The background of the slide is a dark blue field filled with a complex network of thin, light blue lines. These lines connect numerous small, semi-transparent blue circular nodes. The nodes are distributed across the entire frame, with some appearing more prominent than others. The overall effect is a sense of a vast, interconnected web or data structure, typical of network visualization in data science or biology.

# Extracting a Biologically Relevant Latent Space from Cancer Transcriptomes with Variational Autoencoders

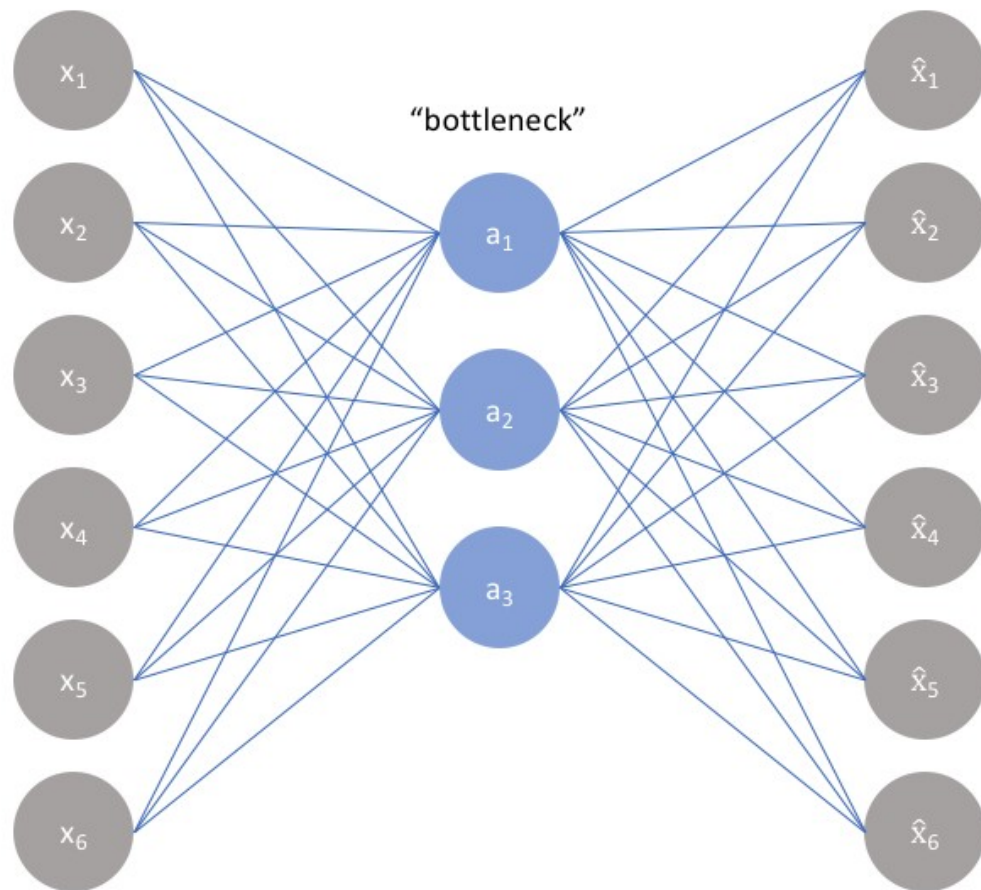
The background is a dark blue field filled with a complex network of thin, light blue lines connecting small, semi-transparent blue circular nodes. The nodes are scattered throughout the frame, with some appearing more prominent than others. The lines form a web-like structure that suggests connectivity and data flow.

Autoencoder

Input layer

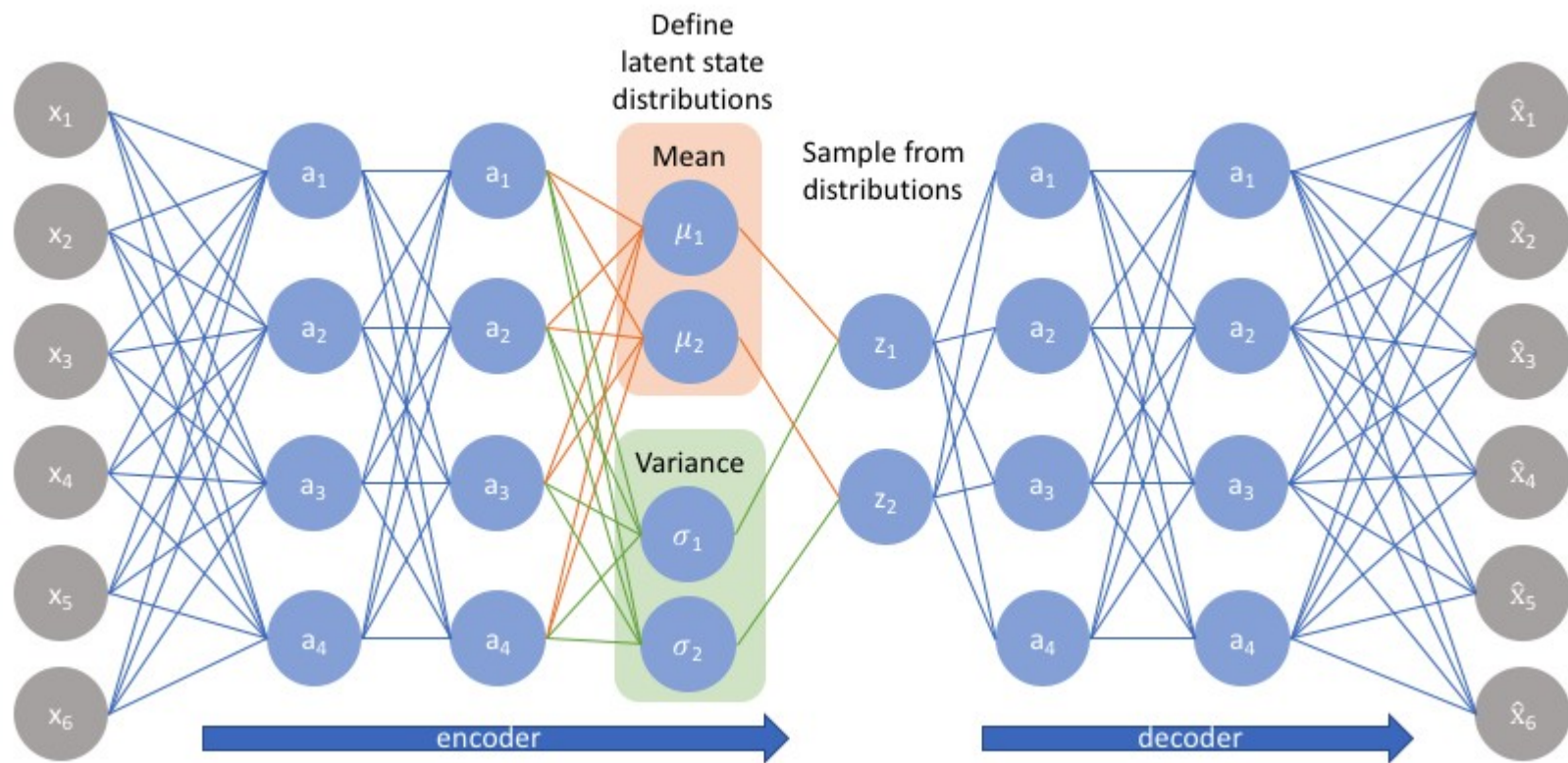
Hidden layer

Output layer





# Variational Autoencoder



## Loss Function

- Generative Loss
- Latent Loss

$$\mathcal{L}(x, \hat{x}) + \sum_j KL(q_j(z|x) || p(z))$$



SPINK1	PPP1A10	ALDH3B2	C15E	NRG	LTG0	C9A	PLA2G2A	NRN	ULFAP4	CORR3	SCLE	MUC13	ZPT	FMO3A3	GDA	ENF	WDR72	CLCA2	SPN	TIGB8	SLC1A2A	KRT23	SLC6A14	KLR8			
	VIL1	ESRP1	CLDN2	TPMRSS2	PCK1	SPRR18	H0XB13	H0XC10	FGFBP1	DDC	FGG	UGT1A9	PKP3	MUC16	TMCS	PITX1	C9orf152	PLP1	SERPINB3	C4BP4	COL11A1	SDR16C5	KLK7				
	C20orf114	UGT2B7	CS1T	GGT6	SLC5A1	A2M1L	C19orf133			CBLC	MPM1	FGA	YVD	FOXA2	C19orf21		DES	SFTPA2	ADHB1	TEFF3	PDZK1IP1	MUC15	DMBT1				
C10orf81		MPM7	APM12	ANXA8L2	WFDC2	GRP110	PRSS58	FOXK1	FOLR1	SYT13	LGAL54	GJB6	TP63	POF1B	TOX3	Cyorf158		TTTY15	DUOX2	TNNT1	SLP1	AQP4	COMP	SERPINA3			
	ABP1	PRR15L	PRAP1	CP	IVL	MPM12	PVRL4	GPXR7	NEFL	CHGA	PCSK9	VTGN1	CDH16	MUC4	MPM13	LTF	HP	BCAS1	SPRR3	PGC	CACNG4	SAA1	CLDN10	EPCAM	EPN3		
PCSK2	SPRR1A	ZG16B	FG8	LAMC2	UPK18	PLA2G4F	SCNN1A	ZNF750	CLDN4	ADH1C	PP2R2C	GJB3	TSIX	MYBPC1	KIAA1324		SFRP2	ATP10B	FAM83E	KLK8	SLC39A5	ADAM6	C19orf77				
ALDH1L1	SALL1	TJ3P	B80X1	CAPN13	GSTT1	PSCA	S100A2	IRX2	KRT8	C20orf56		FUT6	ALDOB	UGT2A3	LRR1C5	COL10A1	HABP2	FAM83B	SLC44A	BMP7	GLYATL1	SLC39A5	ADAM6	C19orf77			
	ELF3	VSIG2	CAPN8	PRSS3	CHGB	PCP4	SERPINA6	AQO5	CYP2B6	KLHDC7A	CHST9	LM03	GCNT3	RERG1A	TCN1	SCN1NG	EP58L3	EMX205	ORM1	WN7B7	FUT3	MSMB	ST6GALNAC1				
	C7	KIF12	HKDC1	CPLX2	FAM3B	NXK2-1	GATA4	CCL21	KLK5	NLRP2	ANKS4B	FABP7	BEX1	ERBB4	RBP4	ATP13A4	C16orf89	FAM32	CNTN1	BARX2	MLPH	EMX2	SPRR2A	XDH			
	NLGN4Y	AMN	C2orf54	CE1	SA2	C20orf151		HSD17B2	IGJ	SLITRK6	GPNS4	FOXJ1	S0X21	CNTNAP2	MPM10	GP2	ALB	CCDC64B	ERN2	PTPR	TRIM15	DNER	CABR2P	BNC1			
B4GALNT4	NTRK2	FAM63F	PDPP6	CKNJ15	ELF5	CYP24A1		EVPL	ACADL	PPAN-PRYV11	PCSK1N	TFAP2C	ZIC1	CXCL14	TCF21	SLC6A15	TM45F5	MAL2	DUOX4A	DUOX2A	MASP1	RNF128	ZIC2				
ABCA12	GRK13	C2orf72	LTPH	TMEM40	GLDC	OVOL2	CWH43	AGEA6	H0XC13	GABRR3	SPRR2D	PPR1R1A	SPINK5	FABP1	GREM1	SERPINB2	PRKY	SCN11B	CYP4F3	CDHR2	C4orf7	CXCL28	AGT	LG13			
	LGALS7	SULT1C2	CDH3	DAPL1	FXDY2	S100A1	BHMT	MAI	CLRN3	PHYHIP1	TM45F4	SERPINA8		LYPD6B	HHLA2	ATP2B2	SMOC1	CAPN6	FAT2	CABR3P	ADH3A1	IHH	CXCL13	TFAP2A	PAH		
CRTAC1	FOXK1	AKR1C2	SLC3A1	NR1H4	SLC04C1	BMPR18	FGAP	FREM2	EDN3	H0XB9	AADAC	SBSN	SHISA9	UGT8	FERMT1	MAPK4	PDZK1	RORC	LPAR3	IGR5	SPOCK1	CHRD1	NMU	NFPA5	MFAP5		
SERPINB3	FXQ01	GM6A	G5TA2	EPHA7	CRYM	FOA3	SYT8	SLC15A1	CYP3A5	CEACAM7	MUC1	RMS4	S100A8	ATP1A2	MYEOV	NKAINA	RORC	LPAR3	IGR5	SPOCK1	CHRD1	NMU	NFPA5	MFAP5			
	LMX18	CDCC2	GAL3S21	BCAN	POU3F3	ORM2	UC1A	SFTPA1	TTR	C6orf223		CC119	S100A9	ZBED2	VSNL1	ADCY2	VGLL1	SCGB1D2	TECAL2	SLC01A2	FABP4	PRSS51	IGSF9	PCRLR			
	IRX4	RHOV	CSCT6	SCRG1	SEMA3E	CHIT1	DLK1	FUT9	PART1	GABBR2	ACTG3	OVOL1	ACE2	C19orf46		ALIM1	ABCC8	ATM1L	LIGAM	CLCA4	SFTA2	SLC9A2	LONRF2	SFRP1	CDH17		
	CDH2	CSCT6	SCRG1	SEMA3E	CHIT1	DLK1	CLX5	HBA1	CA12	MBT	MAPT	SCGP	OVOL1	ACE2	C19orf46		ALIM1	ABCC8	ATM1L	LIGAM	CLCA4	SFTA2	SLC9A2	LONRF2	SFRP1		
GRIA2	KRT80	C6	CYP2B7P1		CLDN1	CLX5	HBA1	CA12	MBT	MAPT	SCGP	OVOL1	ACE2	C19orf46		ALIM1	ABCC8	ATM1L	LIGAM	CLCA4	SFTA2	SLC9A2	LONRF2	SFRP1			
TPMRSS3	BNIP1	CKMT1B	WNK4	NPY	AREG	ELPR1	NCCRPI	MT3	GRB7	CKMT1A	MGC29506		SLC6A13	TPMRSS13		CA4	DACT2	KLK3	LIX1	CHRM1	PITX2	H0XC11	OGN	CLDN7			
PAD13	C3orf157	UGT1A10	G3B4	GALNT5	ASTN1	LPR12	PAX2	GABRA3	GRH13	RASAL1	CXCL6	WNT7A	C4BPB	CKN3J	TMEM125	DYPS	H56S2T	HOXD13	MARCO	ODZ2	GJB2	TM4	AQP3	GPDI			
CYP4F11	BCHC	SOSTDC1	SERPINA1		APOB	RSP28	AKR1C1	GRH13	PIK6	TFAP2B	SLC26A9	CRI5P3	MSA48B	H0XA10	APD0	SCGB2A1	C3orf64	CPA3	APOH	FNDCl	IDRAS5	HOXD11	D4532A4	BHMT2			
STAC2	DHR52	DMKN	METTL7B	NCAM1	CRYAB	MYB		WIF1	ABCA13	TRIM31	DPYSL5	DL13	GAL3S21	STMN2	GRPIN2	C5orf38	CADM3	PIP	CADPS		ZIC5	ATPDV0A4		CLIC6			
PEBP4	MUC6	NLGN1	TRPM8	PAX8	UGT2B15	C1orf106		AP0A1	SLC5A8	COL2A1	OLIG1	G8A3	H0XA11	XRGR	TUBB2B	KRT18	ACMSD	CKN2H	LVDK6		G56S23	RGN	CDX2	SLC17A4	CUX2	TBX5	
EGF6	RASSF6	KLK4	MUC21	SCGN	GBP6	AP0A1	SLC5A8	COL2A1	OLIG1	G8A3	H0XA11	XRGR	TUBB2B	KRT18	ACMSD	CKN2H	LVDK6		G56S23	RGN	CDX2	SLC17A4	CUX2	TBX5			
	FAM12	IGSF1	GRK15	STK32A	HHA1L	ENKP3	COL4A6	AGXT2L1	TP12	MB	ALOX15B	SERPINA4		CILP	GRP158	NTS	SCGB3A1	C1orf172	REG4	DPPI10	TMEEF2	AKR7A3	TPG	SH3GL2	FMN2		
SSTR1	SLC30A2	WNK2	PTPRN	H19	ACSM2B	KLK13	VTN	CKNK3	LYLT18	SLC6A20	PCDP1	CLDN18	PEG10	WBSCR17	LZU2P	SLC01B3	MAT1A	IRX1	CH13L1	SPRR2E	ATCAY	VSTM2L	UGT1A1	VGF			
	MACC1	AR	MYH11	GALNT14	COL7A1	SNAP91	PKLR	UDSP9	ACTH1	SLC27A6	LRRC31	SYT9	DRU2	PRUNE1	ATCAY	VSTM2L	UGT1A1	VGF	CH13L1	SPRR2E	ATCAY	VSTM2L	UGT1A1	VGF			
IL22RA1	C10orf19	HES2	LYGN	HAND2	KRT20	CR2	TMEM195	IGSF11	PLEKHG4B		LRRC31	SYT9	DRU2	PRUNE1	ATCAY	VSTM2L	UGT1A1	VGF	CH13L1	SPRR2E	ATCAY	VSTM2L	UGT1A1	VGF			
C12orf127	SHD	THB54	TMEM92	VWA2	A1CF	FCRL5	CLIC13	COL4A3	BMP3	LYLT18	SLC6A20	PCDP1	CLDN18	PEG10	WBSCR17	LZU2P	SLC01B3	MAT1A	IRX1	CH13L1	SPRR2E	ATCAY	VSTM2L	UGT1A1	VGF		
THRSP	DI01	MS11	NRK	LOC84740	IGF2BP3	TAGLN3	MS1R	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	
	LAMB3	DSP	C2C04A		DSG1	ABCA8	DISCAM1	PNMA2	AOX1	T1HDE	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	
	PIK3C2G	ZNF385B	MAD	LUM	ENTP03	MS4A1	TMEM30B	MKRN3	KL5F	EN1	T1HDE	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9	MYO3M	N8L	CAPN9
PNMAL1	FGFR4	LRRMT1	INSM1	MI2	ACY3	HPGD	SLITRK2	SH3RF2	SFRP4	GAD1	C4orf141	ADAM23	C24	RN186	GDP15	AGTR1	ESR1	SLC22A3	ATP1A3	CD79A	ETV4	PCDH411	UNC80	MAGEA4	WN01		
	SPAG17	PADI1	BARX1	CPA4	KLK2	NCAM2	H0XA11A5	LOD1R	TMEM184A	FOXD1	GALNT9	TBX1	TPSAB1	MIA	LHPFL4	EDN2	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	UCLH1	
ELOVL2	EYAZ	KIAA0408		LOC100130933	CN7A	SLC13A2	RANBP3L	SGK2	SNAP25	C15orf48		CRB3L3	CIQ1L	C11orf41		GRPR1	NIPAL4	LASS5	TMEM63C	UPD3D	LOC389493	PNK3	DSG2	ROS1	PLA2G2D	TPMRSS56	
SMPDL3B	C12orf56	SLC7A4	NTNG1	STYK1	ID01	CXCL9	LAM1	CNNM1	ASCL1	ITIH2	FAM107A	CCLL14-CCLL15	GRPR1	NIPAL4	LASS5	TMEM63C	UPD3D	LOC389493	PNK3	DSG2	ROS1	PLA2G2D	TPMRSS56	NRG3	SCARAS	ISL1	PTN
	STR4E	ATPV61B1		ABCC6	FA2H	CSTA	KLK12	FAM5B	ACSM3	FG1	TYRP1	KRTCAP3	RIC3	GRP109A	PLAC2	AFM3	GD3D	SLC389493	PNK3	DSG2	ROS1	PLA2G2D	TPMRSS56	NRG3	SCARAS	ISL1	PTN
PLEKHG6	SCUBE2	TINAG	TPMRSS110	MUM1L	MPM11	HPD	MAP7D2	PI15	SLT1	ACTN2	CSDC2	H0XD10	PODPD3	C1KAA2022	CRB3	CLRF1	TFPC2L1	IL8	STXBPSL	CYP2C9	IGFBP1	MN1	BAALC	SLC6A19	KTG05	CAPN52	LOC43763
	NTRK3	SCG2	MFS06L	FLJ16779	HPD	MAP7D2	PI15	SLT1	ACTN2	CSDC2	H0XD10	PODPD3	C1KAA2022	CRB3	CLRF1	TFPC2L1	IL8	STXBPSL	CYP2C9	IGFBP1	MN1	BAALC	SLC6A19	KTG05	CAPN52	LOC43763	
RIMBP2	RASSF10	PRG4	LOC554202	ST6GAL2	SIX1	PLXNB2	H0XA7	SLC6A17	NEU4	LOC448905	LOC389332	ZYG11A	VSTM2A	STEAP4	FTCD	STXBPSL	CYP2C9	IGFBP1	MN1	BAALC	SLC6A19	KTG05	CAPN52	LOC43763			
FAM189A1	YMBL2	LAMA3	PRODH	CNXHA10	DMRT2	DCX	RAMP1	GPC3	C1orf168		SEZ6L	DNH11	VAT1L	PCDH20	SCGB2A2	LOC286002	ABCC2	SYTL5	CYP4F22	PEG3	PGR	PDX1	XAGE1D	ROB02	CALB1	TNNT3	KRT75
SPON1	BAIAP2L2		ENTPD8	PALM3	SYN2	SLC47A1	DYPSL4	PTH1L	MEGF10	NTF4	ABCC2	SYTL5	CYP4F22	PEG3	PGR	PDX1	XAGE1D	ROB02	CALB1	TNNT3	KRT75	C11orf92					
PHGR1	SLC16A9	C8orf85	NPR3	CC11	NELL2	NOTUM	TNNC1	MIOX	PKN0X2	MLC1	C1orf130	PLA2G3	PLA2G10	FAM135B	RG520	HIF3A	SYT14	LRN4	PTH2R	C1orf61	CYP4A11	UNC5A	GRN2A	CLU	POU2F3	DACH1	
SLC38A4	COL3A1	ABCC3	CSMD1	ESRRG	ANPEP	HEPACAM2		CACNA2D1		DLX1	EDAR	KIAA0125	NMES	XG	LTPC	PRSS12	CKN05	TMEM35	BAAT	CECR2	PLA2G12B						
NXPH4	FAM189A2	C4A	TMEM100	POU2AF1	CYP2W1	NOL4	DIO2	DLX1	EDAR	KIAA0125	NMES	XG	LTPC	PRSS12	CKN05	TMEM35	BAAT	CECR2	PLA2G12B								
ANKRD43	IL1A	SNORD116-4		APLP1	VEPH1	WSCD2	SYT7	EDAR	KIAA0125	NMES	XG	LTPC	PRSS12	CKN05	TMEM35	BAAT	CECR2	PLA2G12B									
CHMP4C	TRIM9	GRIA3	LHX2	OTX1	IGFN1	CKN4	FXYD1	FUT2	BTX	LGR6	BRKS2	SPOCK1	R1MS1	TCERG1L	CDH4	LOC645323	CEL3F	MEG3	CDH19	UGT3A1	SFTPD	IP6K3	MT1H				
PTPRD	CD1A	NALCN	PPAPDC1A		IGDCD3	C6orf132		CSF3	PPP1R140		HHP1	C1orf188	ACCS5	EN2	EFDH1	SLC14A1	ALPN3	AQP9	TRPA1	COL8A1	NECAB2	ADP2	RAB17	PCSK1			
EPHX3	C5orf23	DNA5E1L3	TGM1	PDPN	RNF212	PTPN20B	PTG2G	GABBR2	PCOLCE2	PLAC8	SLC19A3	IGFL2	ALDH1A1	ELAVL2	LPHK2	SOX15	LPNK3	OSR2	EMID2	KNG1	DNAJC22	SPINT1	GIPC2	NUDT11	OMD		
	SP5	DPF1	KIAA1244		RP56KA6	GRB14	GREM2	RSDC1A	CDKN2A	CKN10	EP58L1	FMRD5	CLSTN2	UNC5D	AKR1C3	SYTL1	LOC84856	DLX6	AN04	STX19	POU3F2	BCL2L14	WDR17	HEPACAM	SLC9A3		
C8orf46	ARHGDTG	ADAM12	STXB8P6	SLC17A3	CYP4F2	SFRP5	FOSB	SLC6A12	SULT1E1	GFR43	SPLEKH81	TSHR	ANKS18	RLG3	COL9A1	TRIM10	FOXO1	C3	GNALNT1	LOC254559	KLF15	F7	ATCSL1	GLYATL2	KANK4		
GRK12	WNT10A	CALN1	TTCT22	LYPD6	SLC38A5	SYT4	TESC	PCDH19	TNNI3	DEGS2	IRX3	FOXG1	YBX2	DN2	CLKMT2	HAP1	TNNT2	TF2F	PDIA2	S100A7A	HRA5L5	NRG1	EDIL3	DMRTA1	C21orf62		
GLT2SD2	PCDHAC2	ATP1B2	ADAMT516		C6orf141		ENHO	TUBBP5	CHST8	PZNRNA	PAEP	FS01	DCLC1	NPNT	H0XB6	FAT3	CALNT1	LOC254559	KLF15	F7	ATCSL1	GLYATL2	KANK4				
ABCC6P1	ENPP5	CNN1	BTRC7	BA11	CKNS1	PCDH4A	AN05	HMP19	SLC17F5	FAP	FLNC	SHOX2	CXCL10	CKMT2	HAP1	TNNT2	TF2F	PDIA2	S100A7A	HRA5L5	NRG1	EDIL3	DMRTA1	C21orf62			
	ST6GALNAC5	ARX	AN09	SGPP2	FCG8P		CC113	H0XB5	DUSP26	SCG5	ALDH1A2	CRB2	COCH	GFRG3	TPRXL	HPX	KRTDAP	ACSM1	AQP7	CST2	TLX1	SYT5	RGMA	RNF182	GPX3		
	MPMED2	B3GALT5	CD5N	TGDF1	FLJ345983		ITIH5L	CASKIN1	CC114	C1QL4	GREB1L	F1BCD1	ARHGAP8	B4GALNT3		CDK12	CXCL11	LOC255167	CSAG3	RIP							

Gene Expression Level



										pancan_scaled_zeroone_rnaseq (1).tsv ~									
0.03900325027085591	0.0	0.31176654347838895	0.13519807298373912	0.5598111658456486	0.3013222035427525	0.30728867577781096	0.116503968003462	0.0	0.203547712600807	0.0	0.756302772339742	0.614186828244523	0.0	0.31308691454816723	0.5002130243738083	0.1629506257831314	0.3258563844649343	0.535506411715639	0.0
0.40806191192027175	0.0	0.1469183422404596	0.8555505957490642	0.0	0.0	0.10971492600299772	0.1637452264164558	0.7590197794503762	0.13702141785723068	0.0	0.2547196579279035	0.3846285974898273	0.1257737761476172	0.048391500678260581	0.1652917588086806	0.5580364742689312	0.11002261664781947	0.32658742482848185	0.0
0.31502677054228483	0.20351019177517002	0.10773715535041904	0.5498956316173327	0.9327448014057111	0.715669158359046	0.332588928673298	0.20245468816897386	0.0	0.10177255181277	0.310895695377658	0.7745450925113724	0.6816458254915744	0.7346297465052778	0.3014612611543607	0.0	0.1958611599297812	0.5468137641941457	0.558076082845765	0.0
0.5393315870861867	0.31553482191859955	0.0	0.1995976002788667	0.4845844584548463	0.20742661115039146	0.8824126404191484	0.5366479118507207	0.821305821734712	0.04500058594512949	0.8317184719750891	0.2224882813066887	0.0	0.2079324217870088	0.0501600156750049	0.0	0.0	0.7318538207953431	0.0	0.11472067315373438
0.3964165132243863	0.530467897205211	0.82173151093466271	0.7663750489319958	0.0	0.0	0.0766340897796191	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.2684049300332217	0.661243881370573	0.12480597235568038	0.6484427668637104	0.0	0.0	0.1960157359723627	0.7095603309784837	0.23664281956838023	0.18766831513489693	0.4033289757050755	0.6276905820210065	0.622375379787589	0.13186699682991502	0.14366646577090791	0.438534621686682	0.816917032252942	0.10326322387968422	0.678991731984138	0.0
0.08340684704717238	0.19938876505906178	0.1094843191369833	0.1784278260896564	0.07358910733600561	0.37517661781922407	0.049189077633629626	0.678991731984138	0.0	0.8946891219101284	0.0	0.0345949080902992	0.7994901828929776	0.5615930809309887	0.20917234299374913	0.2392428521716612	0.415391261363931006	0.27815818012156057	0.0	0.0
0.3327662700820661	0.5618745422265062	0.12127417162347334	0.776545732273338	0.14078626561730187	0.7897628440336864	0.40495711723226413	0.26945146424855065	0.21229683254288953	0.46677940317609937	0.05505858910445844	0.16499733034846994	0.17546160831399454	0.0	0.24952790158946164	0.722243928520019	0.4566231632027104	0.09803149373547488	0.0	0.0
0.6770324361628789	0.2041215287177771	0.1650863512321775	0.2236717962652636	0.09649757140205935	0.17533366118093754	0.2963191137775577	0.09176997559535764	0.4925404061334374	0.5714590615598008	0.8135138794854434	0.8135138794854434	0.681573320911214	0.08452701122544434	0.0	0.0	0.24648380147371599	0.5308889943132459	0.044975111429222114	0.0
0.04377953154887828	0.6491807075444386	0.8382339327042904	0.641208702644024	0.4264903279436915	0.6580390851880728	0.42599583219458864	0.16196164773759433	0.1874406143397872	0.5521632084006942	0.2651209752814031	0.3089138476852113	0.3504445528719742	0.769837711826415	0.09845067020102767	0.6744378363069952	0.6147099779317758	0.0	0.8349812842581933	0.0
0.04109686779080553	0.3567143180568582	0.07569718508846835	0.19752983276940003	0.1778424958110588	0.350471147008026	0.6147099779317758	0.0	0.506590891830665	0.0	0.1976882321826525	0.13968251978677807	0.36100556850483225	0.04561580370618614	0.5659601284779162	0.0	0.09676798607799338	0.3448233553462524	0.0	0.0
0.8734059716666299	0.7306614700150752	0.17691893803703015	0.7468419255178676	0.5474886844794861	0.3413907702104795	0.04745492743076057	0.0	0.16844994061075136	0.0	0.05477456431904271	0.5204334575008466	0.7728382363025441	0.6935751683400575	0.2605531373031065	0.4858978219418236	0.5079680480612748	0.0	0.0	0.0
0.7190179607833347	0.188580107120995718	0.5097548029017628	0.09362040538016332	0.42267577351090335	0.5138985215275713	0.5315181874344609	0.5079680480612748	0.46762519128941314	0.2476364085769017	0.361618895429689	0.8345611139650028	0.2484591916051302	0.6448069483979273	0.2682554706372639	0.2127362794941989	0.0	0.0	0.5018928125597429	0.0
0.594166559106713	0.2476364085769017	0.361618895429689	0.8345611139650028	0.2484591916051302	0.6448069483979273	0.2682554706372639	0.2127362794941989	0.6736518313780568	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.8711904885519964	0.0
0.3094700152919944	0.523348304022184	0.64948124288	0.459852987981762	0.0	0.0	0.0	0.0	0.660500780723996	0.3407870411127741	0.459852987981762	0.0	0.791	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.5615351302155821	0.8670115384364799	0.0	0.791	0.0	0.0	0.0	0.0	0.08606423192546954	0.10846475895037232	0.122936488231519	0.869	0.1052	0.133063115	0.0861	0.17082	0.5328	0.18428	0.0	0.0
0.21609274379234983	0.55578013341195548	0.4332528842800505	0.11953393650051748	0.4771686492403406	0.5107191087103309	0.09961161375043122	0.25823917890949006	0.66357022272115573	0.25475268575846566	0.6618880579093255	0.0	0.39430841868985267	0.76297891400911	0.5116529398749167	0.3337487501267988	0.682398314182387	0.0	0.0	0.0
0.04490148567271027	0.15410456849525964	0.518682343737070	0.467715126119909	0.0880480294106	0.633759511006	0.6049368802808034	0.5591122222874085	0.38850131227708123	0.14430380564746154	0.48344708766814654	0.0	0.20035	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.5500854344320817	0.1598834776787582	0.550017258261071	0.0657112104939018	0.6859750725386774	0.8033890166176769	0.720	0.162768283	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.2977997901623156	0.543684182199817	0.06657112104939018	0.6859750725386774	0.8033890166176769	0.720	0.162768283	0.0	0.1608327019518707	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.9518319579894973	0.0
0.5154540403699463	0.539595536554083	0.7868815969498011	0.5365162923968816	0.5351141909764913	0.6893092735672066	0.13507809912948796	0.08876098384559304	0.7754568311990719	0.08212680446776634	0.78986861185445836	0.059641735408828916	0.7061274246172601	0.540939164111667	0.17232669099073814	0.30154749908812447	0.082265240756874	0.6456262625780775	0.0	0.0
0.07597065218105267	0.22095712783770102	0.2705621700159482	0.2705621700159482	0.2705621700159482	0.2705621700159482	0.2705621700159482	0.2705621700159482	0.362404307101727	0.0994498684323902	0.7201891784317858	0.12883863863179783	0.23750935268988545	0.59808602525806642	0.7433714754215235	0.22790733531208322	0.05425346540876036	0.0	0.0	0.0
0.10575075390981135	0.757696375584522	0.8164863490297238	0.8422924346668938	0.0	0.0	0.0	0.0	0.7209538426625419	0.749759677005849	0.06670280744653856	0.62459575213657148	0.6854869889775505	0.5260451080699985	0.687604469077131	0.6336095561693841	0.564097160909941	0.0	0.0	0.0
0.6986398983796511	0.20019220751225994	0.188586245988616	0.0657112104939018	0.6859750725386774	0.8033890166176769	0.720	0.162768283	0.844321466241134	0.7591892380204921	0.2064118277775582	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.35846616198120745	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.7056989428299848	0.418212550972538	0.7308319501470545	0.5698974584087557	0.0	0.0	0.0	0.0	0.7348178899312697	0.08809605285190382	0.4263830725148776	0.7763945966850813	0.69851119462171888	0.11417019024113366	0.5496812435361129	0.0527931808808029	0.12276800591361037	0.338891701685991	0.0	0.0
0.197287134194756137	0.25123603991692134	0.37980015673981193	0.730966278984489	0.15935007943124083	0.175080734163658033	0.0	0.0	0.86848775910496192	0.33907062315300934	0.51776084117876392	0.78390991977876392	0.4245911872568582	0.3431632091746645	0.7942640042968627	0.45879399410997923	0.0	0.0	0.0	0.0
0.5503963265591173	0.7594912914119775	0.5948087366410034	0.526626823365823	0.4116017287289197	0.2073561594265315	0.5351984257023211	0.0	0.6295686074304412	0.5632721298074132	0.23743293066754595	0.1584762330335698	0.614653917182145	0.6621839567133959	0.3903478320089901	0.797772092574191	0.6669342675035275	0.0	0.0	0.0
0.6174327378782355	0.560658182831513	0.18798472187310325	0.853035019452531	0.45780935528750694	0.22697550425028923	0.18142200432460073	0.08781947123050524	0.8734703461432043	0.760851243281413	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Extracting Decoder  
Network Weights

## Feature 82 → Patient Sex

```
In [15]: # There are 17 genes with high activation in node 82  
# All genes are located on sex chromosomes  
sex_node_plot.head(17)
```

Out[15]:

	encoding 82	encoding 85
<b>EIF1AY</b>	-0.543605	0.013644
<b>UTY</b>	-0.514367	0.019198
<b>CYorf15A</b>	-0.514013	0.016753
<b>KDM5D</b>	-0.499488	0.019061
<b>DDX3Y</b>	-0.497709	0.022053
<b>TMSB4Y</b>	-0.495302	-0.003714
<b>USP9Y</b>	-0.494874	0.022164
<b>TTY15</b>	-0.487078	0.014047
<b>NCRNA00185</b>	-0.473645	-0.019878
<b>CYorf15B</b>	-0.472546	0.019967
<b>ZFY</b>	-0.453348	0.018549
<b>RPS4Y1</b>	-0.452888	0.016435
<b>NLGN4Y</b>	-0.371427	-0.013003
<b>DAZ1</b>	-0.369805	-0.008085
<b>XIST</b>	0.316281	-0.023227
<b>TSIX</b>	0.298300	-0.030515
<b>PRKY</b>	-0.294522	0.017516

Feature 66 and 53 → Primary and Metastatic SKCM tumours

Out[18]:

	encoding 66	direction
genes		
<b>ROPN1</b>	0.115224	positive
<b>ROPN1B</b>	0.108729	positive
<b>ADIPOQ</b>	0.107172	positive
<b>SOX10</b>	0.105733	positive
<b>CIDEA</b>	0.103107	positive

Out[19]:

	encoding 53	direction
genes		
<b>HCG22</b>	0.084451	positive
<b>RXRG</b>	0.081329	positive
<b>MGAT4C</b>	0.076966	positive
<b>PLP1</b>	0.076440	positive
<b>C10orf90</b>	0.076005	positive



										pancan_scaled_zeroone_rnaseq (1).tsv ~									
0.03900325027085591	0.0	0.31176654347838895	0.13519807298373912	0.559811658456486	0.3013222034527525	0.3072886757781096	0.116503968003462	0.0	0.203547712600807										
0.7562308727339742	0.0	0.614186828244523	0.0	0.31308691454816723	0.5002130243738083	0.1629506257831314	0.3258563844649343	0.535506411715639	0.0										
0.40806191192027175	0.0	0.1469183422404596	0.8555505957490642	0.0	0.10971492600299772	0.1637452268164558	0.7590197794503762	0.790705921917515	0.13702141785723068										
0.2547196579279035	0.0	0.3846285974898273	0.1257737761476172	0.04839150068260581	0.1652917588086806	0.5503064742689312	0.11002261664781947	0.32658742482848185											
0.31502677054227843	0.20351019177517002	0.10773715535041904	0.5498953616173327	0.9327448014057111	0.715669158359046	0.332588928673298	0.20245468816897386	0.0											
0.1011772551828487	0.310895695377658	0.7745450925113724	0.6816458254915744	0.7346297465052771	0.3014612611543607	0.0	0.1958611599297812	0.5468137641941457											
0.5393315870861867	0.3155348219185995	0.0	0.19959760027886667	0.4845844554845463	0.20742661115039146	0.8824126404191484	0.0	0.5366479118507207	0.5580076082845765										
0.04670017836873683	0.0	0.28484470118016295	0.0668674730227879	0.487940465514067	0.667903931277676	0.33281895106896126	0.821305821734712	0.0	0.11472067315373438										
0.04500058594512949	0.8317184719750891	0.2224882813066887	0.0	0.2079324217870088	0.0501600156750049	0.0	0.0	0.7318538207953431	0.0										
0.396416532243863	0.530467097205211	0.8217351093466271	0.7663750489319958	0.0	0.07663408977969191	0.0	0.054365810551648935	0.1608176164158213	0.0										
0.2684049300332217	0.661243881370573	0.1248059723568038	0.6484427668637104	0.0	0.1960157359723627	0.7095603309784837	0.2366420195683023	0.18766835113489693											
0.40332389757050755	0.6270905820210065	0.622375379787589	0.13186699682991502	0.14366646577090791	0.438534621686682	0.8169170322552942	0.10326322387968422	0.0											
0.08340684704717238	0.19938876505906178	0.1094843191396833	0.1784278260896564	0.07358910733600561	0.37517661781922407	0.049189077633629626	0.679891731984138	0.0											
0.8946891219101284	0.0	0.0345949080892992	0.7994901828929776	0.561593080309887	0.209172132499374913	0.2392428521716612	0.41539126363931006	0.27815818012156057											
0.3327667200820661	0.5618745242265062	0.2127417162343734	0.7765457322733308	0.14078626561730187	0.7897628440336864	0.40495711723226413	0.26945146424855065	0.0											
0.21229683254288953	0.7786803249169701	0.2972609826548062	0.9368194640338505	0.222388553718366	0.419675826952292	0.2185582820588894	0.08244409754150361	0.0											
0.466779403176709937	0.05505858910445844	0.1649973303484694	0.17546160831399454	0.0	0.24952790158946164	0.722243928520019	0.4566231632027104	0.09803134973574788											
0.6770324361628709	0.2041215287177771	0.16508635132321775	0.2236717962652636	0.09649757140205935	0.17533366118093754	0.2963191137775577	0.09176997559535764	0.0											
0.4925404061334374	0.5714590615958008	0.8135138794854434	0.681573320911214	0.0845270112254434	0.0	0.0	0.2464838014731599	0.5308889943132459	0.044975111429222114										
0.04377953154887828	0.6491807075444386	0.8382339327042904	0.641208702644024	0.4264903279436915	0.6580390851880728	0.42599583219458864	0.16196164773759433	0.0											
0.1874406143397872	0.5521632084006942	0.2651209752814031	0.3089138476852113	0.3504445528719742	0.7698377118264145	0.09845067020102767	0.6744378363069952	0.0											
0.04109686779080553	0.3567143180568582	0.07569718508046835	0.19752983276940003	0.1778424958110588	0.350471147008026	0.6147099779317758	0.0	0.8349812842581933											
0.5065908918303665	0.0	0.4197688232186255	0.13968251978767807	0.36100556850483225	0.04561593078618614	0.5659601284779162	0.0	0.09676798607799338	0.3448233553462524										
0.8734059716666299	0.7306614700150752	0.17691893803703015	0.7468419255518676	0.5474886844794861	0.3413907702104795	0.04745492747807657	0.0	0.05257993108012506											
0.0	0.16844994061075136	0.0	0.05477454631904271	0.5204334575008466	0.7728382363025441	0.6935751683400575	0.2605531373030165	0.4858978219418236											
0.7190179607833347	0.18850107120995718	0.5097548029017628	0.09362040580316332	0.42267577351090335	0.5138985215275713	0.5315181874344609	0.5079680480612748	0.0											
0.46746259128941314	0.0	0.4122125813449024	0.39830719067448805	0.2153172221348256	0.5174037792719685	0.586128519081592	0.17622250793473332	0.5550880810247909											
0.5941665589106713	0.2476364085769017	0.361618895429689	0.03944575067911521	0.596529110191189	0.5754315752112744	0.14653084569444523	0.06627548506137043	0.0											
0.6736518313780568	0.8711904885519964	0.8345611139650028	0.2849591916051302	0.644806483979273	0.2682554706372639	0.2127362794941989	0.0	0.5018920125597429											
0.6016764157870812	0.0	0.3688638760812863	0.0	0.24742510937009006	0.6272378018139417	0.6502668019533846	0.4766919930797503	0.7357681940700808											
0.309470152919944	0.523348304022184	0.6494012428800	0.45985298798762	0.0	0.8087081856705449	0.785090852100889	0.510070078357	0.0											
0.660500780723996	0.6307870411127741	0.8670115384364799	0.0	0.7915277775757575	0.0	0.0	0.23864813370331064	0.15287799390929793											
0.5615351205158221	0.0	0.10846475895037232	0.1229364882105919	0.4357166263333333	0.0	0.0	0.7523068050749712	0.7558041121277124											
0.08606423192546954	0.4670381965708217	0.869210774101629	0.4332528842800505	0.0	0.556037287769673	0.7062379260921043	0.733259944853394	0.843403863269089											
0.3465027755749405	0.55578013341195548	0.42820454079602593	0.11953393650051748	0.4771686492403406	0.5107191087103309	0.09961161375043122	0.25823917890949006	0.46349069534796983											
0.21609274379234983	0.25475268575846566	0.661880527903259	0.03943081668985267	0.79629910409911	0.44511652938974167	0.3373487501267988	0.682398314182387	0.0											
0.66357022272115573	0.15410456849525964	0.5186823437370706	0.46774551261199	0.009084219417506	0.6433759525100603	0.6049360882080034	0.5591122222874085	0.0											
0.04490148567271027	0.48344708766814654	0.0	0.2850685773410818	0.4234044452340445	0.149339256	0.6446020722694693	0.5745379957278078	0.1313213365653854											
0.38850131227708123	0.730067700801893	0.62083757590970048	0.3508006423100000	0.4234044452340445	0.149339256	0.6446020722694693	0.5745379957278078	0.1313213365653854											
0.5500854344320817	0.1598834776787582	0.5500172582610716	0.4811543979289475	0.08991512220691065	0.05716589787426212	0.2065175483900483	0.3344982290436836	0.3507390233299522											
0.2977997901623156	0.543684182199817	0.06657112104939810	0.6859750725386774	0.803389016176769	0.7281017162768283	0.0	0.06824967840156727	0.9564921081097436											
0.1608327019518707	0.9518319579894973	0.6991776304583331	0.476020038150381	0.12108923294359503	0.137953886936687	0.675873794336325	0.675873794336325	0.2504286960800351											
0.5154540403699463	0.576955536554083	0.1375944414981515	0.8253812384473197	0.15707220266980879	0.0	0.470975750321408	0.2942020105442744	0.0											
0.77455683611990719	0.7868915969498011	0.5365162923968816	0.5351141909764913	0.6893092735672066	0.13507809912948796	0.08876098384559304	0.112361387145687	0.0											
0.08212680446776634	0.78986861185445836	0.059641735408828916	0.706127426172601	0.540939164111667	0.1723266909073814	0.301547499080212447	0.082265240756874	0.0											
0.07597065218105267	0.22095712783770102	0.8873631041566907	0.6857737128130428	0.603427043303224	0.5842543815905197	0.8253756716813176	0.6456246265780775	0.0											
0.3624043071017127	0.73595272597248625	0.5029472001594882	0.275062656641604	0.07955702297427432	0.1891896141056984	0.6887534947099685	0.099292134645152833	0.0											
0.0994498684323902	0.7201891784317858	0.12883863863179783	0.23750935826898545	0.5980062525806642	0.7433714754215235	0.22790733512030822	0.05425346540876036	0.0											
0.10575075390981135	0.757696375584522	0.8164863490297238	0.0	0.0450843474510426	0.057882660324585056	0.21870022011351903	0.5786954101513082	0.5261282431573473											
0.7209538426625419	0.7497596770058416	0.842292434668938	0.0	0.21408408384594323	0.2589539874092309	0.435776406138824	0.29536390299173753	0.04958026104892520											
0.04790087180695505	0.06670280744653856	0.62459575213657148	0.6893842973531678	0.8407180973248046	0.2875368418535413	0.63680786468373727	0.06610495308958407	0.0											



## GO terms

geneset	description	link	C	O	E	R	PValue	FDR	overlapGene	OverlapGene_UserID		
G0:0030300	regulation of intestinal cholesterol absorption	<a href="http://amigo.geneontology.org/amigo/term/G0:0030300">http://amigo.geneontology.org/amigo/term/G0:0030300</a>								5		
G0:1904729	regulation of intestinal lipid absorption	<a href="http://amigo.geneontology.org/amigo/term/G0:1904729">http://amigo.geneontology.org/amigo/term/G0:1904729</a>								5		
G0:0006069	ethanol oxidation	<a href="http://amigo.geneontology.org/amigo/term/G0:0006069">http://amigo.geneontology.org/amigo/term/G0:0006069</a>							7	3	0.0731343283582	
G0:1904478	regulation of intestinal absorption	<a href="http://amigo.geneontology.org/amigo/term/G0:1904478">http://amigo.geneontology.org/amigo/term/G0:1904478</a>								7	3	
G0:0032371	regulation of sterol transport	<a href="http://amigo.geneontology.org/amigo/term/G0:0032371">http://amigo.geneontology.org/amigo/term/G0:0032371</a>								20	4	0.20895
G0:0032374	regulation of cholesterol transport	<a href="http://amigo.geneontology.org/amigo/term/G0:0032374">http://amigo.geneontology.org/amigo/term/G0:0032374</a>								20	4	
G0:0016042	lipid catabolic process	<a href="http://amigo.geneontology.org/amigo/term/G0:0016042">http://amigo.geneontology.org/amigo/term/G0:0016042</a>								96	7	1.0029850746268
G0:0006067	ethanol metabolic process	<a href="http://amigo.geneontology.org/amigo/term/G0:0006067">http://amigo.geneontology.org/amigo/term/G0:0006067</a>								8	3	0.08358
G0:0030299	intestinal cholesterol absorption	<a href="http://amigo.geneontology.org/amigo/term/G0:0030299">http://amigo.geneontology.org/amigo/term/G0:0030299</a>								9	3	
G0:0098856	intestinal lipid absorption	<a href="http://amigo.geneontology.org/amigo/term/G0:0098856">http://amigo.geneontology.org/amigo/term/G0:0098856</a>								9	3	0.09402

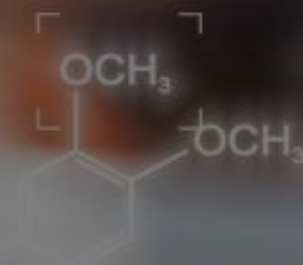
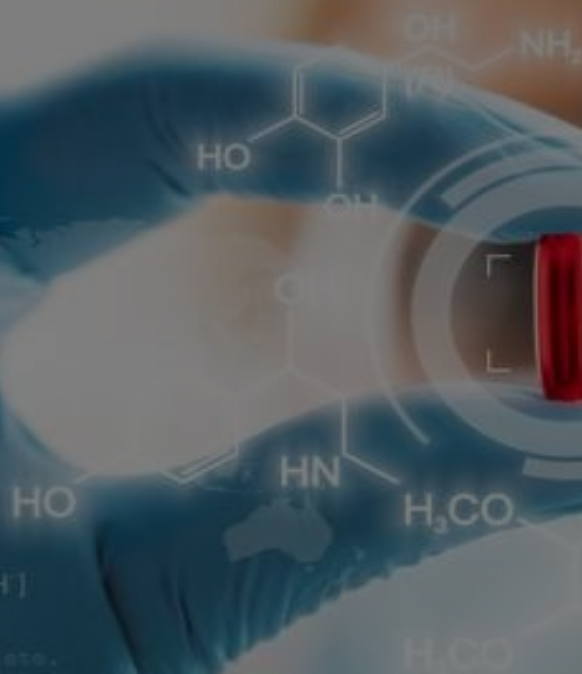
4850-32001/905

• 10722 14-341/  
172009

$C_b = pH[H^+]$        $[OH^-]$

Analysis: Complete.  
Position: #120498 05  
Offset: 14055 880 0110  
Current status: Online.

Awaiting data input...



$C_b = pH[H^+]$	$[OH^-]$	Alpha	Value
7.40108E-08	2.51E-07	0.300	0.300
7.60251E-08	3.98E-07	0.250	0.250
8.00100E-08	1.00E-06	0.500	0.500
8.40398E-09	2.51E-06	0.711	0.711
8.80158E-09	6.31E-06	0.800	0.800
9.00100E-09	1.00E-05	0.900	0.900
9.40398E-10	2.51E-05	0.962	0.962
9.60251E-10	6.31E-05	0.980	0.980

## 5 Key Takeaways

- VAE's are generative models that allows for reconstruction of original input data as well as identification and recapturement of variations/patterns within the data.
- The weights in the decoder network are able to learn which genes contributed to a particular feature.
- Through the decoder network, we are able to understand that the VAE was able to construct features representing patient sex and another capturing SKCM tumours.
- The genes with the highest weight are the most expressed meaning they have a higher chance of being the cause of the state of a cancerous tumour.
- We are able to identify the functional processes of the highly expressed genes within a feature, using ORA. This can help researchers identify which particular gene products or pathways to target when curing for a disease.

The background of the slide is a dark blue field filled with a complex network of thin, light blue lines. These lines connect numerous small, semi-transparent blue circular nodes, creating a web-like or molecular structure that fills the entire frame. The nodes and lines are more densely packed in some areas and more sparse in others, giving a sense of depth and connectivity.

# Discussion Questions



Pro:

- The papers presented in #NIPS2017
- Potential for discovering genetic/biological patterns for certain conditions (strong enough conclusion?)
- The manifolds of the VAE provide the potential for representing differing pathway activations, transitions between cancer states, or indicating particular tumors vulnerability to specific drugs; versatile applications? Transfer learning potential?
- This is a open source project and for code and dataset of this paper search /Greenelab/Tybal
- Very simple VAE structure
- The model has two direct benefits of modeling cancer gene expression data.

Automatically engineer non-linear features

Learning the reduced dimension manifold of cancer expression space

- Side note: VAEs are different from deterministic autoencoders because of the added constraint of normally distributed feature activations per sample. This constraint not only regularizes the model, but also provides the interpretable manifold.

### Cons:

- Is the genetic expression of gender found in this paper enough to validate the hypothesis on genetic expression of disorders?
- What are the evaluation/validation techniques are used by the authors (sounds like pattern matching from select examples)?
- How would validation need to take place for more extensive research?
- Why and how normalization happened and how we can measure it effects
- Predefined type of cancers in latent space!!! Very selective choices
- Measuring the relation of the depth of VAE to latent space size and interpretability of extracted features