

Googlomics

signor.sif

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Abstract

Preliminary study on Google matrix of protein networks.

1 Network structure

Let's consider the directed network provided by Andrei Zinovyev (signor.sif file).

```
# of different proteins = 5824
# of different interactions = 8
6971 links with interaction 1: transcription
3251 links with interaction 2: up-regulates
1754 links with interaction 3: down-regulates
324 links with interaction 4: up-regulates quantity
593 links with interaction 5: up-regulates activity
154 links with interaction 6: down-regulates quantity
198 links with interaction 7: unknown
295 links with interaction 8: down-regulates activity
# of links = 14708
# of 1-links = 12869
# of 2-links = 310
# of 3-links = 13
# of 4-links = 3
```

2 Google matrix

The considered network possesses N nodes and N_ℓ links. We define a $N \times N$ adjacency matrix A whose the elements are $A_{ij} = n$ if node j points toward node i via n directed interactions (links). The elements of the Google matrix G are

$$G_{ij} = \alpha S_{ij} + (1 - \alpha)/N \quad (1)$$

where S_{ij} are the elements of the stochastic matrix S

$$S_{ij} = \begin{cases} 1/N & \text{if } j \text{ is a dangling node} \\ \frac{A_{ij}}{\sum_{k=1}^N A_{kj}} & \text{otherwise} \end{cases} \quad (2)$$

The PageRank probability vector P is such as $GP = P$. Consequently, P is the eigenvector associated to unity eigenvalue.

For the same network, it is possible to consider its inverted network characterized by a $N \times N$ adjacency matrix A' whose the elements are $A'_{ij} = n$ if node j is pointed from node i via n directed interactions (links). The elements of the corresponding Google matrix G^* are

$$G^*_{ij} = \alpha S^*_{ij} + (1 - \alpha)/N \quad (3)$$

where S^*_{ij} are the elements of the stochastic matrix S^*

$$S^*_{ij} = \begin{cases} 1/N & \text{if no nodes points toward node } j \\ \frac{A^*_{ij}}{\sum_{k=1}^N A^*_{kj}} & \text{otherwise} \end{cases} \quad (4)$$

The CheiRank probability vector P^* is such as $G^*P^* = P^*$. Consequently, P^* is the eigenvector associated to unity eigenvalue.

3 PageRank, CheiRank, 2DRank

Table 1 gives top 100 proteins according to PageRank algorithm.

Table 2 gives top 100 proteins according to CheiRank algorithm.

Table 3 gives top 100 proteins according to 2DRank algorithm.

Fig. 1 shows PageRank (CheiRank) probability as a function of K (K^*) index.

Fig. 2 shows the distribution of proteins on the Pagerank-CheiRank plane (K - K^* plane).

Fig. 3 shows the complex spectrum of Google matrices G and G^* .

Fig. 4 shows inverse participation ratios of G and G^* eigenvectors.

Table 1: **Top 100 proteins from PageRanking**

K	PageRank probability ($\alpha = 0.85$)	Protein	aktmtor	cit7	e2f1targets
1	0.61867700062238898E-02	PIK3CB			
2	0.58378209434316237E-02	NOTCH1			
3	0.55108916908452865E-02	MYOD1			
4	0.54466379350716034E-02	TEK			
5	0.39925093635559866E-02	LEF1			
6	0.37697068049365745E-02	CTNNB1			
7	0.37519330888639984E-02	PPARG			
8	0.36138799218548002E-02	AXIN1			
9	0.34514447260332218E-02	CASP3			
10	0.32655115391020529E-02	SMAD4			
11	0.32228655881422384E-02	KIT			
12	0.30198265252946235E-02	TP53			
13	0.29831342755130839E-02	CDKN1A			
14	0.29609358752815603E-02	SMAD3			
15	0.29471354980482364E-02	CASP9			
16	0.28740131032172983E-02	PIK3CD			
17	0.26883592250853291E-02	AKT1			
18	0.24613147291790076E-02	MAPK14			
19	0.24204303400942583E-02	LRP6			
20	0.23319547602142092E-02	BAX			
21	0.22411035354602296E-02	STAT3			
22	0.21756709463379995E-02	MYF5			
23	0.21331586196999574E-02	CCND1			
24	0.20455036536248557E-02	RUNX2			
25	0.19411735065238190E-02	CEBPA			
26	0.19204972447337161E-02	PIK3CA			
27	0.19009882933319348E-02	MAP3K7			
28	0.18931827519769835E-02	SMAD2			
29	0.18412065224268868E-02	PITX2			
30	0.18308926935019800E-02	CDK1			
31	0.18258560922662170E-02	MAPK8			
32	0.18092210223861184E-02	CDK2			
33	0.17900940830109831E-02	EGFR			
34	0.17216202969066358E-02	JAK1			
35	0.16649924261985561E-02	RAC1			
36	0.16600491161659355E-02	TRAF2			
37	0.16484996482973313E-02	MAPK3			
38	0.16196822012765642E-02	GRB2			
39	0.16190253741950021E-02	PLCG1			
40	0.15403542007659129E-02	RELA			
41	0.15341544801827556E-02	MYOG			
42	0.15179894184304518E-02	MYC			
43	0.15116891382109725E-02	RHOA			
44	0.14804281503857753E-02	SMAD1			
45	0.14792707911675751E-02	TYK2			
46	0.14601268959867870E-02	FGFR4			
47	0.14498856797682273E-02	DIABLO			
48	0.14086242059337885E-02	ABL1			

49	0.13985822286391370E-02	RAF1		
50	0.13797043151451020E-02	FABP4		
51	0.13765328416496632E-02	RB1		
52	0.13681190081076896E-02	MAP3K1		
53	0.13555872513933293E-02	IRAK1		
54	0.13486897260899810E-02	CDK4		
55	0.13475652641422088E-02	JAK2		
56	0.13321059120548587E-02	MAP3K5		
57	0.13276253680503558E-02	RIPK1		
58	0.13186361972707339E-02	YAP1		
59	0.13116665370332968E-02	MDM2		
60	0.12685039588276481E-02	AR		
61	0.12580219551198705E-02	FADD		
62	0.12506964670802608E-02	CYCS		
63	0.12438732804647546E-02	HRAS		
64	0.12412442942691619E-02	HDAC1		
65	0.12374915075613313E-02	BCL2L1		
66	0.12306468771592527E-02	TCF3		
67	0.12287619146084201E-02	ATM		
68	0.12282801898717442E-02	BCL2		
69	0.12082306010831385E-02	SMARCA4		
70	0.12049099368817137E-02	NFKB1		
71	0.12042088418893485E-02	MEF2C		
72	0.11970773947846997E-02	MTOR		
73	0.11879755425506715E-02	MAPK1		
74	0.11685919103818283E-02	DVL1		
75	0.11652141840253809E-02	IRS1		
76	0.11632946326733844E-02	NUMB		
77	0.11620652063773895E-02	E2F1		
78	0.11462475497786364E-02	RBPJ		
79	0.11410423727303070E-02	TRAF6		
80	0.11368198032119684E-02	PTEN		
81	0.11273887891024366E-02	CASP8		
82	0.11244465323719059E-02	BAK1		
83	0.11184093188099530E-02	MAP2K1		
84	0.11170470239275979E-02	XIAP		
85	0.11112788034661162E-02	TERT		
86	0.10968170292155285E-02	JAK3		
87	0.10953053536132605E-02	CDKN1B		
88	0.10796270689871911E-02	JUN		
89	0.10787048624256677E-02	MAP2K4		
90	0.10723925815259794E-02	CBL		
91	0.10696031530652584E-02	RXRA		
92	0.10659135192091221E-02	APAF1		
93	0.10463375532361655E-02	GLI1		
94	0.10450579156785790E-02	GSK3B		
95	0.10429603469665969E-02	PIK3C3		
96	0.10393086326329502E-02	IL6ST		
97	0.10284299160876012E-02	BAD		
98	0.10201803491167645E-02	HTRA2		
99	0.10162199240300028E-02	STAT1		
100	0.10099362485530416E-02	PIK3R1		

Table 2: **Top 100 proteins from CheiRanking**

K^*	CheiRank probability ($\alpha = 0.85$)	Protein	aktmtor	cit7	e2fltargets
1	0.53984991303061269E-01	GABPA			
2	0.45705457510481798E-01	REST			
3	0.17735620173326836E-01	EBF1			
4	0.16885096148340473E-01	SPI1			
5	0.16371147239751368E-01	CTCF			
6	0.15204975271077696E-01	PRKAA1			
7	0.15101679186562321E-01	NRF1			
8	0.12824473983975915E-01	PBX3			
9	0.12428778660309659E-01	YY1			
10	0.10976587077341704E-01	HOXB8			
11	0.10265566092383516E-01	MAPK1			
12	0.94453467825880493E-02	ZNF143			
13	0.91694976926730419E-02	SRF			
14	0.79886851285727015E-02	ELF1			
15	0.78818359064447749E-02	MAPK3			
16	0.77862022474473779E-02	FOS			
17	0.76154187317242359E-02	SP1			
18	0.72782355100346950E-02	CSNK2A1			
19	0.72115547623455067E-02	CDK1			
20	0.71559475137776413E-02	PRKACA			
21	0.69944261780450879E-02	ATM			
22	0.63769965085685675E-02	AURKB			
23	0.62717703031558827E-02	SIX5			
24	0.60084275222200907E-02	SRC			
25	0.58840264120814600E-02	STK11			
26	0.58117378288551025E-02	RFX5			
27	0.58004727965493038E-02	EGR1			
28	0.57169649502056148E-02	CHD2			
29	0.53715270613996367E-02	AKT1			
30	0.52818379668668000E-02	RAD21			
31	0.51207720692581941E-02	PLK1			
32	0.49147121083916757E-02	USF1			
33	0.47094172699508203E-02	MAPK14			
34	0.44078250676006698E-02	EP300			
35	0.44034194959263890E-02	PDPK1			
36	0.42145531422599891E-02	BMP7			
37	0.41445302461847564E-02	BATF			
38	0.38108771467831391E-02	PRKCA			
39	0.38079394305040523E-02	GSK3B			
40	0.36401067508999908E-02	PRKCD			
41	0.35791551481483031E-02	PAX5			
42	0.35766294329587112E-02	POU2F2			
43	0.34869584757255413E-02	ZEB1			
44	0.32961871220664530E-02	NOTCH1			
45	0.32453874566025005E-02	CDK2			
46	0.27747275009208535E-02	PRKCZ			
47	0.27196362930472415E-02	USF2			
48	0.26681100116140700E-02	RPS6KA1			
49	0.25777307374288525E-02	MAPK8			
50	0.25216784817754533E-02	DYRK1A			
51	0.24596041058468688E-02	MAPKAPK2			
52	0.24149271449680240E-02	CHEK1			
53	0.23948772406502296E-02	RELA			
54	0.23490571333562790E-02	PRKDC			
55	0.23472760739586349E-02	ATR			
56	0.23287335449732783E-02	PTPN1			
57	0.23197930359863890E-02	CAMKK2			
58	0.22962922753073046E-02	TCF12			

59	0.22606037515026564E-02	CALM3	
60	0.22188601214966236E-02	CAMK2A	
61	0.21633620763249389E-02	ULK1	
62	0.21433188629933259E-02	RET	
63	0.21199617004099767E-02	CAMKK1	
64	0.21137862618269407E-02	ZBTB33	
65	0.21103460223943312E-02	TWIST1	
66	0.20885295971885902E-02	BRCA1	
67	0.20805700708368022E-02	ABL1	
68	0.20374604968783913E-02	SMO	
69	0.20042678081561188E-02	CAMK2B	
70	0.19424963450517748E-02	CTNND1	
71	0.19313203100134340E-02	TLR4	
72	0.19203401840193403E-02	EGFR	
73	0.18944977142705060E-02	BRSK2	
74	0.18443523774423285E-02	PPP2CA	
75	0.18297187543134643E-02	PTK6	
76	0.17707889129509621E-02	NFKB1	
77	0.17706054332034560E-02	MEF2A	
78	0.17680665524500560E-02	AKT2	
79	0.17662660635243983E-02	CDK5	
80	0.16785647680086563E-02	SMARCA4	
81	0.16663032624300786E-02	RPS6KA4	
82	0.16543183720492389E-02	NFE2	
83	0.16507290604374088E-02	PAK1	
84	0.16016912100909523E-02	POU2AF1	
85	0.15880959590370637E-02	ETS1	
86	0.15609522216796101E-02	TP53	
87	0.15347654726908613E-02	PTPRJ	
88	0.15323704341041307E-02	TGFB1	
89	0.15202644691872526E-02	PRKG1	
90	0.14929024018328497E-02	DAPK1	
91	0.14032910327896304E-02	INCENP	
92	0.13133754986986177E-02	LCK	
93	0.12804956001365203E-02	ATF3	
94	0.12804237812410082E-02	CREB1	
95	0.12751816047887511E-02	PRKCE	
96	0.12472674301535558E-02	MKL2	
97	0.12405476454817539E-02	MTOR	
98	0.12278908700843163E-02	CHEK2	
99	0.11884337051269900E-02	IGF1R	
100	0.11811870896252247E-02	EIF2AK2	

Table 3: **Top 100 proteins from 2DRanking**

K_2	K	K^*	Protein	aktmtor	cit7	e2f1targets
1	17	29	AKT1			
2	30	19	CDK1			
3	18	33	MAPK14			
4	37	15	MAPK3			
5	2	44	NOTCH1			
6	32	45	CDK2			
7	31	49	MAPK8			
8	40	53	RELA			
9	67	21	ATM			
10	48	67	ABL1			
11	33	72	EGFR			
12	73	11	MAPK1			
13	70	76	NFKB1			
14	69	80	SMARCA4			
15	12	86	TP53			
16	94	39	GSK3B			
17	72	97	MTOR			
18	110	83	PAK1			
19	112	77	MEF2A			
20	13	112	CDKN1A			
21	83	117	MAP2K1			
22	122	38	PRKCA			
23	71	134	MEF2C			
24	138	110	INSR			
25	87	140	CDKN1B			
26	141	88	TGFB1			
27	142	118	ERBB2			
28	9	143	CASP3			
29	101	144	IKBKB			
30	151	68	SMO			
31	153	78	AKT2			
32	154	94	CREB1			
33	35	154	RAC1			
34	3	157	MYOD1			
35	158	148	CAMP			
36	161	24	SRC			
37	119	163	PIK3CG			
38	164	152	MAP2K2			
39	156	165	ADCY1			
40	8	173	AXIN1			
41	175	13	SRF			
42	116	180	SMAD7			
43	181	34	EP300			
44	187	169	FZD3			
45	6	187	CTNNB1			
46	189	66	BRCA1			
47	77	189	E2F1			
48	191	121	SHH			
49	159	197	ROCK1			
50	201	153	PEA15			
51	148	201	NBN			
52	202	35	PDPK1			
53	59	203	MDM2			
54	90	206	CBL			
55	39	208	PLCG1			
56	209	105	PPP1CA			
57	210	20	PRKACA			
58	27	210	MAP3K7			

59	24	212	RUNX2		
60	41	213	MYOG		
61	217	123	DVL3		
62	55	219	JAK2		
63	223	25	STK11		
64	42	227	MYC		
65	91	228	RXRA		
66	54	236	CDK4		
67	120	238	MAPK9		
68	152	244	MAP2K6		
69	80	245	PTEN		
70	249	31	PLK1		
71	157	249	PTK2		
72	251	183	GSK3A		
73	78	253	RBPJ		
74	257	185	CHUK		
75	199	262	WWTR1		
76	109	266	PTCH1		
77	270	52	CHEK1		
78	58	279	YAP1		
79	26	280	PIK3CA		
80	282	6	PRKAA1		
81	283	74	PPP2CA		
82	233	283	BMP2		
83	284	282	CSNK1D		
84	51	287	RB1		
85	291	194	CDC25C		
86	56	296	MAP3K5		
87	43	297	RHOA		
88	300	149	CDKN2A		
89	208	301	DUSP3		
90	215	302	CREBBP		
91	133	304	HES1		
92	265	307	LRIG1		
93	118	308	ESR1		
94	81	310	CASP8		
95	311	135	PRKAA2		
96	314	252	ITCH		
97	315	56	PTPN1		
98	74	315	DVL1		
99	163	321	TGFBR2		
100	330	294	ILK		

4 Reduced Google matrix analysis

According to arXiv:1602.02394, a reduced Google matrix can be derived for a given subnetwork of n_r nodes. Let G and P be the Google matrix and the PageRank probability vector associated to the complete directed network. It is always possible to decompose G and P such as

$$GP = \begin{pmatrix} G^{(rr)} & G^{(rs)} \\ G^{(sr)} & G^{(ss)} \end{pmatrix} \begin{pmatrix} P^{(R)} \\ P^{(S)} \end{pmatrix} \quad (5)$$

where $G^{(rr)}$ is the $n_r \times n_r$ Google submatrix describing jumps between nodes (proteins) of the subnetwork, $G^{(ss)}$ is the $n_s \times n_s$ Google submatrix describing jumps between nodes (proteins) not belonging to the subnetwork, $G^{(sr)}$ is the $n_s \times n_r$ Google submatrix describing jumps from a node belonging to the subnetwork toward a node not belonging to the subnetwork, and $G^{(rs)}$ is $n_r \times n_s$ the Google submatrix describing jumps from a node not belonging to the subnetwork toward a node belonging to the subnetwork. We are looking for a $n_r \times n_r$ reduced Google matrix $G^{(R)}$ such as

$$G^{(R)} P^{(R)} = P^{(R)} \quad (6)$$

The expression of $G^{(R)}$ is given by (see arXiv:1602.02394)

$$G^{(R)} = G^{(rr)} + G^{(rs)} \left(\mathbf{1}_s - G^{(ss)} \right)^{-1} G^{(sr)} \quad (7)$$

where $\mathbf{1}_s$ is the identity matrix of the subspace of nodes not belonging to the subnetwork. If $n_r \ll n_s$, the $G^{(ss)}$ matrix is quite similar to the global Google matrix G , the biggest eigenvalue of $G^{(ss)}$ is $\lambda_c \approx 1$ and the corresponding right eigenvector of $G^{(ss)}$ is similar to the PageRank probability vector P . Let us define $\mathcal{P}_c$ the projector on the eigenspace associated with the biggest eigenvalue λ_c , and the orthogonal projector $\mathcal{Q}_c = \mathbf{1}_s - \mathcal{P}_c$, we can write

$$\left(\mathbf{1}_s - G^{(ss)} \right)^{-1} = \frac{1}{1 - \lambda_c} \mathcal{P}_c + \mathcal{Q}_c \left(\mathbf{1}_s - G^{(ss)} \right)^{-1} \mathcal{Q}_c \quad (8)$$

and decompose the reduced Google matrix in three terms

$$G^{(R)} = G^{(rr)} + G^{(pr)} + G^{(qr)} \quad (9)$$

The $G^{(pr)} = \frac{1}{1 - \lambda_c} G^{(rs)} \mathcal{P}_c G^{(sr)}$ matrix is a quite homogeneous matrix which mainly encodes the PageRank information, the matrix elements of the residual matrix $G^{(qr)}$ gives the hidden links between proteins.

4.1 aktmtor subnetwork

4.1.1 aktmtor PageRanking

See Fig. 5 page 22 for matrix elements.

Table 4: **PageRanking of aktmtor proteins**

K	PageRank probability ($\alpha = 0.85$)	Protein
1	0.11011196876441225	CASP3
2	8.5767139716074581E-002	AKT1
3	6.0647521873816744E-002	MAP3K7
4	5.2592338474452695E-002	MAPK3
5	3.9479883144174562E-002	BCL2L1
6	3.9186012421124274E-002	BCL2
7	3.8190545147390113E-002	MTOR
8	3.7900167252942756E-002	MAPK1
9	3.3340644672083718E-002	GSK3B
10	3.3273725304403187E-002	PIK3C3
11	3.2174659512789791E-002	IKBKB
12	2.6190215722039046E-002	BECN1
13	2.3578363170135792E-002	FOXO3
14	2.3335080098845221E-002	AKT2
15	1.8627583070759381E-002	RPTOR
16	1.8084160608559299E-002	PDPK1

17	1.6225637679815805E-002	STK11
18	1.5863164723269100E-002	EIF4E
19	1.3244013861128426E-002	PRKAA1
20	1.2974699470764049E-002	MAPK6
21	1.2329204811832912E-002	PRKAA2
22	1.2128875772745119E-002	FOXO1
23	1.1434176215075717E-002	RHEB
24	1.0796689982021344E-002	PRKDC
25	9.9851286357412628E-003	PRDX1
26	9.2030765695063493E-003	AKT1S1
27	8.9689965157480310E-003	CAMKK2
28	8.8410640881464581E-003	RPS6KB1
29	8.8197698925103780E-003	RPS6KB2
30	8.8169575900623152E-003	RPS6KA3
31	8.7057719209003605E-003	DUSP1
32	8.4915057581942174E-003	TSC1
33	8.2744184537359832E-003	PDCD4
34	8.1911744347081660E-003	FKBP8
35	7.9263208283618797E-003	TSC2
36	7.7044835154790403E-003	EIF4EBP1
37	7.3298612379214499E-003	RPS6KA1
38	6.9897390073347526E-003	YWHAG
39	6.9765078273848011E-003	YWHAZ
40	6.2768851374214920E-003	PRKAG3
41	6.2096259180285151E-003	SFN
42	6.0644895401003951E-003	YWHAB
43	5.7293099883198827E-003	DEPTOR
44	5.5762730415027063E-003	PRKAB1
45	4.5154757502822154E-003	EIF4B
46	4.3412113279035795E-003	DAPK1
47	4.0140538615429291E-003	DUSP6
48	3.8377092119449793E-003	RPS6KA2
49	3.8099291369736539E-003	HSP90AA1
50	3.6951739219906309E-003	RICTOR
51	3.3488518135336071E-003	YWHAQ
52	3.3374808364602139E-003	FBXW11
53	3.3374808364602135E-003	BTRC
54	3.3299436469737091E-003	YWHAE
63	3.3194286982411564E-003	PRKAG1
63	3.3194286982411564E-003	YWHAH
63	3.3194286982411564E-003	BNIP3
63	3.3194286982411564E-003	PIM2
63	3.3194286982411564E-003	PIM1
63	3.3194286982411564E-003	RBX1
63	3.3194286982411564E-003	DDB1
63	3.3194286982411564E-003	DUSP16
63	3.3194286982411564E-003	DUSP10

4.1.2 aktmtor CheiRanking

See Fig. 7 page 23 for matrix elements.

Table 5: **CheiRanking of aktmtor proteins**

K'	CheiRank probability ($\alpha = 0.85$)	Protein
1	0.20117448396156373	PRKAA1
2	0.13582198365782974	MAPK1
3	0.10428324943483358	MAPK3
4	7.7850565805533858E-002	STK11
5	7.1069774560411691E-002	AKT1
6	5.8260903475106339E-002	PDPK1

7	5.0382208147200694E-002	GSK3B
8	3.5301316169418513E-002	RPS6KA1
9	3.1079981647456553E-002	PRKDC
10	3.0692792578462250E-002	CAMKK2
11	2.3392991948389029E-002	AKT2
12	1.9752340784286348E-002	DAPK1
13	1.6413477710304956E-002	MTOR
14	1.2595866625250141E-002	DUSP1
15	1.1176640911516121E-002	PRKAA2
16	1.0361146676034825E-002	CASP3
17	1.0344490448397940E-002	IKBKB
18	1.0036382387410047E-002	DUSP6
19	7.3056449105731646E-003	MAP3K7
20	6.8389405119198797E-003	PRKAB1
21	6.5050375790745478E-003	RPS6KA3
22	5.5014375882631063E-003	RPS6KB1
23	4.4467843205570944E-003	BTRC
24	3.3005093258797395E-003	FBXW11
25	3.2545932511794762E-003	PIM1
26	2.9487530140262608E-003	DUSP10
27	2.7958968715168652E-003	FOXO1
28	2.6814868256256159E-003	TSC2
29	2.5641927997518020E-003	RHEB
30	2.5374804269539058E-003	PRKAG1
31	2.5259426926194364E-003	PIK3C3
32	2.3648247610763406E-003	YWHAQ
33	2.3140623547738344E-003	DUSP16
34	2.2940698355078913E-003	TSC1
35	2.2620016640965230E-003	FOXO3
36	2.1713041277830955E-003	RBX1
37	1.8490053963064312E-003	HSP90AA1
38	1.6777693161855983E-003	BCL2
39	1.5675485422392112E-003	FKBP8
40	1.5166032381922481E-003	BCL2L1
41	1.3639727652500298E-003	BNIP3
42	1.1312920872165130E-003	DDB1
43	1.0935612894785143E-003	PIM2
44	1.0824067497294089E-003	YWHAB
45	9.9529335343855377E-004	BECN1
47	9.9111622024228361E-004	YWHAH
47	9.9111622024228361E-004	YWHAE
48	9.4906667579695619E-004	MAPK6
49	8.8127666001521431E-004	RPS6KB2
50	8.6150771522817125E-004	RPS6KA2
51	7.2775709717940948E-004	EIF4EBP1
52	7.0518069087933087E-004	SFN
53	6.3745147198134781E-004	EIF4E
62	6.3745147198134770E-004	RICTOR
62	6.3745147198134770E-004	EIF4B
62	6.3745147198134770E-004	PRKAG3
62	6.3745147198134770E-004	DEPTOR
62	6.3745147198134770E-004	YWHAG
62	6.3745147198134770E-004	PDCD4
62	6.3745147198134770E-004	YWHAZ
62	6.3745147198134770E-004	RPTOR
62	6.3745147198134770E-004	PRDX1
63	6.3745147198134673E-004	AKT1S1

4.1.3 aktmtor 2DRanking

See Fig 9 page 24.

Table 6: **2DRanking of aktmtor proteins**

K_2	K	K^*	Protein
4	4	3	MAPK3
5	2	5	AKT1
8	8	2	MAPK1
9	9	7	GSK3B
13	7	13	MTOR
14	14	11	AKT2
16	16	6	PDPK1
16	1	16	CASP3
17	17	4	STK11
17	11	17	IKBKB
19	19	1	PRKAA1
19	3	19	MAP3K7
21	21	15	PRKAA2
24	24	9	PRKDC
27	27	10	CAMKK2
27	22	27	FOXO1
28	28	22	RPS6KB1
29	23	29	RHEB
30	30	21	RPS6KA3
31	31	14	DUSP1
31	10	31	PIK3C3
34	32	34	TSC1
35	35	28	TSC2
35	13	35	FOXO3
37	37	8	RPS6KA1
38	6	38	BCL2
39	34	39	FKBP8
40	5	40	BCL2L1
44	44	20	PRKAB1
44	42	44	YWHAB
45	12	45	BECN1
46	46	12	DAPK1
47	47	18	DUSP6
48	20	48	MAPK6
49	49	37	HSP90AA1
49	29	49	RPS6KB2
50	48	50	RPS6KA2
51	51	32	YWHAQ
51	36	51	EIF4EBP1
52	52	24	FBXW11
52	41	52	SFN
53	53	23	BTRC
53	18	53	EIF4E
54	54	47	YWHAE
62	15	62	RPTOR
62	25	62	PRDX1
62	33	62	PDCD4
62	38	62	YWHAG
62	39	62	YWHAZ
62	40	62	PRKAG3
62	43	62	DEPTOR
62	45	62	EIF4B
62	50	62	RICTOR
63	63	25	PIM1
63	63	26	DUSP10
63	63	30	PRKAG1
63	63	33	DUSP16
63	63	36	RBX1

63	63	41	BNIP3
63	63	42	DDB1
63	63	43	PIM2
63	63	47	YWHAH
63	26	63	AKT1S1

4.2 cit7 subnetwork

4.2.1 cit7 PageRanking

See Fig. 10 page 25 for matrix elements.

Table 7: **PageRanking of cit7 proteins**

K	PageRank probability ($\alpha = 0.85$)	Protein
1	0.15398844375244986	CDK1
2	6.7246991817989224E-002	CCNB1
3	6.5836696751132920E-002	PCNA
4	4.1049258166215394E-002	CCNE1
5	4.0635830288622443E-002	BIRC5
6	3.6849128158921524E-002	CHEK1
7	3.0310925028075350E-002	CCNA2
8	2.8381554312541610E-002	EZH2
9	2.6793784951995196E-002	CDC25B
10	2.6205725985327694E-002	BLM
11	2.1086300413531239E-002	FOXM1
12	2.0759916307623701E-002	AURKB
13	2.0658242899449904E-002	AURKA
14	1.8380689972115657E-002	MELK
15	1.7531303754825683E-002	CDC6
16	1.6830870142151982E-002	VRK1
17	1.5128283131884863E-002	BUB1
18	1.4561172582167773E-002	BUB1B
19	1.3574162535993761E-002	DNMT1
20	1.3214311715862183E-002	KIF2C
21	1.3088006883541463E-002	MCM2
22	1.2935508939495296E-002	NDC80
23	1.2694265932804075E-002	ECT2
24	1.2394338854874934E-002	TTK
25	1.1513475373981169E-002	GPSM2
26	1.1464404156040968E-002	CDCA3
27	1.1446632571363038E-002	TOP2A
28	1.1342394068958176E-002	BORA
29	1.1272947498601979E-002	DTL
30	1.1116439585240074E-002	PTTG1
31	1.1082660158689374E-002	CDC7
32	1.1012130823998437E-002	RACGAP1
33	1.0956430154477772E-002	CEP55
34	1.0943767781927016E-002	DBF4
35	1.0749268436011662E-002	RRM2
36	1.0365989671560912E-002	CDCA7
37	1.0338304406746799E-002	CKAP2
38	1.0298030331604436E-002	ESPL1
39	1.0255971981035112E-002	CDCA8
40	9.9906623452455118E-003	FAM64A
41	9.8760829273604397E-003	FBXO5
42	9.7986116251741612E-003	FEN1
45	9.7501067779662380E-003	PBK
45	9.7501067779662380E-003	KIF11
45	9.7501067779662380E-003	NUSAP1
46	9.6848325880394080E-003	SPAG5

47	9.6030396606094880E-003	KPNA2
49	8.7509451199207968E-003	STIL
49	8.7509451199207968E-003	CDKN2C

4.2.2 cit7 CheiRanking

See Fig. 12 page 26 for matrix elements.

Table 8: **CheiRanking of cit7 proteins**

K'	CheiRank probability ($\alpha = 0.85$)	Protein
1	0.30892424424290144	CDK1
2	0.27317394028841130	AURKB
3	0.10344919399605236	CHEK1
4	4.9828755092910168E-002	AURKA
5	3.7543245383861008E-002	TTK
6	3.2430006176989455E-002	BORA
7	2.5935292225702327E-002	CDC25B
8	2.5370932538905874E-002	BUB1
9	1.9157576899093181E-002	MCM2
10	1.1153901072262161E-002	CCNE1
11	1.1065673012451023E-002	CDC7
12	7.8492480319121774E-003	MELK
13	7.4061127969560865E-003	BIRC5
14	5.4164998374047835E-003	FBXO5
15	5.0233928561458597E-003	CDKN2C
16	4.1105477606821796E-003	PBK
17	3.8875666318440106E-003	VRK1
18	3.5623314014075033E-003	FAM64A
19	2.7953391745105059E-003	STIL
48	2.0638733526532702E-003	DNMT1
48	2.0638733526532702E-003	DTL
48	2.0638733526532702E-003	FEN1
48	2.0638733526532702E-003	KIF2C
48	2.0638733526532702E-003	PCNA
48	2.0638733526532702E-003	RACGAP1
48	2.0638733526532702E-003	TOP2A
48	2.0638733526532702E-003	BLM
48	2.0638733526532702E-003	FOXO1
48	2.0638733526532702E-003	EZH2
48	2.0638733526532702E-003	CCNA2
48	2.0638733526532702E-003	ECT2
48	2.0638733526532702E-003	KPNA2
48	2.0638733526532702E-003	CKAP2
48	2.0638733526532702E-003	NDC80
48	2.0638733526532702E-003	PTTG1
48	2.0638733526532702E-003	CEP55
48	2.0638733526532702E-003	ESPL1
48	2.0638733526532702E-003	CDCA7
48	2.0638733526532702E-003	CDC6
48	2.0638733526532702E-003	GPSM2
48	2.0638733526532702E-003	RRM2
48	2.0638733526532702E-003	KIF11
48	2.0638733526532702E-003	NUSAP1
48	2.0638733526532702E-003	CCNB1
48	2.0638733526532702E-003	CDCA8
48	2.0638733526532702E-003	SPAG5
48	2.0638733526532702E-003	DBF4
48	2.0638733526532702E-003	CDCA3
49	2.0638733526532650E-003	BUB1B

4.2.3 cit7 2DRanking

See Fig 14 page 27.

Table 9: **2DRanking of cit7 proteins**

K_2	K	K^*	Protein
1	1	1	CDK1
6	6	3	CHEK1
9	9	7	CDC25B
10	4	10	CCNE1
12	12	2	AURKB
13	13	4	AURKA
13	5	13	BIRC5
14	14	12	MELK
17	17	8	BUB1
17	16	17	VRK1
21	21	9	MCM2
24	24	5	TTK
28	28	6	BORA
31	31	11	CDC7
40	40	18	FAM64A
41	41	14	FBXO5
45	45	16	PBK
48	2	48	CCNB1
48	3	48	PCNA
48	7	48	CCNA2
48	8	48	EZH2
48	10	48	BLM
48	11	48	FOXM1
48	15	48	CDC6
48	19	48	DNMT1
48	20	48	KIF2C
48	22	48	NDC80
48	23	48	ECT2
48	25	48	GPSM2
48	26	48	CDCA3
48	27	48	TOP2A
48	29	48	DTL
48	30	48	PTTG1
48	32	48	RACGAP1
48	33	48	CEP55
48	34	48	DBF4
48	35	48	RRM2
48	36	48	CDCA7
48	37	48	CKAP2
48	38	48	ESPL1
48	39	48	CDCA8
48	42	48	FEN1
48	45	48	KIF11
48	45	48	NUSAP1
48	46	48	SPAG5
48	47	48	KPNA2
49	49	15	CDKN2C
49	49	19	STIL
49	18	49	BUB1B

4.3 e2f1targets subnetwork

4.3.1 e2f1targets PageRanking

See Fig. 15 page 28 for matrix elements.

Table 10: **PageRanking of e2f1targets proteins**

<i>K</i>	PageRank probability ($\alpha = 0.85$)	Protein
1	8.4503960010493706E-002	PPARG
2	7.7736123543193272E-002	CASP3
3	6.8014886396177046E-002	TP53
4	6.7188472403152399E-002	CDKN1A
5	6.6377679836696055E-002	CASP9
6	4.1236791440411293E-002	CDK1
7	3.4189340370317234E-002	MYC
8	2.7675133029514319E-002	ATM
9	2.7664283338386404E-002	BCL2
10	2.6172937758734006E-002	E2F1
11	2.5391928370018607E-002	CASP8
12	2.5029087395488786E-002	TERT
13	2.4669320798793345E-002	CDKN1B
14	2.4007334530656406E-002	APAF1
15	1.8701835800004563E-002	CCND3
16	1.8008170672284052E-002	CCNB1
17	1.7630505685770594E-002	PCNA
18	1.6645697765728950E-002	FOXO3
19	1.4080667519642038E-002	FGFR2
20	1.3659755160971111E-002	BRCA1
21	1.1579589596972341E-002	TOPBP1
22	1.0992641113674659E-002	CCNE1
23	1.0881928655278541E-002	BIRC5
24	1.0407325294174950E-002	TP73
25	9.9140815000050234E-003	CASP7
26	9.6086572238577792E-003	GAB2
27	8.8539089989180166E-003	CDKN2A
28	8.5626639514772649E-003	FOXO1
29	8.1170071164064529E-003	CCNA2
30	8.0616250032429539E-003	MYCN
31	7.7910499337263623E-003	CDC25A
32	7.6431752475007988E-003	BCL2L11
33	7.6003380997775507E-003	EZH2
34	7.3810952928632430E-003	STMN1
35	6.7355688085596966E-003	E2F2
36	6.4278569613058526E-003	SKP2
37	5.7876841700342683E-003	MYB
38	5.5593284681135407E-003	AURKB
39	5.4095058432453566E-003	ACTN4
40	4.9221919542214972E-003	MELK
41	4.8966738160064896E-003	RPA2
42	4.8028094709491693E-003	PMAIP1
43	4.6947335723155964E-003	CDC6
44	4.6559345794953879E-003	BBC3
45	4.5613760758307425E-003	MCL1
46	4.5574812431481183E-003	AXIN2
47	4.3405481512278155E-003	TP53BP1
48	4.3054718300420472E-003	NRP1
49	4.1901930466633269E-003	CHEK2
50	3.9175729676460564E-003	PFKFB2
51	3.8847826032946189E-003	EIF2AK2
52	3.6350449153689634E-003	DNMT1
53	3.4765901922437603E-003	RBBP8
54	3.4484220677792801E-003	MCM3
55	3.2474115759921333E-003	ACTG1
56	3.0653105424613227E-003	TOP2A
57	3.0494306271247528E-003	TK1
58	3.0155510367953909E-003	PFKFB3

59	2.9306476422127701E-003	DBF4
60	2.8977849263763789E-003	CDT1
61	2.8785623767419548E-003	RRM2
62	2.8354706596208242E-003	UHRF1
63	2.7876427856255884E-003	SIVA1
65	2.7818636597623570E-003	NPAT
65	2.7818636597623570E-003	MYBL2
66	2.7759235937426445E-003	CDCA7
67	2.7638727020669637E-003	MCM7
68	2.7308581171588313E-003	DUSP2
69	2.6077032454217162E-003	RBL1
70	2.4808617380732523E-003	WWOX
71	2.4547017173779783E-003	CBX5
72	2.3520560338116730E-003	FHIT
76	2.3434284420171627E-003	HRK
76	2.3434284420171627E-003	BMI1
76	2.3434284420171627E-003	PTGS2
76	2.3434284420171627E-003	CDKN2C

4.3.2 e2f1targets CheiRanking

See Fig. 17 page 29 for matrix elements.

Table 11: **CheiRanking of e2f1targets proteins**

K'	CheiRank probability ($\alpha = 0.85$)	Protein
1	0.18525501303961131	CDK1
2	0.17967727095009914	ATM
3	0.16381634919702223	AURKB
4	5.3651479774781616E-002	BRCA1
5	4.0098734321285912E-002	TP53
6	3.1542841634276980E-002	CHEK2
7	3.0343085437001139E-002	EIF2AK2
8	2.7923270706666125E-002	CDKN1A
9	2.1003907023011571E-002	CDKN1B
10	2.0116930394701873E-002	CASP3
11	1.9601139891722980E-002	CDKN2A
12	1.5792460759465179E-002	E2F1
13	1.5581662819998577E-002	RBBP8
14	1.5050343691770027E-002	CDC25A
15	1.3125731985511046E-002	DUSP2
16	1.2775252210827983E-002	MYC
17	1.2072873858173034E-002	FHIT
18	9.0758171582792421E-003	CASP8
19	8.0890567636330239E-003	RPA2
20	6.6887469244883806E-003	CCNE1
21	5.9829902677463655E-003	BMI1
22	5.4939169280700754E-003	STMN1
23	5.4284399703787151E-003	FOXO1
24	4.9710776446841038E-003	AXIN2
25	4.7070198394409280E-003	MELK
26	4.5635653177073304E-003	PTGS2
27	4.4412814738066008E-003	BIRC5
28	4.3918430509875175E-003	FOXO3
29	4.2981600335266481E-003	FGFR2
30	3.2575128610132010E-003	BCL2
31	3.1574216329925010E-003	PPARG
32	3.1375913592543961E-003	CASP9
33	3.0124172071659292E-003	CDKN2C
34	2.8006735365115444E-003	BCL2L11
35	2.7676700575816589E-003	SKP2

36	2.7104320225197561E-003	BBC3
37	2.6590177656527414E-003	E2F2
38	1.9940979325608296E-003	GAB2
39	1.7168174938870682E-003	MCL1
41	1.5883291067210535E-003	TP53BP1
41	1.5883291067210535E-003	CASP7
42	1.5363712538763745E-003	HRK
43	1.4599050988121590E-003	APAF1
44	1.4480610817119068E-003	TOPBP1
45	1.2376590441981884E-003	ACTG1
75	1.2376590441981836E-003	DNMT1
75	1.2376590441981836E-003	PCNA
75	1.2376590441981836E-003	PFKFB3
75	1.2376590441981836E-003	TOP2A
75	1.2376590441981836E-003	TP73
75	1.2376590441981836E-003	WWOX
75	1.2376590441981836E-003	TERT
75	1.2376590441981836E-003	EZH2
75	1.2376590441981836E-003	MYB
75	1.2376590441981836E-003	NRP1
75	1.2376590441981836E-003	RBL1
75	1.2376590441981836E-003	CCNA2
75	1.2376590441981836E-003	PFKFB2
75	1.2376590441981836E-003	MYCN
75	1.2376590441981836E-003	SIVA1
75	1.2376590441981836E-003	PMAIP1
75	1.2376590441981836E-003	MCM3
75	1.2376590441981836E-003	CDCA7
75	1.2376590441981836E-003	CDT1
75	1.2376590441981836E-003	NPAT
75	1.2376590441981836E-003	TK1
75	1.2376590441981836E-003	MYBL2
75	1.2376590441981836E-003	CDC6
75	1.2376590441981836E-003	RRM2
75	1.2376590441981836E-003	CCNB1
75	1.2376590441981836E-003	MCM7
75	1.2376590441981836E-003	CCND3
75	1.2376590441981836E-003	UHRF1
75	1.2376590441981836E-003	DBF4
75	1.2376590441981836E-003	CBX5
76	1.2376590441981656E-003	ACTN4

4.3.3 e2f1targets 2DRanking

See Fig 19 page 30.

Table 12: 2DRanking of e2f1targets proteins

K_2	K	K^*	Protein
5	3	5	TP53
6	6	1	CDK1
8	8	2	ATM
8	4	8	CDKN1A
10	2	10	CASP3
12	10	12	E2F1
13	13	9	CDKN1B
16	7	16	MYC
18	11	18	CASP8
20	20	4	BRCA1
22	22	20	CCNE1
27	27	11	CDKN2A

27	23	27	BIRC5
28	28	23	FOXO1
28	18	28	FOXO3
29	19	29	FGFR2
30	9	30	BCL2
31	31	14	CDC25A
31	1	31	PPARG
32	5	32	CASP9
34	34	22	STMN1
34	32	34	BCL2L11
36	36	35	SKP2
37	35	37	E2F2
38	38	3	AURKB
38	26	38	GAB2
40	40	25	MELK
41	41	19	RPA2
41	25	41	CASP7
43	14	43	APAF1
44	44	36	BBC3
44	21	44	TOPBP1
45	45	39	MCL1
46	46	24	AXIN2
47	47	41	TP53BP1
49	49	6	CHEK2
51	51	7	EIF2AK2
53	53	13	RBBP8
55	55	45	ACTG1
68	68	15	DUSP2
72	72	17	FHIT
75	12	75	TERT
75	15	75	CCND3
75	16	75	CCNB1
75	17	75	PCNA
75	24	75	TP73
75	29	75	CCNA2
75	30	75	MYCN
75	33	75	EZH2
75	37	75	MYB
75	42	75	PMAIP1
75	43	75	CDC6
75	48	75	NRP1
75	50	75	PFKFB2
75	52	75	DNMT1
75	54	75	MCM3
75	56	75	TOP2A
75	57	75	TK1
75	58	75	PFKFB3
75	59	75	DBF4
75	60	75	CDT1
75	61	75	RRM2
75	62	75	UHRF1
75	63	75	SIVA1
75	65	75	NPAT
75	65	75	MYBL2
75	66	75	CDCA7
75	67	75	MCM7
75	69	75	RBL1
75	70	75	WWOX
75	71	75	CBX5
76	76	21	BMI1
76	76	26	PTGS2

76	76	33	CDKN2C
76	76	42	HRK
76	39	76	ACTN4

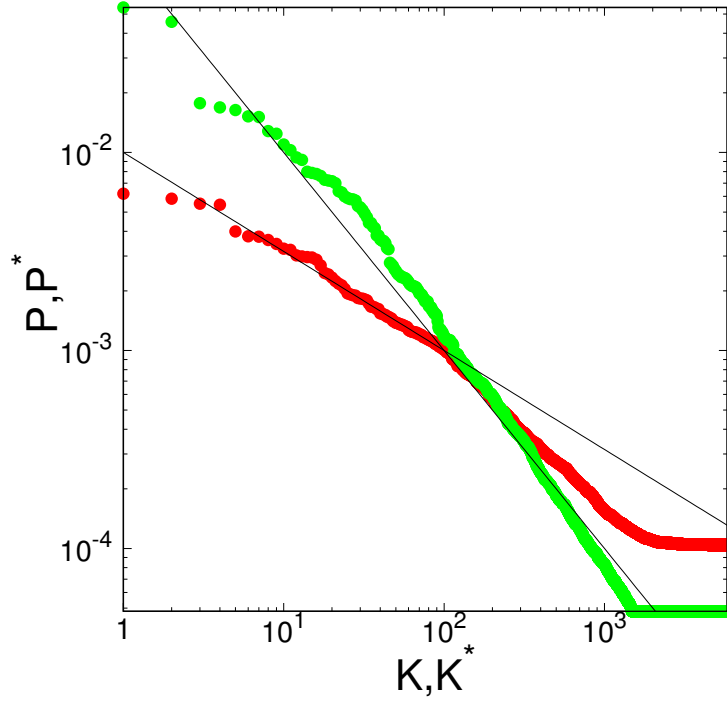


Figure 1: PageRank probability P (red points) and CheiRank probability P^* (green points) as a function of K and K^* indexes. Straight dashed lines are drawn to adapt an eye and show algebraic decay with exponents -0.5 and -1 . The damping factor is $\alpha = 0.85$.

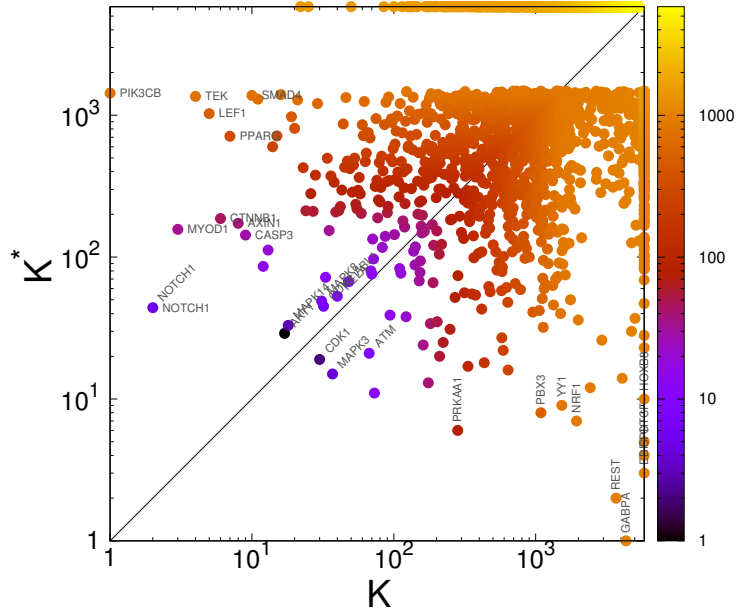


Figure 2: Distribution of proteins in PageRank - CheiRank plane (K, K^*). The colors correspond to 2DRank indexes from $K_2 = 1$ (black) to $K_2 = 2432$ (bright yellow). Top 10 proteins ranked using PageRank, CheiRank and 2DRank algorithms are horizontally, vertically and diagonally marked, respectively.

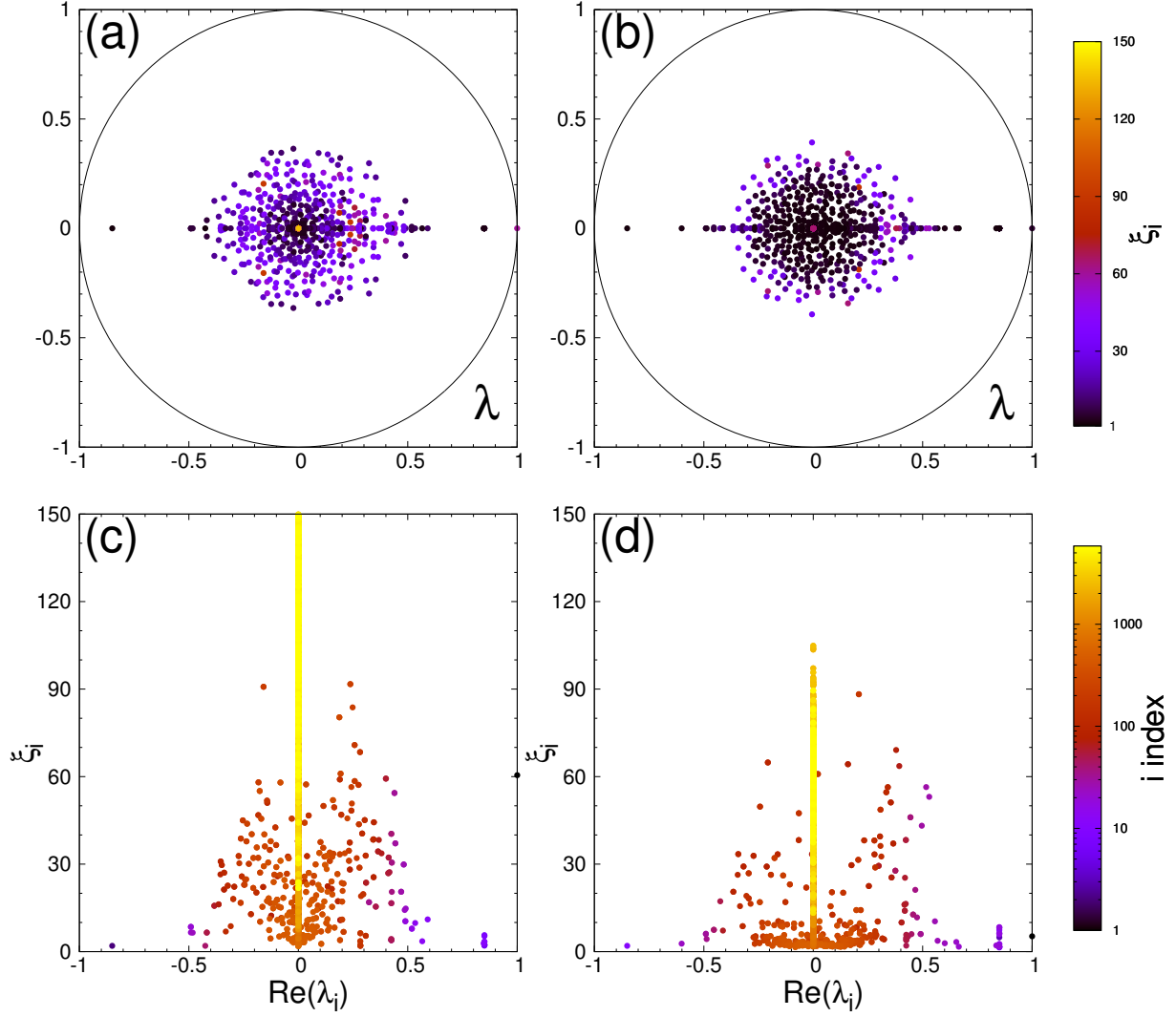


Figure 3: (a,b) Complex spectrum $\{\lambda_i\}_{i=1,\dots,N}$ of Google matrices G (a) and G^* (b). Colors give the inverse participation ratio ξ_i from $\xi_i = 1$ (black) to $\xi_i = 150$ (bright yellow). (c,d) Inverse participation ratio $\xi_i = \left(\sum_{n=1}^N |\psi_i(n)|^2 \right) / \sum_{n=1}^N |\psi_i(n)|^4$ of the i th eigenvector as a function of $\text{Re}(\lambda_i)$ for Google matrices G (c) and G^* (d). Colors give in logarithmic scale i indexes of eigenvalues ranked by decreasing modulus; from $i = 1$ (black) to $i = N = 2432$ (bright yellow). The damping factor is $\alpha = 0.85$.

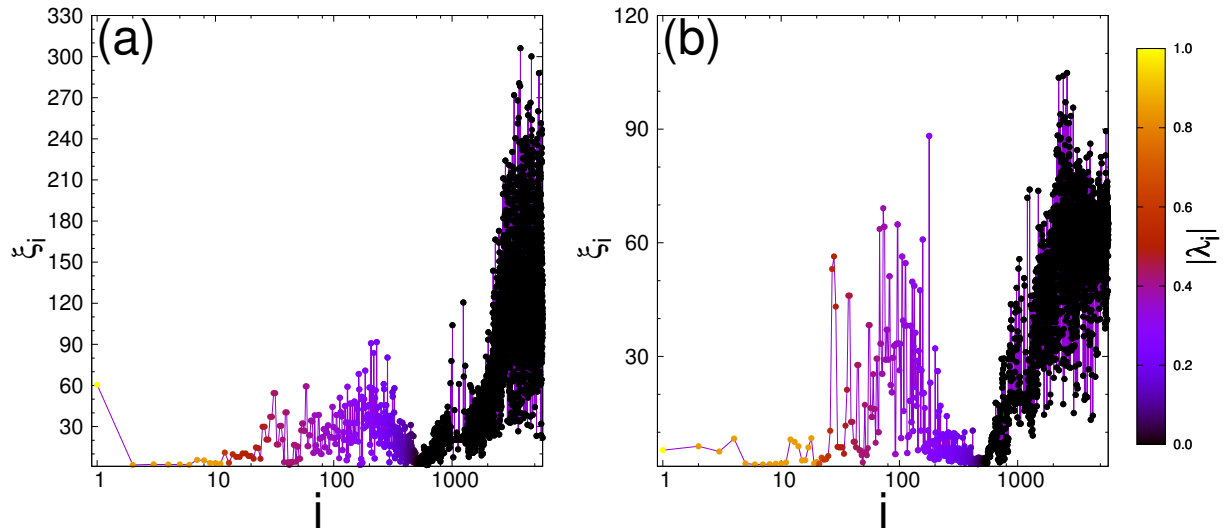


Figure 4: Inverse participation ratio $\xi_i = \left(\sum_{n=1}^N |\psi_i(n)|^2 \right) / \sum_{n=1}^N |\psi_i(n)|^4$ of the i th eigenvector of Google matrices G (a) and G^* (b). Colors give the modulus of the eigenvalue λ_i associated to eigenvector ψ_i from $|\lambda_i| = 0$ (black) to $|\lambda_i| = 1$ (bright yellow). The damping factor is $\alpha = 0.85$.

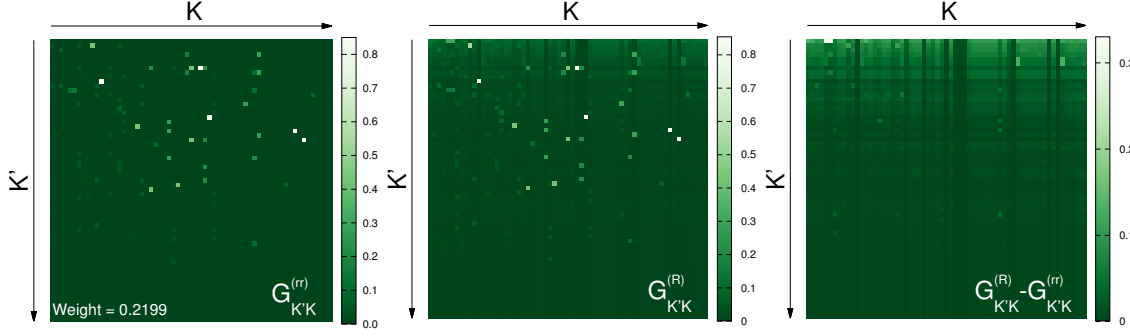


Figure 5: aktmtor reduced Google matrix elements: elements of $G^{(rr)}$ (left panel), $G^{(R)}$ (middle panel), and $G^{(R)} - G^{(rr)}$ (right panel) are shown. Matrix elements are ordered according to PageRank.

aktmtor reduced network: the 10 biggest matrix elements $G_{K'K}^{(R)} - G_{K'K}^{(rr)}$						
Source		Target		$G_{K'K}^{(R)}$	$G_{K'K}^{(rr)}$	$G_{K'K}^{(R)} - G_{K'K}^{(rr)}$
Protein	PageRank	Protein	PageRank			
BCL2L1	5	CASP3	1	0.330173969888	2.57554945055e-05	0.33014821439349451
BCL2	6	CASP3	1	0.313039409216	2.57554945055e-05	0.31301365372149448
CASP3	1	CASP3	1	0.135485990256	2.57554945055e-05	0.13546023476149449
AKT2	14	CASP3	1	0.132278296945	2.57554945055e-05	0.1322525414504945
PIM2	58	BCL2	6	0.131395839867	2.57554945055e-05	0.13137008437249451
PIM2	58	BCL2L1	5	0.130233558782	2.57554945055e-05	0.13020780328749448
RPS6KA2	48	BCL2L1	5	0.129178021096	2.57554945055e-05	0.12915226560149448
RPS6KA2	48	BCL2	6	0.128969645278	2.57554945055e-05	0.1289438897834945
AKT1	2	CASP3	1	0.118142248202	2.57554945055e-05	0.11811649270749451
PIM2	58	CASP3	1	0.117786563125	2.57554945055e-05	0.1177608076304945

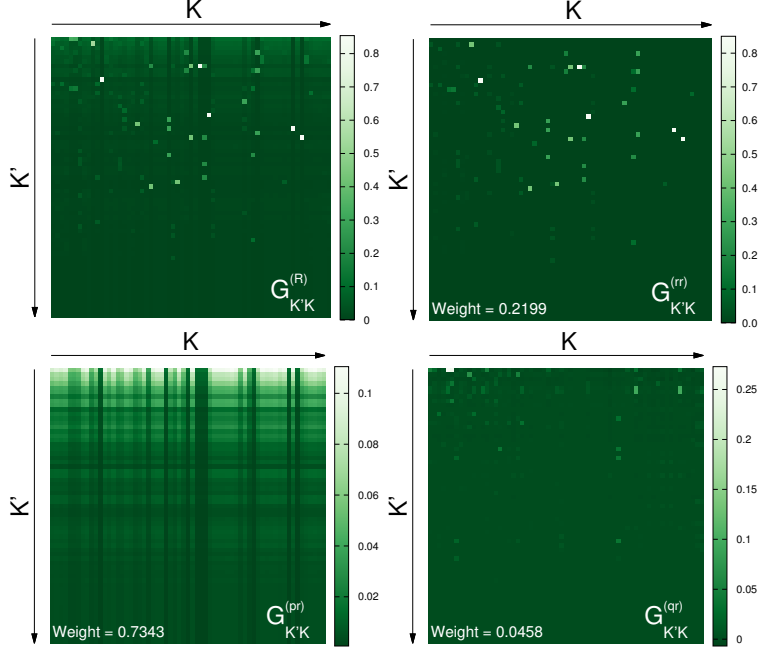


Figure 6: aktmtor reduced Google matrix elements: elements of $G^{(R)}$ (top left panel), $G^{(rr)}$ (top right panel), $G^{(pr)}$ (bottom left panel), and $G^{(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to PageRank.

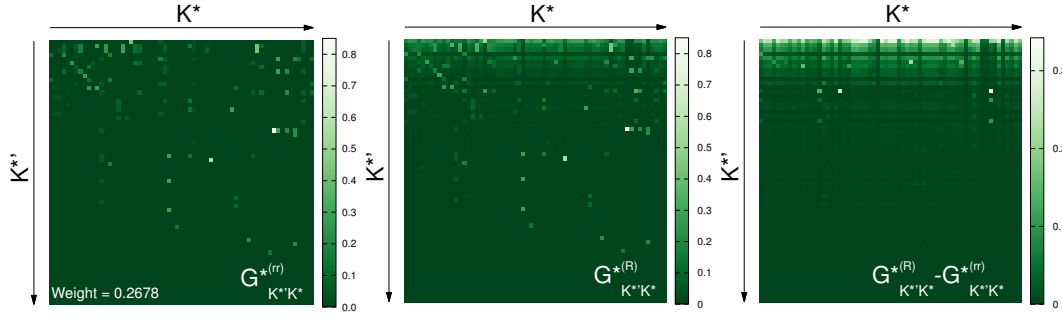


Figure 7: aktmtor reduced inverted Google matrix elements: elements of $G^{*(rr)}$ (left panel), $G^{*(R)}$ (middle panel), and $G^{*(R)} - G^{*(rr)}$ (right panel) are shown. Matrix elements are ordered according to CheiRank.

aktmtor reduced inverted network: the 10 biggest matrix elements $G^{*(R)}_{K^{*'}K^*} - G^{*(rr)}_{K^{*'}K^*}$							
Source		Target		$G^{*(R)}_{K^{*'}K^*}$	$G^{*(rr)}_{K^{*'}K^*}$	$G^{*(R)}_{K^{*'}K^*} - G^{*(rr)}_{K^{*'}K^*}$	
Protein	CheiRank K^*	Protein	CheiRank $K^{*'}$				
PRKAG3	56	MTOR	13	0.342370498834	2.57554945055e-05	0.34234474333949449	
YWHAQ	32	PRKAA1	1	0.291510943176	2.57554945055e-05	0.29148518768149451	
YWHAH	46	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
RBX1	36	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
PRKAG1	30	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
PIM2	43	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
PIM1	25	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
DUSP16	33	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
DUSP10	26	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	
DDB1	42	PRKAA1	1	0.291510943176	0.000171703296703	0.291339239879297	

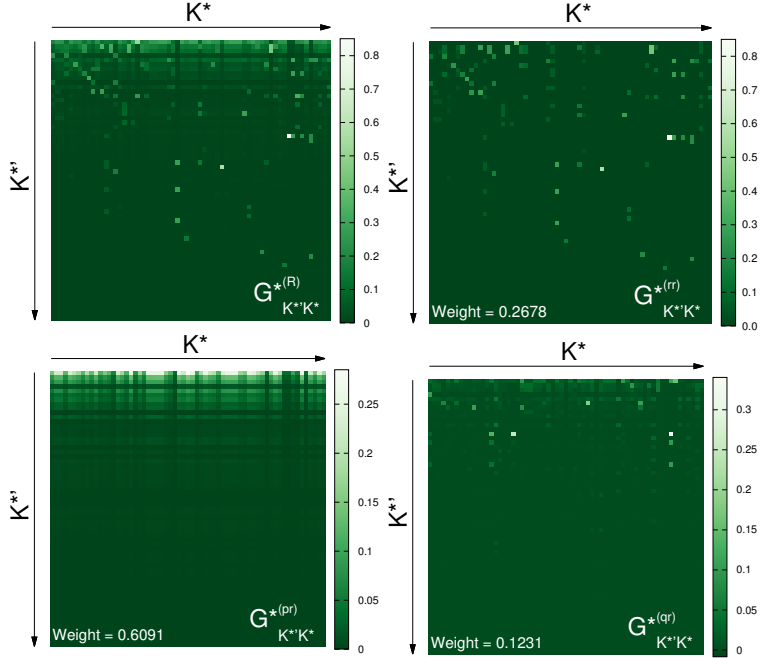


Figure 8: aktmtor reduced inverted Google matrix elements: elements of $G^{*(R)}$ (top left panel), $G^{*(rr)}$ (top right panel), $G^{*(pr)}$ (bottom left panel), and $G^{*(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to CheiRank.

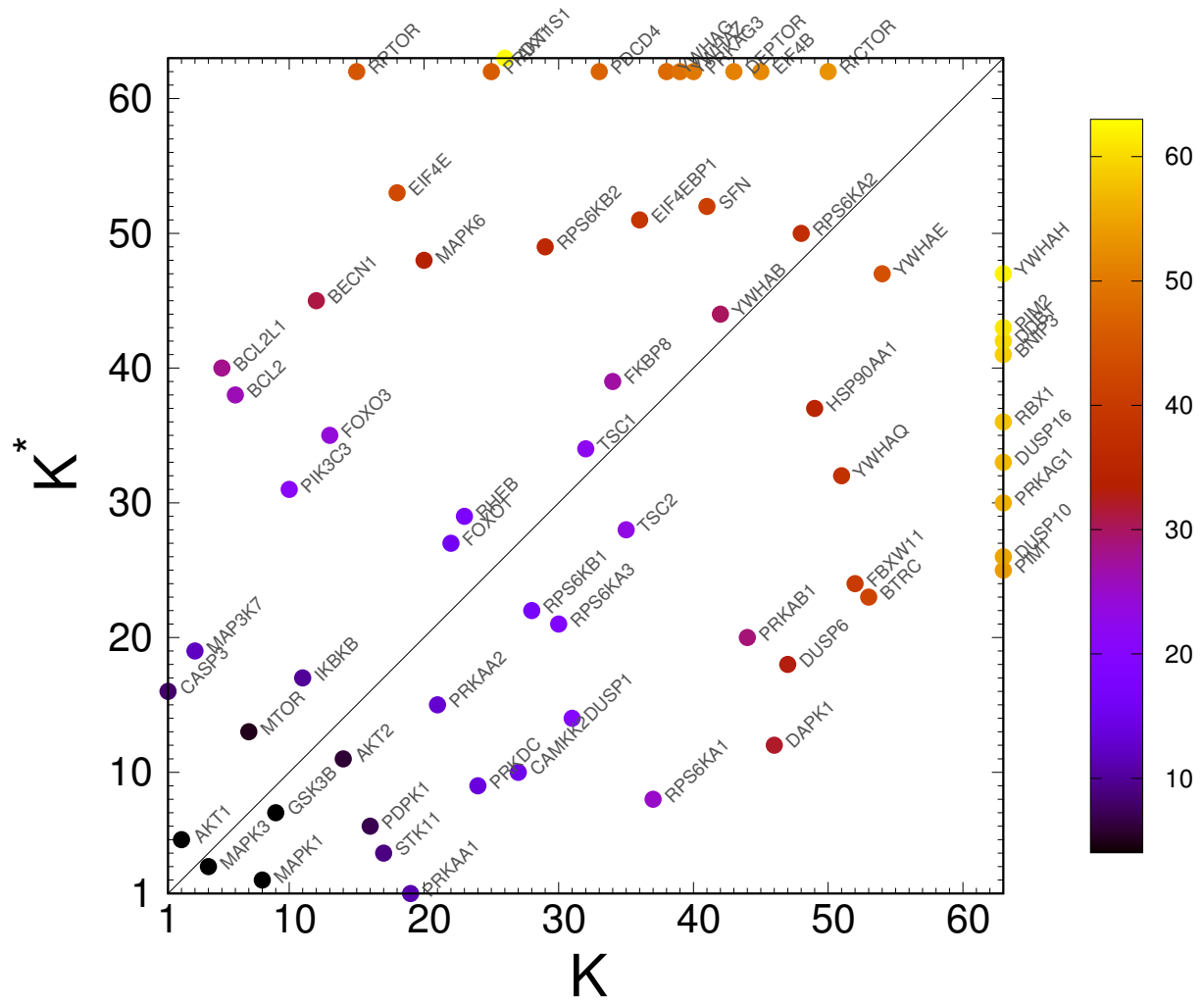


Figure 9: **Distribution of aktmtor proteins in PageRank - CheiRank plane** (K, K^*). The colors correspond to 2DRank indexes from $K_2 = 1$ (black) to $K_2 = 63$ (bright yellow).

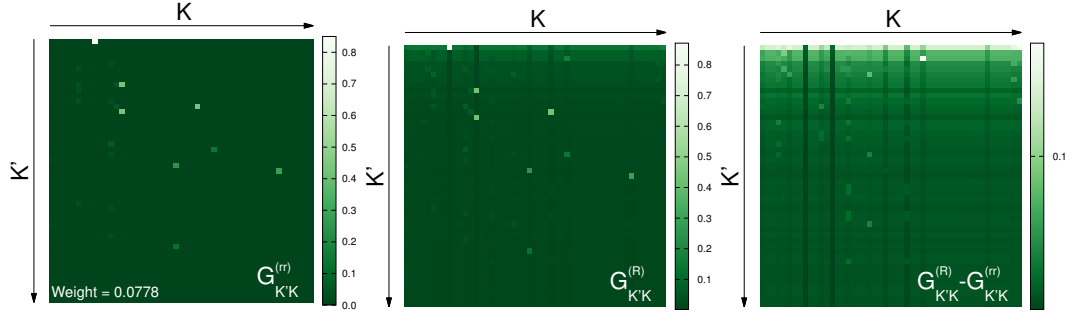


Figure 10: cit7 reduced Google matrix elements: elements of $G^{(rr)}$ (left panel), $G^{(R)}$ (middle panel), and $G^{(R)} - G^{(rr)}$ (right panel) are shown. Matrix elements are ordered according to PageRank.

cit7 reduced network: the 10 biggest matrix elements $G_{K'K}^{(R)} - G_{K'K}^{(rr)}$						
Source		Target		$G_{K'K}^{(R)}$	$G_{K'K}^{(rr)}$	$G_{K'K}^{(R)} - G_{K'K}^{(rr)}$
Protein	PageRank K	Protein	PageRank K'			
CDC7	31	PCNA	3	0.172831189301	2.57554945055e-05	0.17280543380649449
CDKN2C	49	CDK1	1	0.169383762486	2.57554945055e-05	0.1693580069914945
STIL	48	CDK1	1	0.153423889239	2.57554945055e-05	0.15339813374449449
CHEK1	6	CDK1	1	0.150815899712	2.57554945055e-05	0.15079014421749448
CCNE1	4	CDK1	1	0.147057766219	2.57554945055e-05	0.14703201072449448
VRK1	16	CDK1	1	0.141750814892	2.57554945055e-05	0.1417250593974945
FBXO5	41	CDK1	1	0.141243041057	2.57554945055e-05	0.14121728556249449
FAM64A	40	CDK1	1	0.140941174412	2.57554945055e-05	0.14091541891749448
TOP2A	27	CDK1	1	0.140941174412	0.000171703296703	0.140769471115297
SPAG5	46	CDK1	1	0.140941174412	0.000171703296703	0.140769471115297

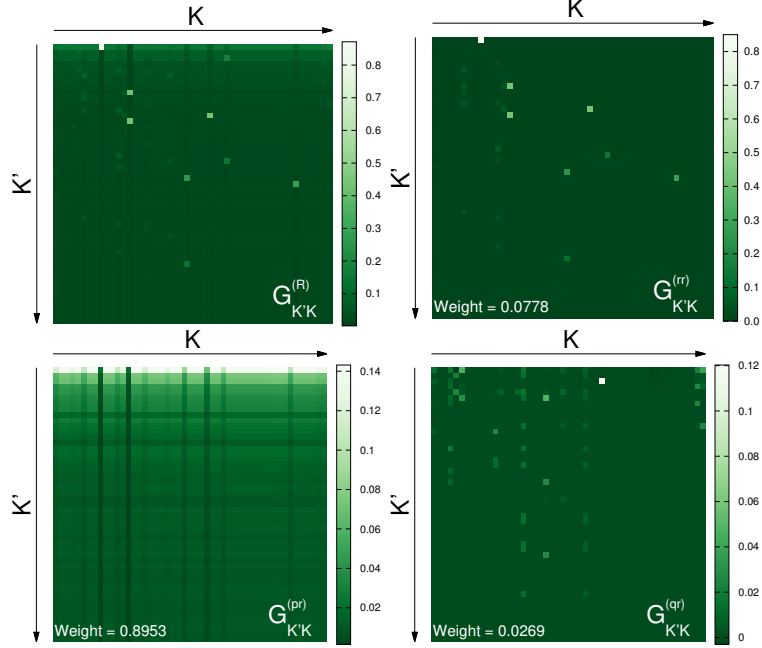


Figure 11: cit7 reduced Google matrix elements: elements of $G^{(R)}$ (top left panel), $G^{(rr)}$ (top right panel), $G^{(pr)}$ (bottom left panel), and $G^{(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to PageRank.

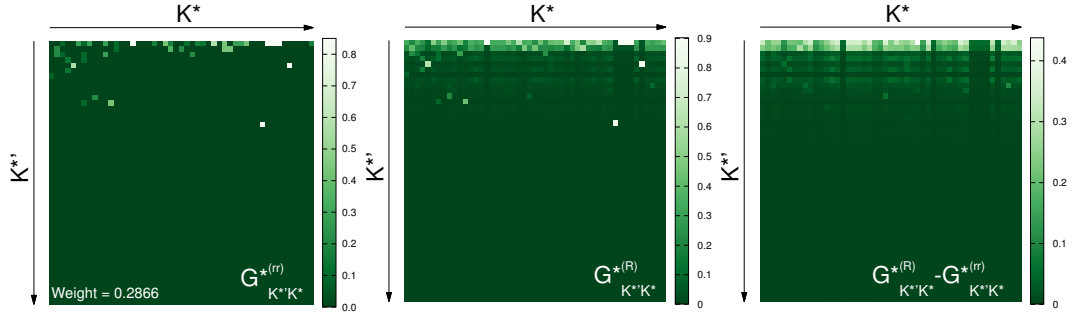


Figure 12: cit7 reduced inverted Google matrix elements: elements of $G^{*(rr)}$ (left panel), $G^{*(R)}$ (middle panel), and $G^{*(R)} - G^{*(rr)}$ (right panel) are shown. Matrix elements are ordered according to CheiRank.

cit7 reduced inverted network: the 10 biggest matrix elements $G^{*(R)}_{K^*!K^*} - G^{*(rr)}_{K^*!K^*}$						
Source		Target		$G^{*(R)}_{K^*!K^*}$	$G^{*(rr)}_{K^*!K^*}$	$G^{*(R)}_{K^*!K^*} - G^{*(rr)}_{K^*!K^*}$
Protein	CheiRank	Protein	CheiRank			
CCNA2	30	CDK1	1	0.437780054111	2.57554945055e-05	0.43775429861649451
PCNA	24	CDK1	1	0.364590003488	2.57554945055e-05	0.36456424799349452
CDCA7	38	CDK1	1	0.357878444652	2.57554945055e-05	0.35785268915749452
CDCA3	48	CDK1	1	0.354933417077	2.57554945055e-05	0.35490766158249448
KPNA2	32	CDK1	1	0.351388954047	2.57554945055e-05	0.35136319855249448
SPAG5	46	CDK1	1	0.348593240082	2.57554945055e-05	0.34856748458749448
DTL	21	CDK1	1	0.346637821671	2.57554945055e-05	0.34661206617649448
FAM64A	18	CDK1	1	0.346211965883	2.57554945055e-05	0.34618621038849451
STIL	19	CDK1	1	0.346211965883	0.000171703296703	0.346040262586297
CDKN2C	15	CDK1	1	0.346211965883	0.000171703296703	0.346040262586297

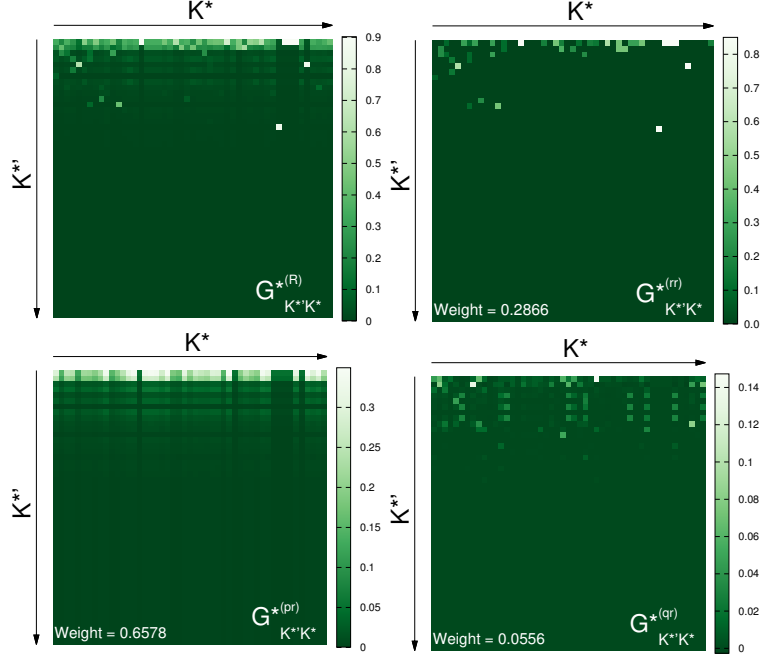


Figure 13: cit7 reduced inverted Google matrix elements: elements of $G^{*(R)}$ (top left panel), $G^{*(rr)}$ (top right panel), $G^{*(pr)}$ (bottom left panel), and $G^{*(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to CheiRank.

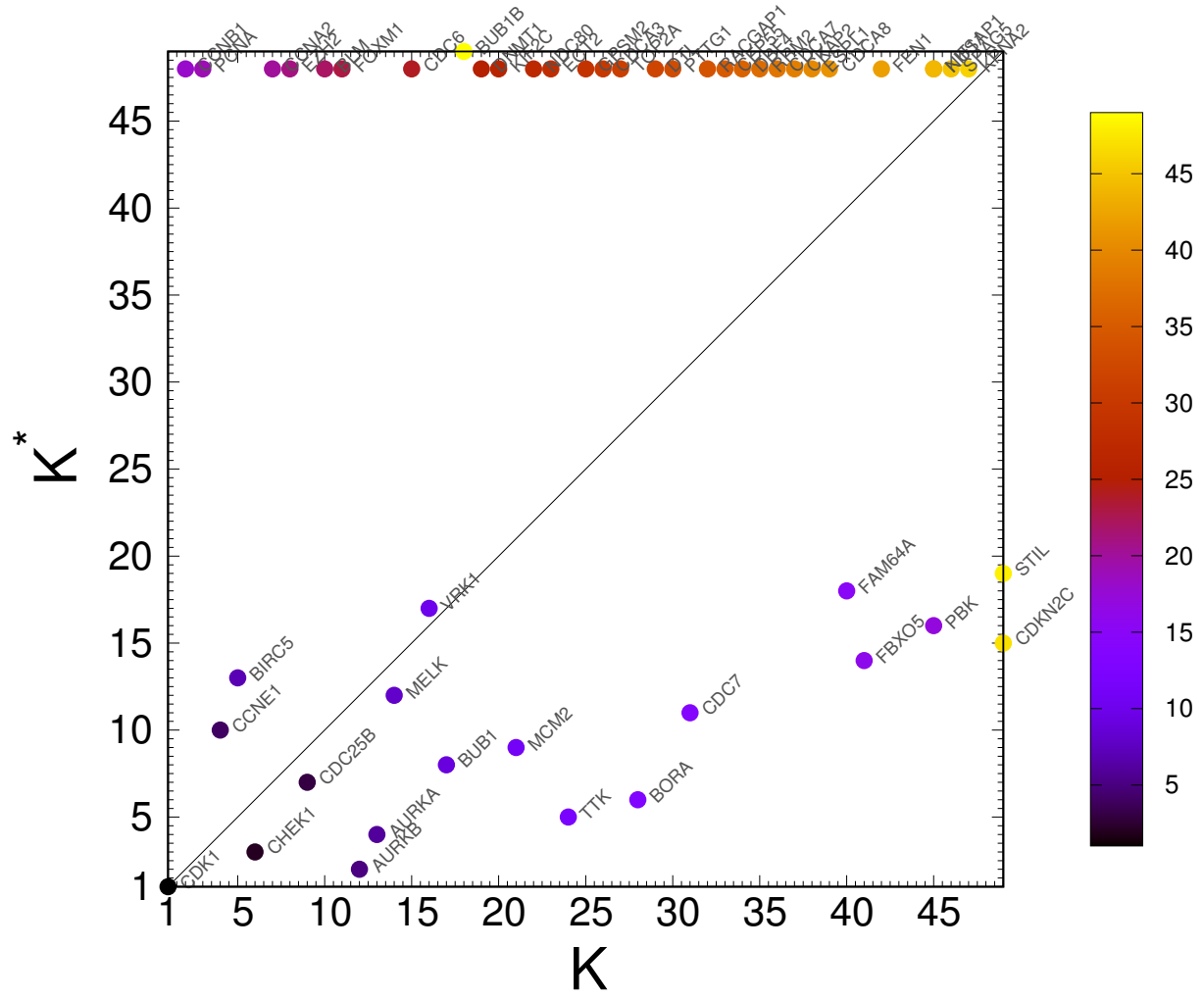


Figure 14: **Distribution of cit7 proteins in PageRank - CheiRank plane (K, K^*).** The colors correspond to 2DRank indexes from $K_2 = 1$ (black) to $K_2 = 49$ (bright yellow).

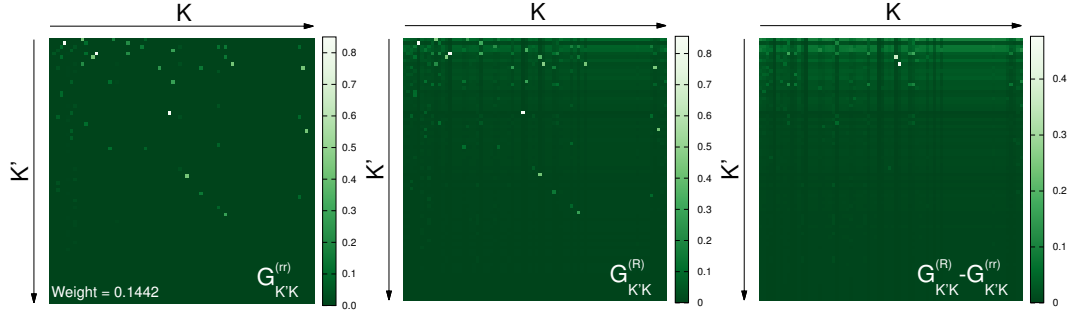


Figure 15: e2f1targets reduced Google matrix elements: elements of $G^{(rr)}$ (left panel), $G^{(R)}$ (middle panel), and $G^{(R)} - G^{(rr)}$ (right panel) are shown. Matrix elements are ordered according to PageRank.

e2f1targets reduced network: the 10 biggest matrix elements $G_{K'K}^{(R)} - G_{K'K}^{(rr)}$						
Source			Target		$G_{K'K}^{(R)}$	$G_{K'K}^{(rr)}$
Protein	PageRank	K	Protein	PageRank	K'	$G_{K'K}^{(R)} - G_{K'K}^{(rr)}$
RPA2	41	41	ATM	8	8	0.476338692864
MELK	40	40	CDK1	6	6	0.367107006375
MCL1	45	45	CASP9	5	5	0.173144076119
BCL2	9	9	CASP9	5	5	0.171844650226
AXIN2	46	46	PPARG	1	1	0.122922349358
BCL2L11	32	32	CASP9	5	5	0.121089778404
CDKN2C	76	76	CDKN1A	4	4	0.115453704301
BBC3	44	44	CASP9	5	5	0.113045828645
PTGS2	75	75	PPARG	1	1	0.109699422777
FOXO3	18	18	CDKN1A	4	4	0.108343528884

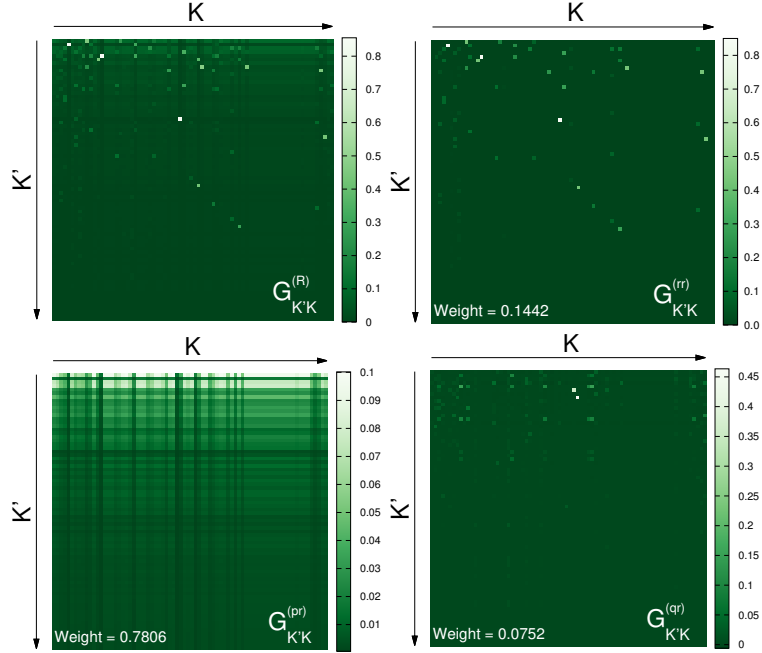


Figure 16: e2f1targets reduced Google matrix elements: elements of $G^{(R)}$ (top left panel), $G^{(rr)}$ (top right panel), $G^{(pr)}$ (bottom left panel), and $G^{(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to PageRank.

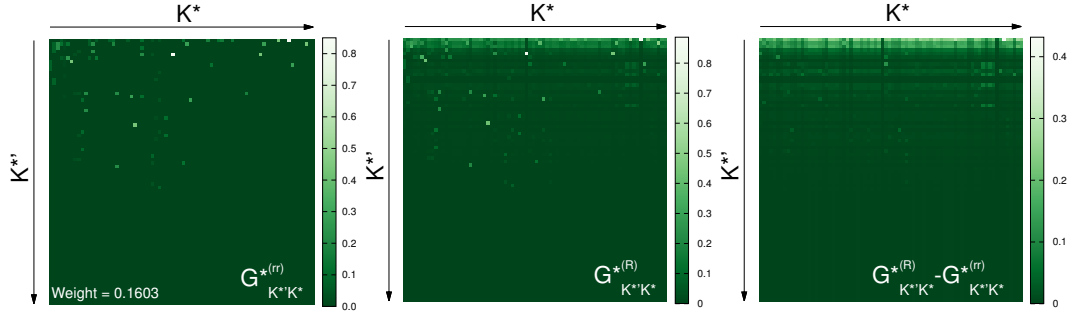


Figure 17: e2f1targets reduced inverted Google matrix elements: elements of $G^{*(rr)}$ (left panel), $G^{*(R)}$ (middle panel), and $G^{*(R)} - G^{*(rr)}$ (right panel) are shown. Matrix elements are ordered according to CheiRank.

e2f1targets reduced inverted network: the 10 biggest matrix elements $G^{*(R)}_{K^{*'}K^*} - G^{*(rr)}_{K^{*'}K^*}$						
Source		Target		$G^{*(R)}_{K^{*'}K^*}$	$G^{*(rr)}_{K^{*'}K^*}$	$G^{*(R)}_{K^{*'}K^*} - G^{*(rr)}_{K^{*'}K^*}$
Protein	CheiRank K^*	Protein	CheiRank $K^{*'}$			
MCM7	71	CDK1	1	0.431618668928	2.57554945055e-05	0.43159291343349448
CCNA2	57	CDK1	1	0.296028384983	2.57554945055e-05	0.29600262948849448
CBX5	75	CDK1	1	0.27463652062	2.57554945055e-05	0.27461076512549448
WWOX	51	CDK1	1	0.261492889491	2.57554945055e-05	0.26146713399649452
PCNA	47	CDK1	1	0.259381431003	2.57554945055e-05	0.25935567550849448
CCND3	72	CDK1	1	0.257836204626	2.57554945055e-05	0.25781044913149448
PFKFB2	58	CDK1	1	0.250097848358	2.57554945055e-05	0.25007209286349447
TOPBP1	44	CDK1	1	0.249608354837	2.57554945055e-05	0.24958259934249449
RBL1	56	CDK1	1	0.249584619217	2.57554945055e-05	0.2495588637224945
FOXO3	28	CDK1	1	0.247591269132	2.57554945055e-05	0.24756551363749449

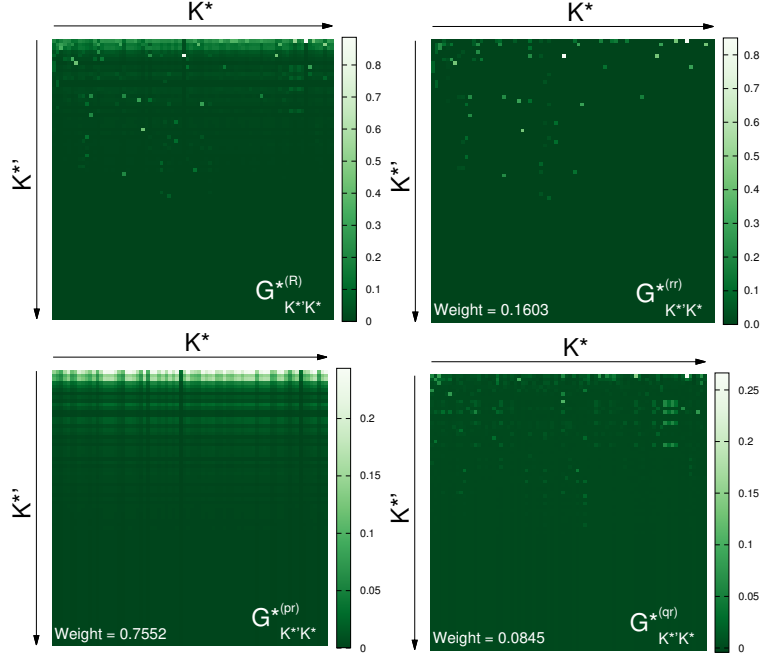


Figure 18: e2f1targets reduced inverted Google matrix elements: elements of $G^{*(R)}$ (top left panel), $G^{*(rr)}$ (top right panel), $G^{*(pr)}$ (bottom left panel), and $G^{*(qr)}$ (bottom right panel) are shown. Matrix elements are ordered according to CheiRank.



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