# LabBook_18_03_16

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Monday

After admin, I had to think about how I was going to approach the next stage of my analysis. In my monday meeting with Win, we talked about how we need to understand the context of the consensus genes I generated with MA and RNAseq data. What I need to work out how to do is to generate a kind of network in which the nodes are not co-expression values, but the presence of coexpression in multiple data sets. See the image below:
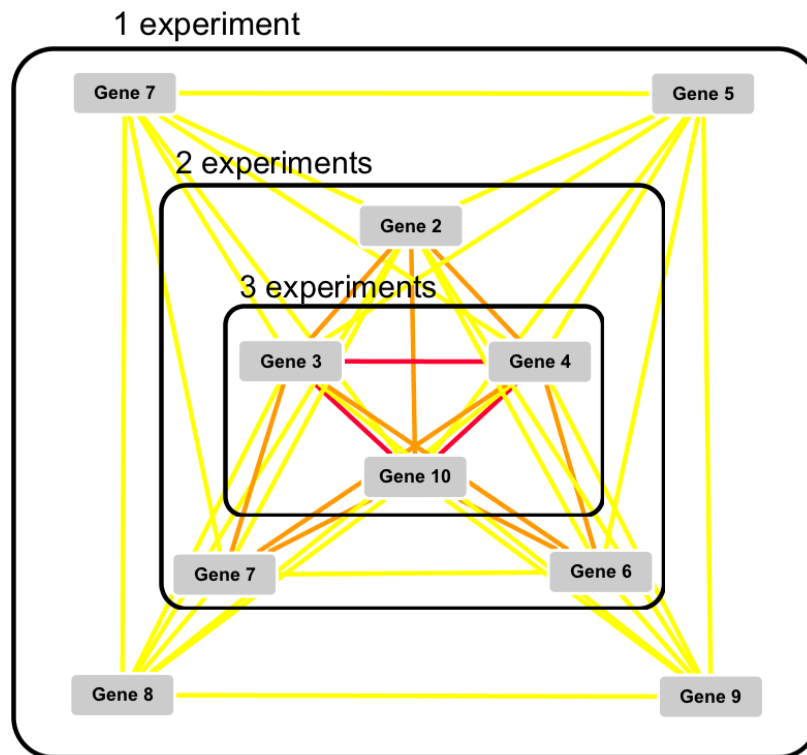
Using this I can investigate how consistently genes are coexpressed in different disease contexts.

Also, I managed to get Jiantao's GRAIL analysis to work. The seed genes are a list of genes known to be associated with the disease or that represent some kind of disease signature. The query genes are those that you have found via your own analysis. I managed to generate this table:

ID	tmBestGene	tmBestPv	coBestGene	coBestPv	Flag
CST3	CST3	0.052951201	CST3	0.001231177	TRUE
ATXN2	ATXN2	0.000718823	ATXN2	0.003215914	FALSE
SPG11	SPG11	0.468656424	SPG11	0.006591873	FALSE
TARDBP	TARDBP	0.021439303	TARDBP	0.007150317	TRUE
FIG4	FIG4	1	FIG4	0.010119741	FALSE
VCP	VCP	0.003218942	VCP	0.010514627	FALSE
ALS2	ALS2	5.48E-08	ALS2	0.020922795	FALSE
PFN1	PFN1	0.206251512	PFN1	0.024407396	FALSE
ACTN1	ACTN1	0.201768694	ACTN1	0.048444135	TRUE
UBQLN2	UBQLN2	0.015915903	UBQLN2	0.052282078	FALSE
SIGMAR1	SIGMAR1	0.218781207	SIGMAR1	0.061560365	FALSE
HNRNPA1	HNRNPA1	0.001313368	HNRNPA1	0.064107491	FALSE
RPLP2	RPLP2	0.793242641	RPLP2	0.076818327	TRUE
GRN	GRN	0.179913159	GRN	0.083107837	FALSE
RGS2	RGS2	0.443510298	RGS2	0.086157508	TRUE
SERBP1	SERBP1	0.304169308	SERBP1	0.093179592	TRUE
SETX	SETX	1.35E-07	SETX	0.110166356	FALSE
OPTN	OPTN	0.009115922	OPTN	0.111098532	FALSE
HNRNPA2B1	HNRNPA2B1	0.00048968	HNRNPA2B1	0.123012254	FALSE
C9orf72	C9orf72	1	C9orf72	0.126143766	FALSE
ANXA1	ANXA1	0.114425196	ANXA1	0.140357244	TRUE
TARS	TARS	1	TARS	0.150617296	TRUE
KCTD12	KCTD12	0.781257367	KCTD12	0.156459409	TRUE
JAG1	JAG1	0.202839734	JAG1	0.170970564	TRUE
ETS2	ETS2	0.184360756	ETS2	0.173973587	TRUE
TCF4	TCF4	0.277906629	TCF4	0.217432273	TRUE
PLEKHB1	PLEKHB1	0.303471505	PLEKHB1	0.224219972	TRUE
VAPB	VAPB	0.009797937	VAPB	0.341290234	FALSE
NIPA1	NIPA1	0.000181018	NIPA1	0.371141516	FALSE
SYNM	SYNM	0.053162771	SYNM	0.399472304	TRUE
GBAS	GBAS	0.497238086	GBAS	0.438578165	TRUE
CHMP2B	CHMP2B	0.010602707	CHMP2B	0.542451571	FALSE
SQSTM1	SQSTM1	1.17E-05	SQSTM1	0.582233211	FALSE
COX6A1	COX6A1	0.813982412	COX6A1	0.597855078	TRUE
SPARC	SPARC	0.027254148	SPARC	0.640741503	TRUE
RAB40B	RAB40B	0.789049901	RAB40B	0.67444711	TRUE
PFDN1	PFDN1	0.457723279	PFDN1	0.679673863	TRUE
ANG	ANG	0.110533633	ANG	0.685218181	FALSE
BGN	BGN	0.211052052	BGN	0.797808694	TRUE
DCN	DCN	0.212907252	DCN	0.836665496	TRUE
GFAP	GFAP	0.21162059	GFAP	1	FALSE
HBB	HBB	0.307807658	HBB	1	TRUE

I believe this performs some kind of prioritisation, but I may need to talk to Jiantao more about how to interpret this.