Experiment number and size analysis

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):	0.08119916171
Avg consistent (s):	0.01084955176
Avg repaired (s):	0.1150069015
Number of consistent models:	779
Number of repaired models:	1621
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.1178148913
Avg consistent (s):	0.01733011755
Avg repaired (s):	0.1554535179
Number of consistent models:	654
Number of repaired models:	1746
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.1169106275
Avg consistent (s):	0.0163065396
Avg repaired (s):	0.1521815035
Number of consistent models:	623
Number of repaired models:	1777
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.2595802992
Avg consistent (s):	0.04508887573
Avg repaired (s):	0.3313955588
Number of consistent models:	602
Number of repaired models:	1798
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):	0.08231274505
Avg consistent (s):	0.01128241937
Avg repaired (s):	0.1149132897
Number of consistent models:	755
Number of repaired models:	1645
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.1196672039
Avg consistent (s):	0.01708223896
Avg repaired (s):	0.1584974692
Number of consistent models:	659
Number of repaired models:	1741
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.1201970723
Avg consistent (s):	0.01641566683
Avg repaired (s):	0.1581774046
Number of consistent models:	643
Number of repaired models:	1757
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.2715633413
Avg consistent (s):	0.04486856101
Avg repaired (s):	0.3378505065
Number of consistent models:	543
Number of repaired models:	1857
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):	0.3182965571
Avg consistent (s):	0.01193746434
Avg repaired (s):	0.4100218296
Number of consistent models:	553
Number of repaired models:	1847
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.493782043
Avg consistent (s):	0.0222827084
Avg repaired (s):	0.589215776
Number of consistent models:	404
Number of repaired models:	1996
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.5991790357
Avg consistent (s):	0.02191270068
Avg repaired (s):	0.6879892411
Number of consistent models:	320
Number of repaired models:	2080
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	1.094701636
Avg consistent (s):	0.07479503186
Avg repaired (s):	1.243742429
Number of consistent models:	306
Number of repaired models:	2094
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):	0.2992319376
Avg consistent (s):	0.01090229767
Avg repaired (s):	0.3853563755
Number of consistent models:	552
Number of repaired models:	1848
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.4071502714
Avg consistent (s):	0.02297780145
Avg repaired (s):	0.4979978571
Number of consistent models:	459
Number of repaired models:	1941
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.4750732775
Avg consistent (s):	0.02275391548
Avg repaired (s):	0.5580431012
Number of consistent models:	372
Number of repaired models:	2028
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.9639199459
Avg consistent (s):	0.08478897044
Avg repaired (s):	1.118047707
Number of consistent models:	358
Number of repaired models:	2042
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):	1.127914875
Avg consistent (s):	0.01334985715
Avg repaired (s):	1.40365965
Number of consistent models:	476
Number of repaired models:	1924
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps	
Average (s):	1.3676606
Avg consistent (s):	0.03329478
Avg repaired (s):	1.629744415
Number of consistent models:	394
Number of repaired models:	2006
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps	
Average (s):	1.247842313
Avg consistent (s):	0.03109594263
Avg repaired (s):	1.540238727
Number of consistent models:	465
Number of repaired models:	1935
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps	
Average (s):	2.244703837
Avg consistent (s):	0.1402644653
Avg repaired (s):	2.653027894
Number of consistent models:	390
Number of repaired models:	2010
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

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	0.018367	0.026812	0.026230	0.058297
25F	0.042536	0.069645	0.067443	0.160749
50F	0.078730	0.116117	0.119176	0.248171
100F	0.158682	0.209942	0.218543	0.442630
5E	0.033418	0.057763	0.046666	0.111027
10E	0.051814	0.078844	0.074468	0.168398
15E	0.076057	0.100440	0.094892	0.229014
20E	0.088724	0.117906	0.113792	0.247440
25E	0.107190	0.145824	0.153736	0.305145
50E	0.196509	0.260581	0.254327	0.565637
75E	0.244431	0.333370	0.312580	0.673657
1R	0.015131	0.026035	0.026910	0.070956
5R	0.026518	0.049948	0.050286	0.124363
10R	0.040382	0.083335	0.077795	0.200658
15R	0.061319	0.112773	0.110743	0.266988
1A	0.010086	0.020725	0.019463	0.051842
5A	0.021537	0.034280	0.035065	0.094786
10A	0.029921	0.043216	0.055198	0.133941
15A	0.031513	0.046504	0.053191	0.141821
25F 5E	0.067812	0.085376	0.099848	0.188645
50F 25E	0.133693	0.194541	0.189053	0.425525
100F 50E	0.204212	0.293809	0.296033	0.605187
5F 25E 5R 5A	0.123861	0.192266	0.178038	0.417391
10F 10E 5R 5A	0.086335	0.127504	0.132379	0.297658

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
5F	0.028530	0.035835	0.038507	0.078700
25F	0.071005	0.086449	0.087243	0.198461
50F	0.124890	0.182483	0.172940	0.341023
100F	0.215817	0.312858	0.315203	0.625259
5E	0.026944	0.038915	0.039541	0.098491
10E	0.039711	0.058470	0.057590	0.161783
15E	0.054920	0.079249	0.105073	0.209100
20E	0.068134	0.102374	0.099042	0.243570
25E	0.077370	0.112685	0.108586	0.288051
50E	0.130177	0.184628	0.172735	0.428361
75E	0.174448	0.261042	0.243402	0.546829
1R	0.013869	0.022650	0.021065	0.068591
5R	0.029348	0.065768	0.050606	0.150122
10R	0.066716	0.085049	0.081062	0.236025
15R	0.064981	0.109664	0.108783	0.290217
1A	0.013462	0.019579	0.020317	0.054778
5A	0.019352	0.031325	0.034430	0.084863
10A	0.026912	0.044381	0.045955	0.112742
15A	0.035201	0.056449	0.083878	0.144059
25F 5E	0.076564	0.111444	0.113774	0.235046
50F 25E	0.165133	0.230431	0.240183	0.529254
100F 50E	0.274042	0.379848	0.375277	0.767359
5F 25E 5R 5A	0.098853	0.141852	0.146187	0.347270
10F 10E 5R 5A	0.079127	0.118586	0.123349	0.277566

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
5F	0.047711	0.071548	0.079227	0.163565
25F	0.220167	0.308913	0.368300	0.622178
50F	0.383022	0.565587	0.689272	1.118648
100F	0.764769	1.104990	1.342607	2.194313
5E	0.129800	0.180024	0.200689	0.409716
10E	0.190953	0.294194	0.363655	0.660353
15E	0.289163	0.443073	0.496617	0.946947
20E	0.398340	0.551382	0.653266	1.228598
25E	0.434221	0.651964	0.755368	1.383697
50E	0.677535	0.998147	1.139585	2.191940
75E	0.869147	1.306733	1.427935	2.795676
1R	0.023194	0.045113	0.062418	0.140466
5R	0.056760	0.146505	0.208900	0.469769
10R	0.099506	0.277477	0.381704	0.798835
15R	0.141548	0.347656	0.556800	1.088047
1A	0.014854	0.034729	0.037657	0.109980
5A	0.036988	0.067963	0.102724	0.214712
10A	0.057815	0.112332	0.168774	0.337296
15A	0.082815	0.158559	0.247638	0.484050
25F 5E	0.263881	0.379829	0.481204	0.795149
50F 25E	0.675780	0.992242	1.202535	2.019554
100F 50E	0.989475	1.526006	1.797446	3.130848
5F 25E 5R 5A	0.485956	0.772261	0.954489	1.729914
10F 10E 5R 5A	0.305719	0.513541	0.661486	1.238587

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	0.033373	0.048393	0.064842	0.165738
25F	0.126264	0.181148	0.228470	0.486821
50F	0.249335	0.340747	0.454032	0.862128
100F	0.462315	0.658482	0.838971	1.583532
5E	0.090678	0.120195	0.128535	0.327973
10E	0.185818	0.228645	0.240048	0.559288
15E	0.296732	0.344961	0.384355	0.829306
20E	0.362086	0.432937	0.441351	0.993062
25E	0.423032	0.511947	0.510152	1.174502
50E	0.732978	0.846136	0.906870	1.908704
75E	1.062925	1.293423	1.268959	2.585258
1R	0.017114	0.042463	0.051348	0.130057
5R	0.046445	0.140756	0.189937	0.377266
10R	0.081812	0.213319	0.327640	0.645478
15R	0.127381	0.351196	0.496615	0.937015
1A	0.012245	0.032989	0.055922	0.138044
5A	0.046847	0.088262	0.134446	0.294396
10A	0.122389	0.192407	0.277796	0.551119
15A	0.161491	0.265990	0.405461	0.794475
25F 5E	0.201498	0.277872	0.317118	0.630201
50F 25E	0.585847	0.776701	0.852442	1.661508
100F 50E	0.965393	1.257212	1.410112	2.777777
5F 25E 5R 5A	0.514183	0.705415	0.831177	1.630311
10F 10E 5R 5A	0.273384	0.420010	0.585160	1.090119

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	0.072003	0.106511	0.090664	0.257937
25F	0.291842	0.416217	0.321891	0.699538
50F	0.446604	0.714295	0.495202	1.128203
100F	0.965723	1.463966	0.991946	2.113947
5E	0.391699	0.456112	0.417691	0.816534
10E	0.668398	0.793405	0.734070	1.316084
15E	0.965143	1.149379	1.073295	1.816490
20E	1.291320	1.530567	1.451794	2.390405
25E	1.520214	1.824413	1.697544	2.939892
50E	3.347763	3.933694	3.754378	6.332271
75E	4.893460	5.689748	5.305602	9.538417
1R	0.036279	0.066497	0.063388	0.199752
5R	0.194208	0.303465	0.276454	0.643893
10R	0.272733	0.474355	0.357194	0.841885
15R	0.457051	0.763102	0.705264	1.454032
1A	0.046995	0.075466	0.068882	0.200923
5A	0.164503	0.219839	0.190125	0.428501
10A	0.329835	0.460899	0.383454	0.756746
15A	0.541949	0.717626	0.615052	1.158838
25F 5E	0.618479	0.784745	0.652690	1.244870
50F 25E	2.150003	2.440751	2.281193	3.968516
100F 50E	4.397057	4.815835	4.546196	7.815249
5F 25E 5R 5A	1.954106	2.333192	2.169661	3.704439
10F 10E 5R 5A	1.052590	1.289776	1.304587	2.105529

Corruption type analysis

- **Possible explanation:**
  - The higher the probability of applying a given corruption, the more likely it is that the functions within will be rendered inconsistent, and thus the longer it will take to fully repair the model.

Repair type frequency and impact analysis

Percentage of times each repair type is applied to an inconsistent function (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	0.00%	0.00%	0.00%	47.62%	100.00%
25F	0.00%	0.00%	0.00%	46.46%	100.00%
50F	0.00%	0.00%	0.00%	50.00%	100.00%
100F	0.00%	0.00%	0.00%	51.92%	100.00%
5E	0.00%	0.00%	92.19%	48.44%	7.81%
10E	0.00%	0.00%	92.13%	42.52%	7.87%
15E	0.00%	0.00%	91.95%	42.53%	8.05%
20E	0.00%	0.00%	91.39%	41.15%	8.61%
25E	0.00%	0.00%	94.40%	38.06%	5.60%
50E	0.00%	0.00%	90.36%	40.08%	9.64%
75E	0.00%	0.00%	89.47%	38.13%	10.53%
1R	100.00%	24.00%	0.00%	24.00%	100.00%
5R	100.00%	11.54%	0.00%	33.33%	100.00%
10R	100.00%	12.34%	0.00%	27.92%	100.00%
15R	100.00%	14.57%	0.00%	24.29%	98.38%
1A	50.00%	30.00%	0.00%	0.00%	100.00%
5A	31.37%	19.61%	9.80%	31.37%	98.04%
10A	25.53%	22.34%	9.57%	27.66%	96.81%
15A	22.64%	25.47%	10.38%	30.19%	98.11%
25F 5E	0.00%	0.00%	28.65%	42.69%	76.02%
50F 25E	0.00%	0.00%	56.55%	43.22%	62.07%
100F 50E	0.00%	0.00%	64.23%	34.65%	73.94%
5F 25E 5R 5A	26.08%	3.49%	65.59%	38.71%	45.43%
10F 10E 5R 5A	31.20%	7.52%	43.23%	38.72%	65.04%

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

When a repair is applied to a function, the average number of times that type of repair is applied (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	-	-	-	1.40	2.03
25F	-	-	-	1.42	2.13
50F	-	-	-	1.49	2.21
100F	-	-	-	1.49	2.17
5E	-	-	1.02	1.87	1.00
10E	-	-	1.02	1.80	1.00
15E	-	-	1.05	1.83	1.00
20E	-	-	1.09	1.80	1.00
25E	-	-	1.15	1.85	1.00
50E	-	-	1.22	1.78	1.00
75E	-	-	1.38	1.77	1.00
1R	1.00	1.00	-	1.00	1.56
5R	1.07	1.00	-	1.00	1.53
10R	1.08	1.00	-	1.00	1.56
15R	1.09	1.00	-	1.00	1.54
1A	1.00	1.00	-	-	1.40
5A	1.00	1.00	1.00	1.06	1.55
10A	1.00	1.00	1.00	1.26	1.38
15A	1.00	1.00	1.00	1.24	1.48
25F 5E	-	-	1.04	1.56	2.06
50F 25E	-	-	1.08	1.56	2.21
100F 50E	-	-	1.23	1.40	2.26
5F 25E 5R 5A	1.05	1.00	1.08	1.50	1.64
10F 10E 5R 5A	1.02	1.00	1.03	1.51	1.69

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

Percentage of times each repair type is applied to an inconsistent function
(5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	0.00%	0.00%	0.00%	71.05%	97.37%
25F	0.00%	0.00%	0.00%	64.29%	100.00%
50F	0.00%	0.00%	0.00%	59.94%	99.72%
100F	0.00%	0.00%	0.00%	63.83%	99.57%
5E	0.00%	0.00%	66.67%	36.84%	64.91%
10E	0.00%	0.00%	62.28%	36.84%	70.18%
15E	0.00%	0.00%	71.18%	33.53%	67.65%
20E	0.00%	0.00%	70.83%	30.09%	64.35%
25E	0.00%	0.00%	74.81%	29.32%	60.15%
50E	0.00%	0.00%	77.00%	23.24%	63.38%
75E	0.00%	0.00%	84.55%	17.01%	58.68%
1R	78.57%	3.57%	21.43%	35.71%	96.43%
5R	98.40%	4.00%	1.60%	18.40%	95.20%
10R	96.10%	5.19%	4.76%	14.72%	98.27%
15R	98.18%	6.08%	2.43%	15.81%	96.66%
1A	18.18%	9.09%	0.00%	36.36%	100.00%
5A	9.76%	17.07%	2.44%	24.39%	97.56%
10A	12.00%	12.00%	8.00%	28.00%	98.67%
15A	18.35%	11.01%	4.59%	17.43%	97.25%
25F 5E	0.00%	0.00%	19.20%	50.00%	91.07%
50F 25E	0.00%	0.00%	35.86%	52.94%	84.63%
100F 50E	0.00%	0.00%	40.61%	53.25%	86.30%
5F 25E 5R 5A	31.68%	3.31%	48.21%	25.07%	74.10%
10F 10E 5R 5A	43.45%	3.79%	21.38%	30.69%	86.55%

Legend:	
Regulator+ : Introduced a regulator that was not present in the function before	
Regulator- : Removed an existing regulator from the function	
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)	
N Number Change: Added/removed a node from the original function	
N Format Change: Added/removed a regulator from one of the nodes of the original function	

When a repair is applied to a function, the average number of times that type of repair is applied (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	-	-	-	1.14	2.33
25F	-	-	-	1.15	2.46
50F	-	-	-	1.12	2.56
100F	-	-	-	1.13	2.49
5E	-	-	1.02	1.00	2.32
10E	-	-	1.00	1.00	2.46
15E	-	-	1.03	1.00	2.86
20E	-	-	1.07	1.00	2.65
25E	-	-	1.05	1.00	2.80
50E	-	-	1.18	1.00	3.54
75E	-	-	1.21	1.00	4.09
1R	1.00	1.00	1.00	1.00	1.33
5R	1.09	1.00	1.00	1.00	1.66
10R	1.22	1.00	1.00	1.00	1.84
15R	1.21	1.00	1.00	1.00	1.63
1A	1.00	1.00	-	1.25	2.20
5A	1.00	1.00	1.00	1.10	2.32
10A	1.00	1.00	1.00	1.00	1.74
15A	1.00	1.00	1.00	1.06	2.12
25F 5E	-	-	1.00	1.05	2.73
50F 25E	-	-	1.04	1.13	2.68
100F 50E	-	-	1.11	1.20	2.69
5F 25E 5R 5A	1.10	1.00	1.06	1.06	2.44
10F 10E 5R 5A	1.13	1.00	1.02	1.11	2.50

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

Percentage of times each repair type is applied to an inconsistent function (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	0.00%	0.00%	0.00%	86.00%	100.00%
25F	0.00%	0.00%	0.00%	74.67%	100.00%
50F	0.00%	0.00%	0.00%	73.32%	100.00%
100F	0.00%	0.00%	0.00%	73.09%	100.00%
5E	0.00%	0.00%	89.06%	8.85%	22.92%
10E	0.00%	0.00%	86.58%	15.62%	27.12%
15E	0.00%	0.00%	89.23%	12.59%	22.81%
20E	0.00%	0.00%	90.76%	12.89%	22.83%
25E	0.00%	0.00%	91.60%	15.91%	26.57%
50E	0.00%	0.00%	94.29%	19.78%	27.29%
75E	0.00%	0.00%	96.54%	23.55%	29.73%
1R	97.50%	2.50%	2.50%	10.00%	90.00%
5R	96.86%	5.83%	0.90%	9.87%	90.58%
10R	97.13%	8.13%	2.63%	13.16%	87.56%
15R	97.18%	6.35%	3.35%	14.64%	88.18%
1A	25.00%	15.00%	0.00%	25.00%	100.00%
5A	13.58%	9.88%	7.41%	41.98%	98.77%
10A	13.29%	11.39%	11.39%	29.75%	98.10%
15A	10.73%	17.60%	12.45%	31.76%	98.28%
25F 5E	0.00%	0.00%	36.72%	51.96%	72.29%
50F 25E	0.00%	0.00%	65.77%	47.27%	63.99%
100F 50E	0.00%	0.00%	78.56%	57.57%	76.97%
5F 25E 5R 5A	22.28%	2.26%	72.90%	19.51%	46.10%
10F 10E 5R 5A	33.08%	4.38%	43.96%	28.85%	68.43%

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

When a repair is applied to a function, the average number of times that type of repair is applied (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	-	-	-	1.64	2.28
25F	-	-	-	1.40	2.29
50F	-	-	-	1.36	2.27
100F	-	-	-	1.36	2.29
5E	-	-	1.04	1.25	7.19
10E	-	-	1.07	1.17	4.78
15E	-	-	1.11	1.14	5.72
20E	-	-	1.14	1.22	5.42
25E	-	-	1.18	1.26	4.83
50E	-	-	1.41	1.20	3.96
75E	-	-	1.62	1.17	3.13
1R	1.00	1.00	1.00	1.00	2.03
5R	1.03	1.00	1.00	1.00	1.79
10R	1.07	1.00	1.00	1.00	1.73
15R	1.15	1.00	1.00	1.02	1.64
1A	1.00	1.00	-	1.00	2.80
5A	1.00	1.00	1.00	1.00	1.87
10A	1.00	1.00	1.00	1.00	1.51
15A	1.00	1.00	1.00	1.00	1.52
25F 5E	-	-	1.05	1.30	2.60
50F 25E	-	-	1.18	1.32	2.73
100F 50E	-	-	1.40	1.32	2.54
5F 25E 5R 5A	1.08	1.00	1.17	1.19	2.95
10F 10E 5R 5A	1.04	1.00	1.05	1.17	2.40

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

Percentage of times each repair type is applied to an inconsistent function (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	0.00%	0.00%	0.00%	56.41%	100.00%
25F	0.00%	0.00%	0.00%	69.65%	100.00%
50F	0.00%	0.00%	0.00%	74.40%	100.00%
100F	0.00%	0.00%	0.00%	72.95%	99.87%
5E	0.00%	0.00%	89.92%	9.30%	10.08%
10E	0.00%	0.00%	87.65%	7.97%	12.35%
15E	0.00%	0.00%	92.13%	5.33%	7.87%
20E	0.00%	0.00%	92.77%	5.47%	7.23%
25E	0.00%	0.00%	93.66%	4.62%	6.34%
50E	0.00%	0.00%	96.34%	3.26%	3.66%
75E	0.00%	0.00%	98.88%	0.91%	1.12%
1R	100.00%	28.00%	0.00%	20.00%	92.00%
5R	100.00%	25.00%	0.00%	34.56%	77.94%
10R	100.00%	26.36%	0.00%	27.20%	89.12%
15R	100.00%	29.49%	0.56%	32.58%	87.64%
1A	33.33%	11.11%	22.22%	22.22%	88.89%
5A	38.71%	34.41%	12.90%	17.20%	97.85%
10A	43.84%	36.99%	14.61%	12.33%	96.80%
15A	40.13%	34.48%	14.11%	18.50%	97.81%
25F 5E	0.00%	0.00%	39.14%	50.00%	65.46%
50F 25E	0.00%	0.00%	64.38%	38.77%	49.36%
100F 50E	0.00%	0.00%	74.40%	40.97%	54.48%
5F 25E 5R 5A	25.44%	10.08%	65.87%	14.99%	39.55%
10F 10E 5R 5A	29.82%	14.12%	46.52%	22.86%	58.85%

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

When a repair is applied to a function, the average number of times that type of repair is applied (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	-	-	-	1.00	1.99
25F	-	-	-	1.00	1.83
50F	-	-	-	1.00	1.65
100F	-	-	-	1.00	1.72
5E	-	-	1.00	1.67	5.46
10E	-	-	1.02	1.40	6.10
15E	-	-	1.01	1.52	5.97
20E	-	-	1.04	1.46	5.92
25E	-	-	1.06	1.37	6.05
50E	-	-	1.09	1.15	6.35
75E	-	-	1.15	1.00	6.88
1R	1.14	1.00	-	1.00	1.38
5R	1.12	1.00	-	1.00	1.60
10R	1.15	1.00	-	1.00	1.52
15R	1.21	1.00	1.00	1.00	1.55
1A	1.00	1.00	1.00	1.00	1.64
5A	1.00	1.00	1.00	1.00	1.50
10A	1.00	1.00	1.04	1.00	1.30
15A	1.01	1.00	1.03	1.00	1.42
25F 5E	-	-	1.00	1.02	1.59
50F 25E	-	-	1.02	1.02	1.80
100F 50E	-	-	1.10	1.02	1.70
5F 25E 5R 5A	1.08	1.00	1.06	1.05	1.92
10F 10E 5R 5A	1.08	1.00	1.02	1.04	1.70

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

Percentage of times each repair type is applied to an inconsistent function (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	0.00%	0.00%	0.00%	100.00%	100.00%
25F	0.00%	0.00%	0.00%	100.00%	100.00%
50F	0.00%	0.00%	0.00%	100.00%	100.00%
100F	0.00%	0.00%	0.00%	100.00%	100.00%
5E	0.00%	0.00%	89.59%	10.86%	10.86%
10E	0.00%	0.00%	84.99%	16.28%	16.28%
15E	0.00%	0.00%	87.70%	13.18%	13.18%
20E	0.00%	0.00%	90.29%	11.57%	11.57%
25E	0.00%	0.00%	88.79%	13.54%	13.54%
50E	0.00%	0.00%	92.32%	13.15%	13.15%
75E	0.00%	0.00%	95.71%	12.25%	12.25%
1R	94.44%	5.56%	72.22%	5.56%	100.00%
5R	92.42%	6.82%	61.36%	7.58%	100.00%
10R	91.94%	2.37%	60.66%	8.06%	100.00%
15R	93.53%	6.20%	55.53%	6.47%	100.00%
1A	0.00%	0.00%	36.84%	78.95%	78.95%
5A	1.27%	0.00%	18.99%	86.08%	89.87%
10A	0.00%	0.00%	19.77%	87.01%	92.66%
15A	0.71%	0.35%	19.15%	85.46%	90.07%
25F 5E	0.00%	0.00%	53.58%	49.53%	49.84%
50F 25E	0.00%	0.00%	75.73%	29.79%	30.92%
100F 50E	0.00%	0.00%	80.21%	32.65%	34.33%
5F 25E 5R 5A	9.91%	0.70%	79.74%	20.61%	31.32%
10F 10E 5R 5A	19.74%	1.13%	65.21%	29.77%	49.68%

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

When a repair is applied to a function, the average number of times that type of repair is applied (5 experiments, 20 timesteps)

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

%Corrptn\Repr	Regulator +	Regulator -	Sign Change	N Number Change	N Format Change
5F	-	-	-	1.40	1.40
25F	-	-	-	1.38	1.38
50F	-	-	-	1.27	1.29
100F	-	-	-	1.34	1.37
5E	-	-	1.00	1.00	1.00
10E	-	-	1.01	1.00	1.00
15E	-	-	1.01	1.00	1.00
20E	-	-	1.02	1.00	1.00
25E	-	-	1.01	1.00	1.00
50E	-	-	1.05	1.00	1.00
75E	-	-	1.06	1.00	1.00
1R	1.00	1.00	1.00	1.00	1.07
5R	1.00	1.00	1.00	1.00	1.07
10R	1.00	1.00	1.00	1.00	1.01
15R	1.00	1.00	1.00	1.00	1.06
1A	-	-	1.00	1.25	1.25
5A	1.00	-	1.00	1.06	1.05
10A	-	-	1.00	1.04	1.04
15A	1.00	1.00	1.00	1.09	1.10
25F 5E	-	-	1.00	1.29	1.31
50F 25E	-	-	1.02	1.18	1.28
100F 50E	-	-	1.04	1.26	1.40
5F 25E 5R 5A	1.00	1.00	1.03	1.10	1.09
10F 10E 5R 5A	1.00	1.00	1.01	1.12	1.14

Legend:
Regulator+ : Introduced a regulator that was not present in the function before
Regulator- : Removed an existing regulator from the function
Sign Change: Changed the sign of a regulator (activator to inhibitor or vice-versa)
N Number Change: Added/removed a node from the original function
N Format Change: Added/removed a regulator from one of the nodes of the original function

Repair type frequency and impact analysis

- Whenever the corruptions change only the format of the function, the repairs affect only the function's format. Mostly, these changes are done to the format of the nodes, and not to the number of nodes. Still, when the node number is altered, the variation is 1 for most cases.

- When the sign of regulators is changed, it is almost inevitable that the repairs will also have to change the sign of regulators. Still, in some instances, it is possible to find solutions that change only the format of the function, leaving the signs as they are.

- When regulators are added or removed, the repairs seem to become more unpredictable, since the removal (addition) of regulators can prompt further removals (additions).

Model type analysis

Model type analysis

- As we have seen, models with more nodes and edges will typically take longer to revise than those with fewer. For models with a relatively similar number of nodes, the ones with the most edges will usually take longer to revise, as well.

- **Possible explanation:**
  - Since in consistency checking every node's state must be compared with its observed state, and that in order to determine its state, all of its regulators must also be taken into account, the more nodes and edges there are in our model, the longer this process will take;

  - For repairs, more nodes in the model (compounds) translates into more possibilities for nodes in the functions (terms). Besides that, more edges in a model typically translates into more complex functions, and the more complex a function is (in terms of regulator number and term number), the longer it will take to explore the possible search space and to find optimal solutions.