

Experiment number and size analysis

- Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5

1 Experiment 3 Timesteps

Average (s):	0.01966190994
Number of consistent models:	777
Number of repaired models:	1623
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.03389309212
Number of consistent models:	650
Number of repaired models:	1750
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.03856939241
Number of consistent models:	618
Number of repaired models:	1782
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.1344615325
Number of consistent models:	597
Number of repaired models:	1803
Percentage of successfully revised models:	100.00%

Experiment number and size analysis

- Mammalian Cell Cycle || Nodes: 10 || Edges: 35 || Average Regulator Number: 3.5 || Maximum Regulator Number: 6

1 Experiment 3 Timesteps

Average (s):	0.02143733
Number of consistent models:	730
Number of repaired models:	1670
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.04031834
Number of consistent models:	640
Number of repaired models:	1760
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.03526924
Number of consistent models:	629
Number of repaired models:	1771
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.12520426
Number of consistent models:	549
Number of repaired models:	1851
Percentage of successfully revised models:	100.00%

Experiment number and size analysis

- Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8

1 Experiment 3 Timesteps

Average (s):	0.03648955514
Number of consistent models:	565
Number of repaired models:	1835
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.09065838035
Number of consistent models:	423
Number of repaired models:	1977
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.115883463
Number of consistent models:	333
Number of repaired models:	2067
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.4274355308
Number of consistent models:	315
Number of repaired models:	2085
Percentage of successfully revised models:	100.00%

Experiment number and size analysis

- Th Cell Differentiation || Nodes: 23 || Edges: 35 || Average Regulator Number: 1.52 || Maximum Regulator Number: 5

1 Experiment 3 Timesteps		
Average (s):		0.0395876206
Number of consistent models:		523
Number of repaired models:		1877
Percentage of successfully revised models:		100.00%

1 Experiment 20 Timesteps		
Average (s):		0.09084864376
Number of consistent models:		454
Number of repaired models:		1946
Percentage of successfully revised models:		100.00%

5 Experiments 3 Timesteps		
Average (s):		0.09816700536
Number of consistent models:		361
Number of repaired models:		2039
Percentage of successfully revised models:		100.00%

5 Experiments 20 Timesteps		
Average (s):		0.8409210309
Number of consistent models:		347
Number of repaired models:		2053
Percentage of successfully revised models:		100.00%

Experiment number and size analysis

- TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5

1 Experiment 3 Timesteps

Average (s):	0.07993006239
Number of consistent models:	491
Number of repaired models:	1909
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.1897897519
Number of consistent models:	402
Number of repaired models:	1998
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.1692304311
Number of consistent models:	476
Number of repaired models:	1924
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.7666389204
Number of consistent models:	400
Number of repaired models:	2000
Percentage of successfully revised models:	100.00%

Experiment number and size analysis

- **Possible explanation:**

- Both consistency checking as well as repairs take longer depending on how many observations they have to work with.
- This is because consistency checking will have to take each observation into account when seeing if a model is consistent with it or not, and the repairs will also have to ensure that the produced solutions do not violate any of the observations.
- So naturally, increasing either the size of the experiments, or the number of experiments, will increase the number of observations, therefore resulting in longer solving times.

Corruption type analysis (avg time taken in seconds)

- Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F	0.016794	0.022113	0.022945	0.056216
25F	0.012928	0.025407	0.028035	0.097139
50F	0.018771	0.037314	0.042611	0.150633
100F	0.028172	0.059591	0.070994	0.288387

- Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F	0.020114	0.026693	0.034202	0.100725
25F	0.023963	0.064287	0.076527	0.271279
50F	0.037766	0.104175	0.133882	0.477672
100F	0.064587	0.197617	0.254358	0.931522

Corruption type analysis (avg time taken in seconds)

- TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F	0.02237	0.04685	0.04381	0.16855
25F	0.02452	0.07413	0.06036	0.28828
50F	0.03198	0.10275	0.07710	0.40731
100F	0.05177	0.16972	0.12531	0.65409

- Mammalian Cell Cycle || Nodes: 10 || Edges: 35 || Average Regulator Number: 3.5 || Maximum Regulator Number: 6

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F	0.013758	0.022232	0.021017	0.059721
25F	0.016823	0.034259	0.032141	0.105613
50F	0.025922	0.056928	0.049587	0.172203
100F	0.040569	0.098279	0.095984	0.301198

Corruption type analysis (avg time taken in seconds)

- Th Cell Differentiation || Nodes: 23 || Edges: 35 || Average Regulator Number: 1.52 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F	0.017992	0.032635	0.034731	0.118937
25F	0.019474	0.049003	0.058023	0.254856
50F	0.029039	0.076182	0.096742	0.430739
100F	0.044635	0.121751	0.168776	0.748880

- Possible explanation:**

- While the repair process does not depend on the function format (it only depends on the regulators and their signs), the consistency checking process does need to look at a function's implicants to check whether it is consistent.
- The more implicants a function has, the longer that process takes. Due to the nature of our function change corruption operation, the number of implicants a corrupted function may end up with is directly linked to the number of regulators in that function.
- This means that more regulators = more implicants, and therefore the more likely it is that this corruption is applied, the higher the probability that the resulting functions in our model have more implicants than the original functions, and so the longer the consistency checking process takes.

Corruption type analysis (avg time taken in seconds)

- Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5E	0.015335	0.027176	0.029637	0.096513
10E	0.011466	0.020236	0.022003	0.069660
15E	0.019213	0.032155	0.035774	0.115881
20E	0.020158	0.035960	0.039479	0.137234
25E	0.024200	0.042104	0.047308	0.159475
50E	0.037263	0.070410	0.076541	0.275523
75E	0.044433	0.087807	0.093265	0.344134
1R	0.008915	0.016495	0.018525	0.060113
5R	0.011021	0.021912	0.027830	0.094949
10R	0.014248	0.030475	0.041687	0.146739
15R	0.016124	0.033587	0.050150	0.185963
1A	0.007431	0.014395	0.013721	0.041761
5A	0.009843	0.018026	0.018998	0.059435
10A	0.011698	0.020696	0.023731	0.074408
15A	0.011290	0.021981	0.023809	0.078580

Corruption type analysis (avg time taken in seconds)

- Mammalian Cell Cycle || Nodes: 10 || Edges: 35 || Average Regulator Number: 3.5 || Maximum Regulator Number: 6

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5E	0.013826	0.027997	0.025374	0.084864
10E	0.011680	0.021171	0.019750	0.063534
15E	0.015626	0.036335	0.029147	0.107457
20E	0.017965	0.041380	0.033883	0.123973
25E	0.019991	0.045440	0.037104	0.139341
50E	0.028117	0.068761	0.051301	0.213196
75E	0.048584	0.092500	0.068780	0.291284
1R	0.008439	0.016346	0.014980	0.048196
5R	0.012210	0.026624	0.024210	0.086972
10R	0.015811	0.037935	0.031545	0.131115
15R	0.019482	0.047731	0.039467	0.157481
1A	0.008283	0.015081	0.014108	0.043208
5A	0.009800	0.018211	0.018413	0.057041
10A	0.010781	0.021671	0.022490	0.068059
15A	0.011993	0.024218	0.025402	0.079877

Corruption type analysis (avg time taken in seconds)

- Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5E	0.026930	0.071613	0.092462	0.327179
10E	0.021110	0.050139	0.060531	0.213345
15E	0.035718	0.096689	0.126501	0.452210
20E	0.045118	0.126676	0.164179	0.569641
25E	0.048420	0.136641	0.178229	0.641143
50E	0.070970	0.214250	0.276141	1.001548
75E	0.090380	0.283414	0.344025	1.358367
1R	0.009751	0.021859	0.023112	0.089478
5R	0.013707	0.039172	0.052461	0.205751
10R	0.020034	0.061672	0.083392	0.333620
15R	0.021831	0.075227	0.107612	0.419507
1A	0.009244	0.021182	0.019622	0.079919
5A	0.012045	0.027351	0.033892	0.125895
10A	0.013842	0.036203	0.046744	0.182055
15A	0.016673	0.043857	0.060390	0.225662

Corruption type analysis (avg time taken in seconds)

- Th Cell Differentiation || Nodes: 23 || Edges: 35 || Average Regulator Number: 1.52 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5E	0.029176	0.069948	0.071570	0.310703
10E	0.019447	0.045463	0.045462	0.195938
15E	0.038331	0.094321	0.096171	0.429464
20E	0.048534	0.123397	0.122008	0.554767
25E	0.052707	0.131142	0.132099	0.614307
50E	0.088145	0.229809	0.225930	1.087981
75E	0.125949	0.344168	0.321200	1.503093
1R	0.009435	0.022721	0.024750	0.101917
5R	0.014771	0.044526	0.053392	2.050455
10R	0.022190	0.066379	0.086319	2.264901
15R	0.026560	0.079543	0.103433	4.909819
1A	0.008592	0.021656	0.022069	0.090375
5A	0.012643	0.033124	0.040449	0.165573
10A	0.021293	0.057362	0.064592	0.271482
15A	0.026010	0.069655	0.082421	0.351356

Corruption type analysis (avg time taken in seconds)

- TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5E	0.05628	0.14213	0.13246	0.55817
10E	0.03718	0.09542	0.09168	0.37648
15E	0.07172	0.19071	0.18034	0.75009
20E	0.09124	0.24505	0.22881	0.96584
25E	0.10656	0.28516	0.27003	1.12672
50E	0.22394	0.64509	0.58995	2.60317
75E	0.33835	0.99327	0.89335	4.11834
1R	0.01376	0.03688	0.03324	0.15783
5R	0.01927	0.06184	0.05046	0.25314
10R	0.02922	0.09470	0.07640	0.40795
15R	0.03834	0.12871	0.09814	0.51914
1A	0.01380	0.03634	0.03388	0.15870
5A	0.02149	0.05595	0.05092	0.23186
10A	0.03058	0.08367	0.07542	0.34794
15A	0.04072	0.11096	0.09815	0.45384

Corruption type analysis (avg time taken in seconds)

- **Possible explanation:**

- The repair process will iteratively explore all possibilities of functions with an increasing number of n nodes, and then settle for the smallest n that allows us to find a consistent function.
- During this process, we attempt to minimize the changes done both to the original regulators, as well as their signs.
- By changing the original regulators/signs, the minimization will take longer to find consistent functions that keep those corrupted signs, as they may not exist.

Corruption type analysis (avg time taken in seconds)

- Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
25F 5E	0.016491	0.031060	0.034194	0.115388
50F 25E	0.027963	0.055336	0.061674	0.228135
100F 50E	0.040782	0.085173	0.093276	0.356141

- Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
25F 5E	0.031058	0.077914	0.101782	0.368384
50F 25E	0.063084	0.186081	0.236734	0.875159
100F 50E	0.089423	0.284952	0.335912	1.355028

Corruption type analysis (avg time taken in seconds)

- TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
25F 5E	0.04668	0.12190	0.10865	0.49459
50F 25E	0.13666	0.36953	0.33266	1.47499
100F 50E	0.26333	0.74417	0.67312	3.08442

- Mammalian Cell Cycle || Nodes: 10 || Edges: 35 || Average Regulator Number: 3.5 || Maximum Regulator Number: 6

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
25F 5E	0.019506	0.039517	0.037134	0.123290
50F 25E	0.033787	0.080562	0.068537	0.253363
100F 50E	0.067577	0.121071	0.101306	0.388974

Corruption type analysis (avg time taken in seconds)

- Th Cell Differentiation || Nodes: 23 || Edges: 35 || Average Regulator Number: 1.52 || Maximum Regulator Number: 5

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
25F 5E	0.028733	0.071316	0.077633	0.349161
50F 25E	0.065312	0.171291	0.184389	0.856555
100F 50E	0.102165	0.289566	0.304913	1.450926

- Possible explanation:**
 - Increasing both the number of corruptions, when it comes to function changes as well as regulator sign changes, will affect both consistency checking and repairing (respectively, as we've seen before). This explains why these these configurations took longer than most others.

Corruption type analysis (avg time taken in seconds)

- **Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5**

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F 25E 5R 5A	0.027781	0.052071	0.063273	0.226898
10F 10E 5R 5A	0.019566	0.037773	0.049333	0.180299

- **Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8**

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F 25E 5R 5A	0.053187	0.153136	0.202773	0.758002
10F 10E 5R 5A	0.036794	0.103146	0.138789	0.517851

- **TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5**

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F 25E 5R 5A	0.12952	0.35515	0.32028	1.39997
10F 10E 5R 5A	0.07904	0.21050	0.18899	0.84410

Corruption type analysis (avg time taken in seconds)

- **Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5**

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F 25E 5R 5A	0.024232	0.055433	0.047888	0.181041
10F 10E 5R 5A	0.019733	0.044437	0.039893	0.145038

- **Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8**

%Corrptn\Exps	1E 3T	1E 20T	5E 3T	5E 20T
5F 25E 5R 5A	0.059317	0.159611	0.174834	3.139553
10F 10E 5R 5A	0.039651	0.107687	0.121850	2.511259

- **Possible explanation (1st configuration slower than 2nd):**
 - The first configuration will affect the repair process more, and the second will affect the consistency checking process more. Because repairing takes longer than consistency checking, more function changes and fewer sign changes ends up being faster than fewer function changes and more sign changes.

Model complexity analysis (5 experiments, 20 time steps)

%Corrptn\Exps	FY	MCC	SP_1	TH	TCR
5F	0.056216	0.059721	0.100725	0.118937	0.16855
25F	0.097139	0.105613	0.271279	0.254856	0.28828
50F	0.150633	0.172203	0.477672	0.430739	0.40731
100F	0.288387	0.301198	0.931522	0.748880	0.65409
5E	0.096513	0.084864	0.327179	0.310703	0.55817
10E	0.069660	0.063534	0.213345	0.195938	0.37648
15E	0.115881	0.107457	0.452210	0.429464	0.75009
20E	0.137234	0.123973	0.569641	0.554767	0.96584
25E	0.159475	0.139341	0.641143	0.614307	1.12672
50E	0.275523	0.213196	1.001548	1.087981	2.60317
75E	0.344134	0.291284	1.358367	1.503093	4.11834
1R	0.060113	0.048196	0.089478	0.101917	0.15783
5R	0.094949	0.086972	0.205751	2.050455	0.25314
10R	0.146739	0.131115	0.333620	2.264901	0.40795
15R	0.185963	0.157481	0.419507	4.909819	0.51914
1A	0.041761	0.043208	0.079919	0.090375	0.15870
5A	0.059435	0.057041	0.125895	0.165573	0.23186
10A	0.074408	0.068059	0.182055	0.271482	0.34794
15A	0.078580	0.079877	0.225662	0.351356	0.45384
25F 5E	0.115388	0.123290	0.368384	0.349161	0.49459
50F 25E	0.228135	0.253363	0.875159	0.856555	1.47499
100F 50E	0.356141	0.388974	1.355028	1.450926	3.08442
5F 25E 5R 5A	0.226898	0.181041	0.758002	3.139553	1.39997
10F 10E 5R 5A	0.180299	0.145038	0.517851	2.511259	0.84410

- **Fission Yeast || Nodes: 10 || Edges: 27 || Average Regulator Number: 2.7 || Maximum Regulator Number: 5**
- **Mammalian Cell Cycle || Nodes: 10 || Edges: 35 || Average Regulator Number: 3.5 || Maximum Regulator Number: 6**
- **Segment Polarity (1 Cell) || Nodes: 19 || Edges: 57 || Average Regulator Number: 3 || Maximum Regulator Number: 8**
- **Th Cell Differentiation || Nodes: 23 || Edges: 35 || Average Regulator Number: 1.52 || Maximum Regulator Number: 5**
- **TCR Signalisation || Nodes: 40 || Edges: 57 || Average Regulator Number: 1.425 || Maximum Regulator Number: 5**