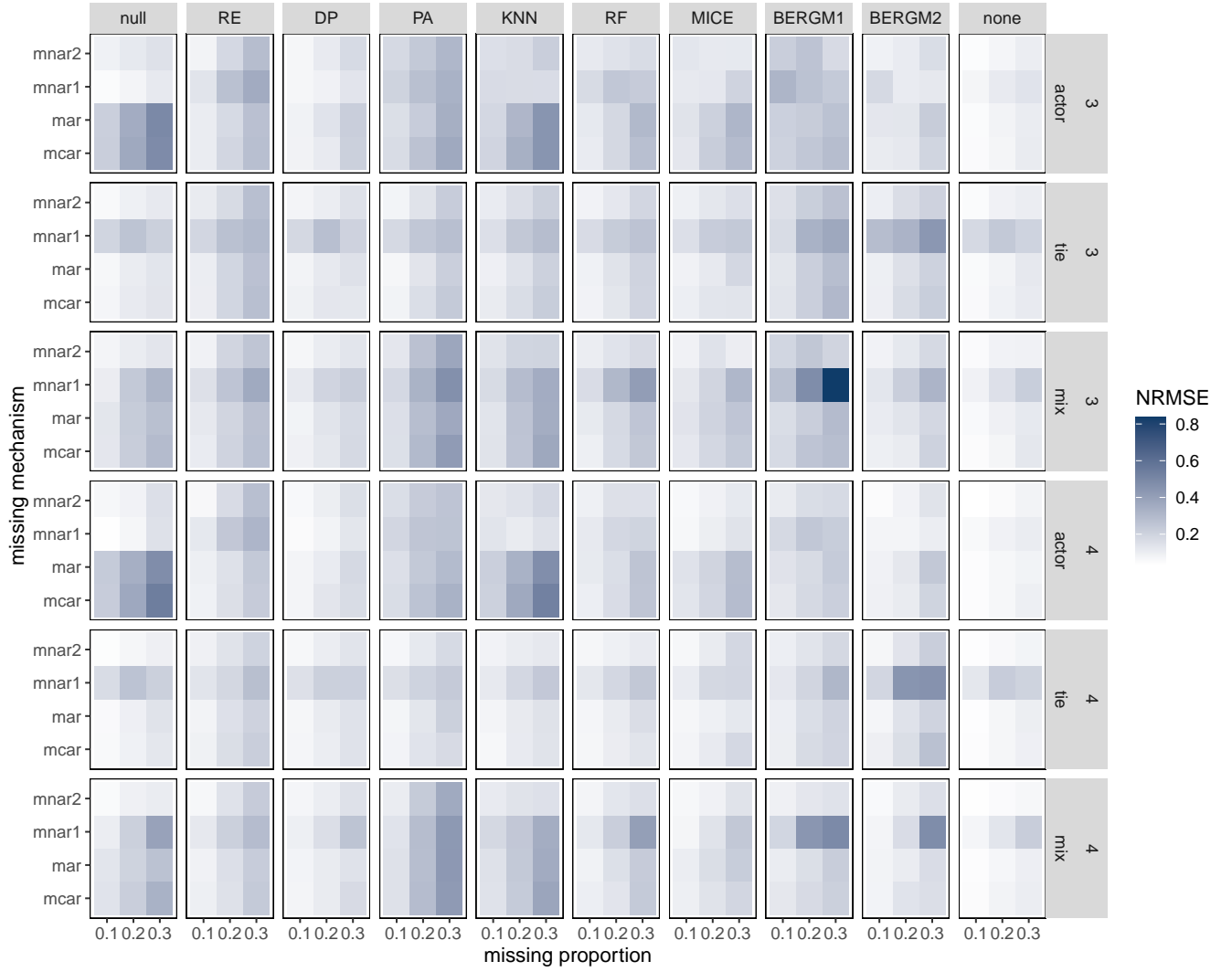


Figure 14: NRMSEs of the Gwesp Coefficient in Networks with 100 Actors

