

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):	0.05315317065
Avg consistent (s):	0.008628353075
Avg repaired (s):	0.07455035318
Number of consistent models:	779
Number of repaired models:	1621
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps	
Average (s):	0.08094427824
Avg consistent (s):	0.01454450924
Avg repaired (s):	0.1058156694
Number of consistent models:	654
Number of repaired models:	1746
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps	
Average (s):	0.07889626622
Avg consistent (s):	0.01389119177
Avg repaired (s):	0.1016864527
Number of consistent models:	623
Number of repaired models:	1777
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps	
Average (s):	0.2017968286
Avg consistent (s):	0.04377796444
Avg repaired (s):	0.2547041458
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):	0.05162403951
Avg consistent (s):	0.008923868786
Avg repaired (s):	0.07122199021
Number of consistent models:	755
Number of repaired models:	1645
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.07713593235
Avg consistent (s):	0.01427266847
Avg repaired (s):	0.1009308151
Number of consistent models:	659
Number of repaired models:	1741
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.08122233192
Avg consistent (s):	0.01427960618
Avg repaired (s):	0.1057210073
Number of consistent models:	643
Number of repaired models:	1757
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.1997733688
Avg consistent (s):	0.04218388438
Avg repaired (s):	0.2458536543
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):	0.1557346492
Avg consistent (s):	0.01071642881
Avg repaired (s):	0.1991537482
Number of consistent models:	553
Number of repaired models:	1847
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps	
Average (s):	0.2553063052
Avg consistent (s):	0.02061434725
Avg repaired (s):	0.3028090863
Number of consistent models:	404
Number of repaired models:	1996
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps	
Average (s):	0.3415534433
Avg consistent (s):	0.02025294751
Avg repaired (s):	0.3909842888
Number of consistent models:	320
Number of repaired models:	2080
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps	
Average (s):	0.7002359806
Avg consistent (s):	0.07536066513
Avg repaired (s):	0.7915501384
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):	0.1109914383
Avg consistent (s):	0.01147598849
Avg repaired (s):	0.1407168324
Number of consistent models:	552
Number of repaired models:	1848
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.1956195967
Avg consistent (s):	0.02389827377
Avg repaired (s):	0.2362275757
Number of consistent models:	459
Number of repaired models:	1941
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.2199652185
Avg consistent (s):	0.02255478662
Avg repaired (s):	0.2561765995
Number of consistent models:	372
Number of repaired models:	2028
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	0.6608513817
Avg consistent (s):	0.09095381292
Avg repaired (s):	0.7607648634
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):	0.2840270749
Avg consistent (s):	0.01463261823
Avg repaired (s):	0.3506755995
Number of consistent models:	476
Number of repaired models:	1924
Percentage of successfully revised models:	100.00%

1 Experiment 20 Timesteps

Average (s):	0.4597498351
Avg consistent (s):	0.03547059461
Avg repaired (s):	0.5430828465
Number of consistent models:	394
Number of repaired models:	2006
Percentage of successfully revised models:	100.00%

5 Experiments 3 Timesteps

Average (s):	0.4138025376
Avg consistent (s):	0.0336376585
Avg repaired (s):	0.5051599892
Number of consistent models:	465
Number of repaired models:	1935
Percentage of successfully revised models:	100.00%

5 Experiments 20 Timesteps

Average (s):	1.21797917
Avg consistent (s):	0.1462052455
Avg repaired (s):	1.425935304
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	0.013502	0.021062	0.020472	0.070411
25F	0.024617	0.044706	0.043494	0.120575
50F	0.046040	0.077243	0.074612	0.185775
100F	0.100603	0.153487	0.136130	0.333923
5E	0.026519	0.039890	0.038274	0.095739
10E	0.038690	0.059005	0.057549	0.141365
15E	0.054675	0.078250	0.075268	0.178077
20E	0.062528	0.089773	0.085017	0.213120
25E	0.076696	0.108464	0.106192	0.251892
50E	0.144250	0.191415	0.197020	0.446801
75E	0.162740	0.224045	0.214750	0.551278
1R	0.010705	0.019823	0.018466	0.056196
5R	0.017328	0.032634	0.032297	0.094974
10R	0.023783	0.048309	0.049060	0.132843
15R	0.034314	0.064582	0.065423	0.179848
1A	0.009034	0.015473	0.015180	0.046705
5A	0.014682	0.023950	0.024887	0.079269
10A	0.016623	0.030412	0.036152	0.109066
15A	0.015651	0.031722	0.033433	0.111195
25F 5E	0.039967	0.059336	0.060285	0.147665
50F 25E	0.083506	0.140070	0.128341	0.322739
100F 50E	0.114476	0.172289	0.166550	0.422726
5F 25E 5R 5A	0.086083	0.124478	0.121326	0.311035
10F 10E 5R 5A	0.058666	0.092245	0.093334	0.239905

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	0.017945	0.025608	0.026569	0.066847
25F	0.036873	0.056154	0.058980	0.143442
50F	0.076590	0.119686	0.114338	0.252709
100F	0.152866	0.189489	0.212505	0.454967
5E	0.020063	0.027760	0.028979	0.095753
10E	0.026305	0.041294	0.041498	0.121279
15E	0.036799	0.055268	0.061411	0.155477
20E	0.044274	0.064974	0.068748	0.187375
25E	0.048246	0.073977	0.076894	0.210577
50E	0.079207	0.122816	0.117274	0.309865
75E	0.108958	0.168890	0.176571	0.413840
1R	0.009952	0.017512	0.017074	0.056510
5R	0.019507	0.034099	0.034267	0.103650
10R	0.031226	0.050960	0.050814	0.151757
15R	0.036934	0.061927	0.061324	0.185424
1A	0.010033	0.015723	0.017682	0.050312
5A	0.013878	0.024213	0.027573	0.072616
10A	0.020209	0.032601	0.036118	0.092644
15A	0.024221	0.043563	0.051062	0.116524
25F 5E	0.049347	0.070639	0.073840	0.175575
50F 25E	0.109689	0.166919	0.163373	0.396452
100F 50E	0.161720	0.222226	0.261104	0.535487
5F 25E 5R 5A	0.058593	0.092099	0.095595	0.243397
10F 10E 5R 5A	0.045540	0.072865	0.075742	0.202082

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	0.034257	0.050458	0.060436	0.139889
25F	0.122829	0.193298	0.265603	0.483323
50F	0.222977	0.317298	0.421033	0.796917
100F	0.427221	0.641613	0.901233	1.582413
5E	0.062525	0.103581	0.114557	0.268623
10E	0.093594	0.159738	0.184484	0.425584
15E	0.133737	0.218978	0.244348	0.581427
20E	0.171279	0.278090	0.308259	0.751253
25E	0.205051	0.312382	0.357417	0.847217
50E	0.278900	0.470968	0.512794	1.310074
75E	0.331622	0.567341	0.639418	1.722263
1R	0.014944	0.030349	0.037101	0.111913
5R	0.026726	0.068225	0.100557	0.273449
10R	0.045162	0.106031	0.160189	0.442858
15R	0.057703	0.129954	0.212029	0.596735
1A	0.011309	0.026365	0.026082	0.100956
5A	0.021961	0.044553	0.060719	0.163192
10A	0.031395	0.064276	0.095947	0.240772
15A	0.041252	0.078814	0.131312	0.324213
25F 5E	0.139987	0.211122	0.267008	0.546450
50F 25E	0.358111	0.562721	0.824758	1.328447
100F 50E	0.549773	0.853341	1.492617	2.047594
5F 25E 5R 5A	0.206820	0.368619	0.445676	0.993957
10F 10E 5R 5A	0.148495	0.269235	0.333704	0.726143

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	0.022203	0.036573	0.046477	0.150452
25F	0.064885	0.112764	0.132920	0.364962
50F	0.118624	0.190319	0.231808	0.628180
100F	0.221503	0.375034	0.456947	1.151084
5E	0.036636	0.065047	0.073289	0.282886
10E	0.078043	0.116696	0.130516	0.447783
15E	0.103425	0.162099	0.192008	0.626898
20E	0.126614	0.199811	0.213135	0.757582
25E	0.150816	0.234249	0.254905	0.828667
50E	0.232463	0.385086	0.391249	1.294657
75E	0.325963	0.554969	0.531587	1.763993
1R	0.012561	0.029490	0.028870	0.113683
5R	0.019540	0.068496	0.079975	0.252601
10R	0.027730	0.090293	0.116516	0.368926
15R	0.037605	0.117373	0.145574	0.443165
1A	0.010673	0.031296	0.035226	0.117139
5A	0.027328	0.056599	0.072758	0.220941
10A	0.046191	0.100012	0.130719	0.359364
15A	0.069509	0.138378	0.186947	0.499349
25F 5E	0.085623	0.144046	0.159954	0.455154
50F 25E	0.206633	0.353286	0.401212	1.124079
100F 50E	0.346095	0.614712	0.676130	1.857956
5F 25E 5R 5A	0.185092	0.313114	0.346593	1.049580
10F 10E 5R 5A	0.108040	0.205128	0.243852	0.701350

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	0.044063	0.075079	0.069050	0.216688
25F	0.165649	0.244035	0.207515	0.525838
50F	0.240989	0.377684	0.290393	0.750914
100F	0.497192	0.754297	0.589388	1.369736
5E	0.076245	0.140714	0.136176	0.463835
10E	0.131074	0.226512	0.216775	0.710833
15E	0.181579	0.306643	0.301391	0.934606
20E	0.237114	0.400599	0.380791	1.191175
25E	0.283005	0.477179	0.461370	1.410421
50E	0.610137	1.055368	0.993595	3.210001
75E	0.886868	1.595885	1.477340	4.954631
1R	0.018024	0.043216	0.040295	0.173012
5R	0.047844	0.101256	0.086546	0.353948
10R	0.060792	0.139412	0.113011	0.454131
15R	0.094558	0.206077	0.168502	0.669761
1A	0.029302	0.054793	0.050775	0.180288
5A	0.071290	0.112540	0.101062	0.307014
10A	0.130672	0.200779	0.185840	0.487868
15A	0.211685	0.323913	0.281940	0.695670
25F 5E	0.211351	0.319612	0.270834	0.737020
50F 25E	0.577907	0.859698	0.781840	2.043714
100F 50E	1.291584	1.883766	1.693376	4.414118
5F 25E 5R 5A	0.432170	0.695368	0.629644	1.861737
10F 10E 5R 5A	0.285555	0.439569	0.403813	1.114541

Corruption type analysis

- **Possible explanation:**
 - TODO

OLD 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.

OLD 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.

OLD Corruption type analysis (avg time taken in seconds)

Th Set 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.

OLD 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.

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%	2.38%	64.29%	100.00%
50F	0.00%	0.00%	2.24%	59.94%	99.72%
100F	0.00%	0.00%	1.99%	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%	20.09%	50.00%	91.07%
50F 25E	0.00%	0.00%	37.00%	52.94%	84.63%
100F 50E	0.00%	0.00%	41.09%	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%	21.72%	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	-	-	1.00	1.10	2.46
50F	-	-	1.00	1.09	2.56
100F	-	-	1.00	1.10	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	1.03	2.73
50F 25E	-	-	1.04	1.10	2.68
100F 50E	-	-	1.13	1.18	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	1.10	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	4.00%	6.00%	2.00%	86.00%	100.00%
25F	1.32%	1.64%	0.33%	74.67%	100.00%
50F	1.34%	2.01%	0.67%	73.32%	100.00%
100F	0.84%	1.09%	0.25%	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%	6.53%	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	1.15%	1.39%	36.72%	51.96%	72.29%
50F 25E	0.45%	0.80%	66.13%	47.27%	63.99%
100F 50E	0.83%	0.95%	78.88%	57.57%	76.97%
5F 25E 5R 5A	22.28%	2.36%	73.00%	19.51%	46.00%
10F 10E 5R 5A	33.23%	4.68%	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	1.00	1.67	1.00	1.56	2.30
25F	1.00	1.80	1.00	1.38	2.30
50F	1.00	1.67	1.00	1.33	2.27
100F	1.00	1.79	1.00	1.35	2.30
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	1.00	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	1.00	1.83	1.05	1.27	2.62
50F 25E	1.00	1.56	1.19	1.29	2.72
100F 50E	1.00	1.89	1.42	1.25	2.53
5F 25E 5R 5A	1.08	1.00	1.17	1.18	2.95
10F 10E 5R 5A	1.04	1.04	1.05	1.16	2.41

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%	64.49%	38.77%	49.36%
100F 50E	0.00%	0.00%	74.61%	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	1.01	1.71
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

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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

%Corrupt\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)

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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)

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Repair type frequency and impact analysis

- TODO

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 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.