A single-source k shortest paths algorithm to infer regulatory pathways in a gene network - Supplementary Material

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(a) UNKNOWNCAUSAL using different λ. (b) UNKNOWNTARGET using different λ.

Figure 1: The sorted e-values of the top GO term in GO_{ann} with different λ. $k = 5$.

Table 1: The number of gold standards found by the k diverse paths algorithm with a significantly less e-value of a GO term in GO_{ann} than the k-shortest paths algorithm ($\lambda = 0$). $k = 5$.

$\lambda = 0.25$	33	$\lambda = 0.75$	445
$\lambda = 0.5$	167	$\lambda = 1.0$	604

Table 2: Case study - other examples: The e-values of some enriched GO terms found by $k = 5$ diverse short paths algorithm with different λ. E-values larger than 0.01 are denoted by "-", representing insignificance.

GO number	function name	$\lambda = 0$	$\lambda = 0.25$	$\lambda = 0.5$	$\lambda = 0.75$	$\lambda = 1.0$
Starting node: CMD1						
GO:0000780	condensed nuclear chromosome...	3.32E-3	2.61E-3	5.72E-4	2.43E-5	**8.51E-7**
*GO:0005934	cellular bud tip	-	-	-	-	**1.61E-4**
*GO:0006606	protein import into nucleus	5.28E-5	6.50E-5	1.55E-5	1.23E-8	
GO:0010499	proteasomal ubiquitin-independent ...	1.42E-11	**1.39E-11**	4.05E-9	-	-
*GO:0031023	microtubule organizing center ...	**1.98E-9**	3.58E-9	2.55E-8	4.80E-8	3.20 E-8
*GO:0034504	protein localization in nucleus	-	-	1.02E-5	6.73E-9	**4.08E-12**
Starting node: RRP6						
GO:0000462	maturation of SSU-rRNA ...	3.00E-11	2.26E-11	5.42E-12	4.38E-4	-
*GO:0000466	maturation of 5.8S rRNA ...	**1.46E-31**	2.18E-31	1.67E-31	1.37E-21	6.20E-20
GO:0008094	DNA-dependent ATPase activity	-	-	-	3.53E-3	**4.92E-5**
*GO:0031126	snoRNA 3'-end processing	**1.10E-25**	2.27E-25	3.58E-25	1.76E-19	1.25E-20
Starting node: BUB3						
*GO:0000777	condensed chromosome kinetochore	2.53E-35	4.50E-35	**2.51E-36**	1.55E-3	5.03E-5
*GO:0007091	mitotic metaphase/anaphase transition	**9.36E-21**	1.67E-20	3.62E-18	7.30E-7	2.66E-11
GO:0016251	general RNA polymerase II transcription	-	-	-	**2.73E-9**	-
GO:0031145	anaphase-promoting complex-...	8.45E-13	**7.77E-13**	3.19E-11	-	4.19E-4
*GO:0033597	mitotic checkpoint complex	3.20E-4	8.94E-4	5.67E-3	1.05E-3	**6.11E-5**

*These GO terms are in GO_{ann}, i.e., they annotate the starting node.

Table 3: The top 10 genes and their corresponding paths found when $\lambda = 0$ and 1.0. The starting node is RTS1.

$\lambda = 0$			
1.PPH21	RTS1 → PPH21 RTS1→RRD2→PPH21 RTS1→SGO1→PPH21 RTS1→RRD2→TAP24→PPH21 RTS1→RRD2→TPD3→PPH21	6.PPH22	RTS1→RRD2→PPH22 RTS1→SGO1→PPH22 RTS1→PPH21→RRD2→PPH22 RTS1→RRD2→TAP24→PPH22 RTS1→RRD2→TPD3→PPH22
2.RRD2	RTS1→RRD2 RTS1→PPH21→RRD2 RTS1→PPH21→TAP24→RRD2 RTS1→SGO1→PPH21→RRD2 RTS1→SGO1→TPD3→RRD2	7.SIT4	RTS1→RRD2→SIT4 RTS1→PPH21→RRD2→SIT4 RTS1→PPH21→TOR2→SIT4 RTS1→RRD2→TAP24→SIT4 RTS1→PPH21→RRD1→SIT4
3.SGO1	RTS1→SGO1 RTS1→PPH21→SGO1 RTS1→RRD2→PPH21→SGO1 RTS1→RRD2→TPD3→SGO1 RTS1→RRD2→PPH22→SGO1	8.RRD1	RTS1→PPH21→RRD1 RTS1→RRD2→TAP24→RRD1 RTS1→RRD2→SIT4→RRD1 RTS1→RRD2→PPH21→RRD1 RTS1→RRD2→TPD3→RRD1
4.TPD3	RTS1→RRD2→TPD3 RTS1→SGO1→TPD3 RTS1→PPH21→TPD3 RTS1→PPH21→RRD2→TPD3 RTS1→PPH21→RRD1→TPD3	9.TOR2	RTS1→PPH21→TOR2 RTS1→RRD2→TAP24→TOR2 RTS1→RRD2→SIT4→TOR2 RTS1→RRD2→PPH21→TOR2 RTS1→PPH21→TAP24→TOR2
5.TAP24	RTS1→RRD2→TAP24 RTS1→PPH21→TAP24 RTS1→PPH21→RRD2→TAP24 RTS1→PPH21→TOR2→TAP24 RTS1→RRD2→SIT4→TAP24	10.CDC55	RTS1→PPH21→CDC55 RTS1→RRD2→PPH21→CDC55 RTS1→RRD2→TPD3→CDC55 RTS1→RRD2→PPH22→CDC55 RTS1→PPH21→ZDS2→CDC55
$\lambda = 1.0$			
1.PPH21	RTS1→PPH21 RTS1→RRD2→PPH21 RTS1→SGO1→PPH21	6.TAP24	RTS1→RRD2→TAP24 RTS1→PPH21→TAP24
2.RRD2	RTS1→RRD2 RTS1→PPH21→RRD2 RTS1→SGO1→TPD3→RRD2	7.ZDS2	RTS1→PPH21→ZDS2 RTS1→RRD2→TPD3→ZDS2 RTS1→SGO1→TPD3→CDC55→ZDS2
3.SGO1	RTS1→SGO1 RTS1→PPH21→SGO1 RTS1→RRD2→TPD3→SGO1	8.PPH22	RTS1→RRD2→PPH22 RTS1→SGO1→PPH22
4.TPD3	RTS1→RRD2→TPD3 RTS1→SGO1→TPD3 RTS1→PPH21→TPD3	9.SIT4	RTS1→RRD2→SIT4 RTS1→PPH21→TOR2→SIT4 RTS1→PPH21→TOR2→SIT4
5.CDC55	RTS1→PPH21→CDC55 RTS1→RRD2→TPD3→CDC55 RTS1→SGO1→PPH22→CDC55	10.TOR2	RTS1→PPH21→TOR2 RTS1→RRD2→TAP24→TOR2