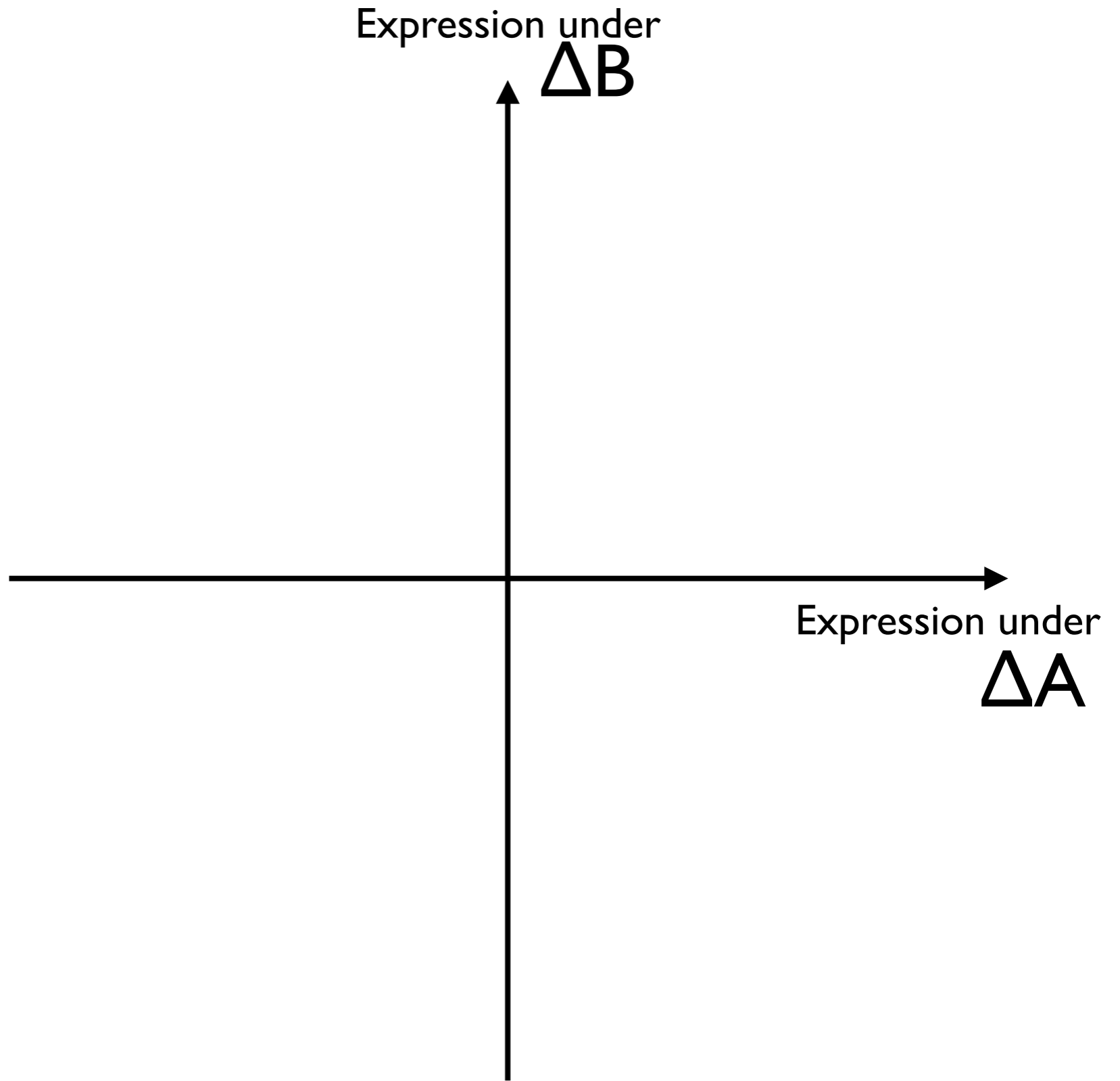
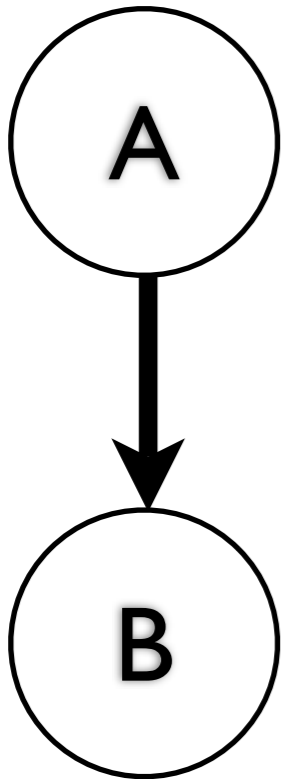
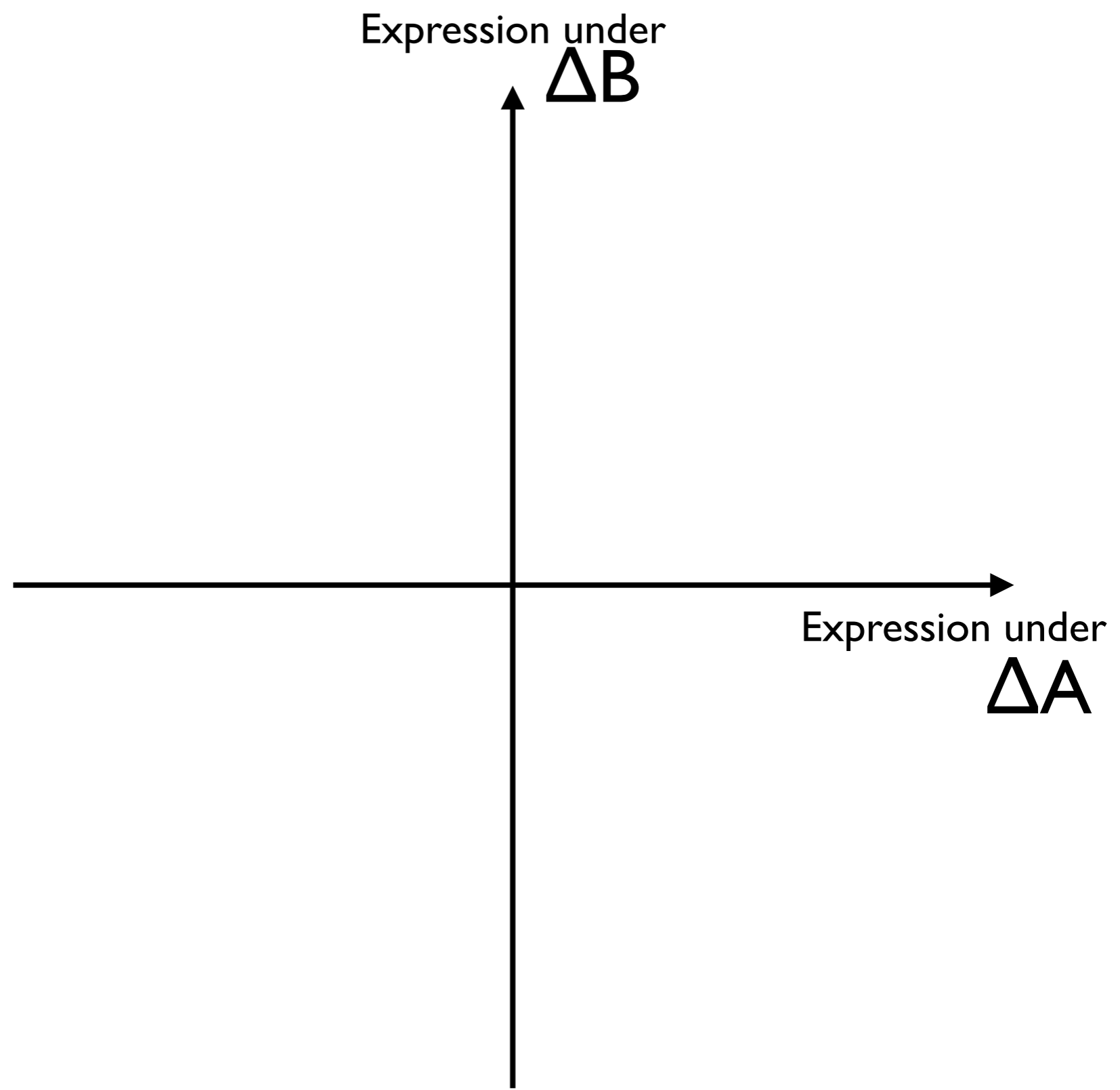
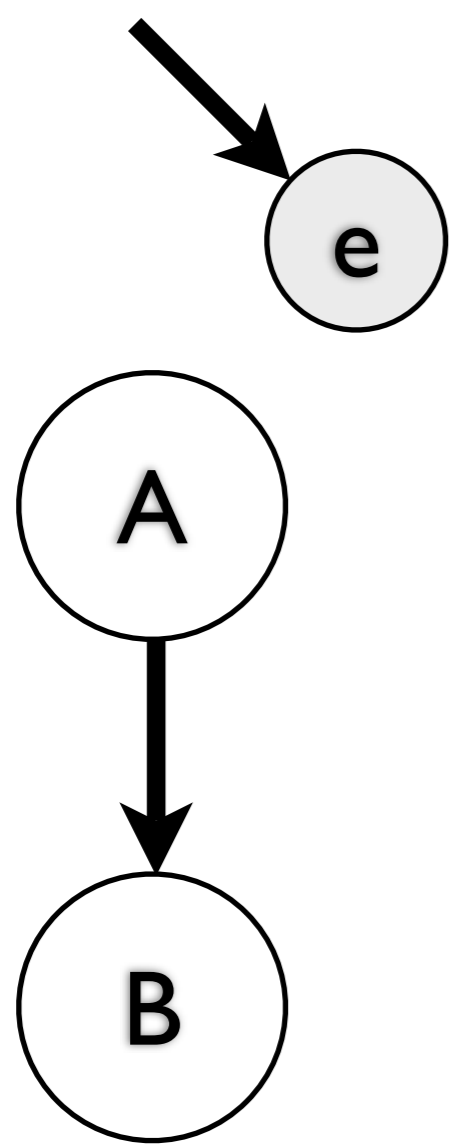


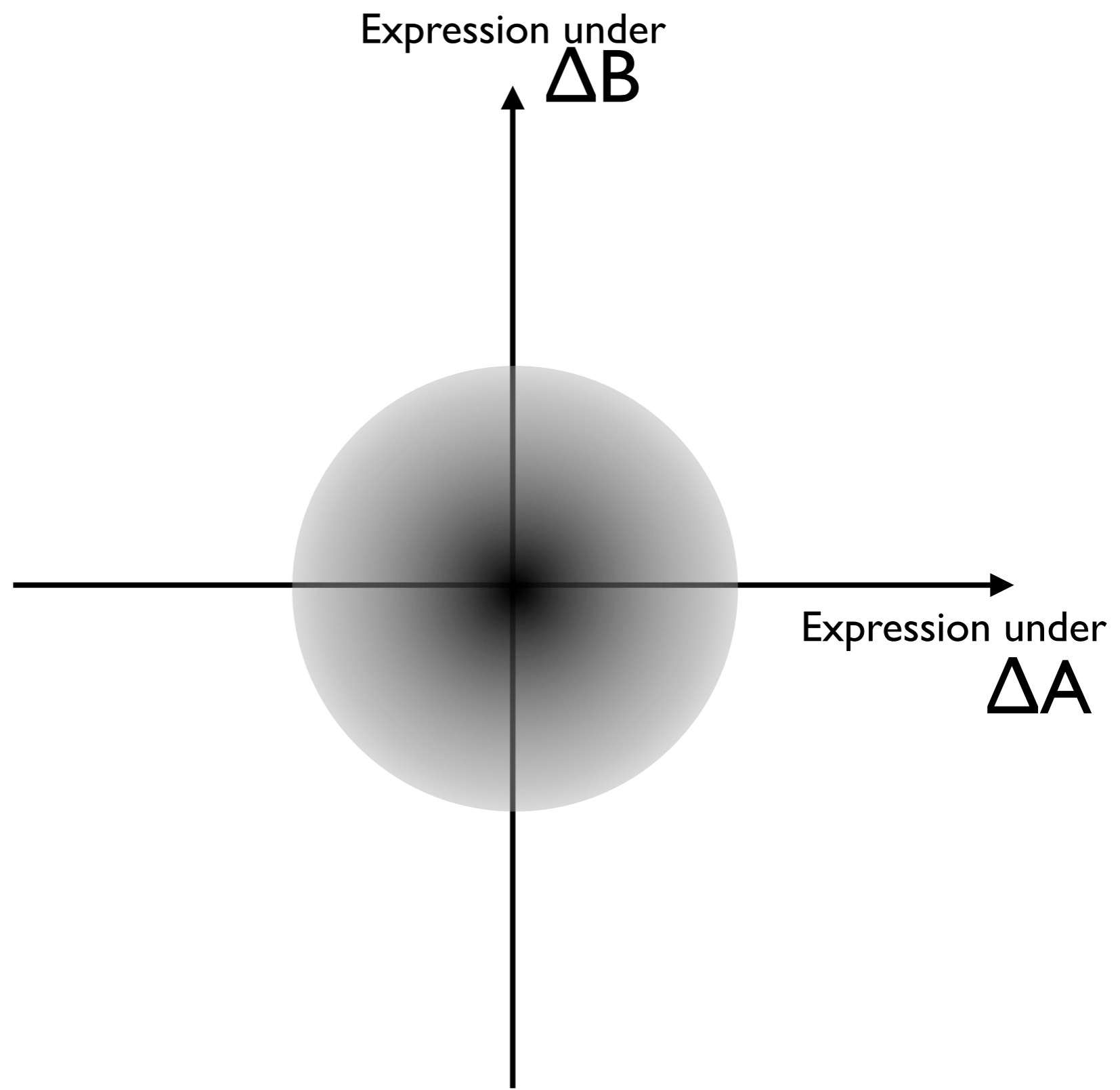
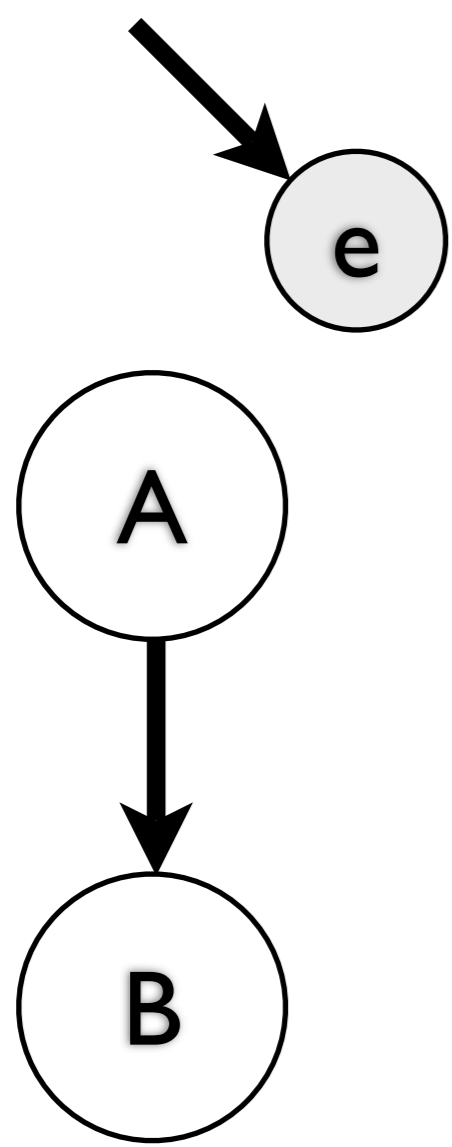
# Predicting new network members from perturbation

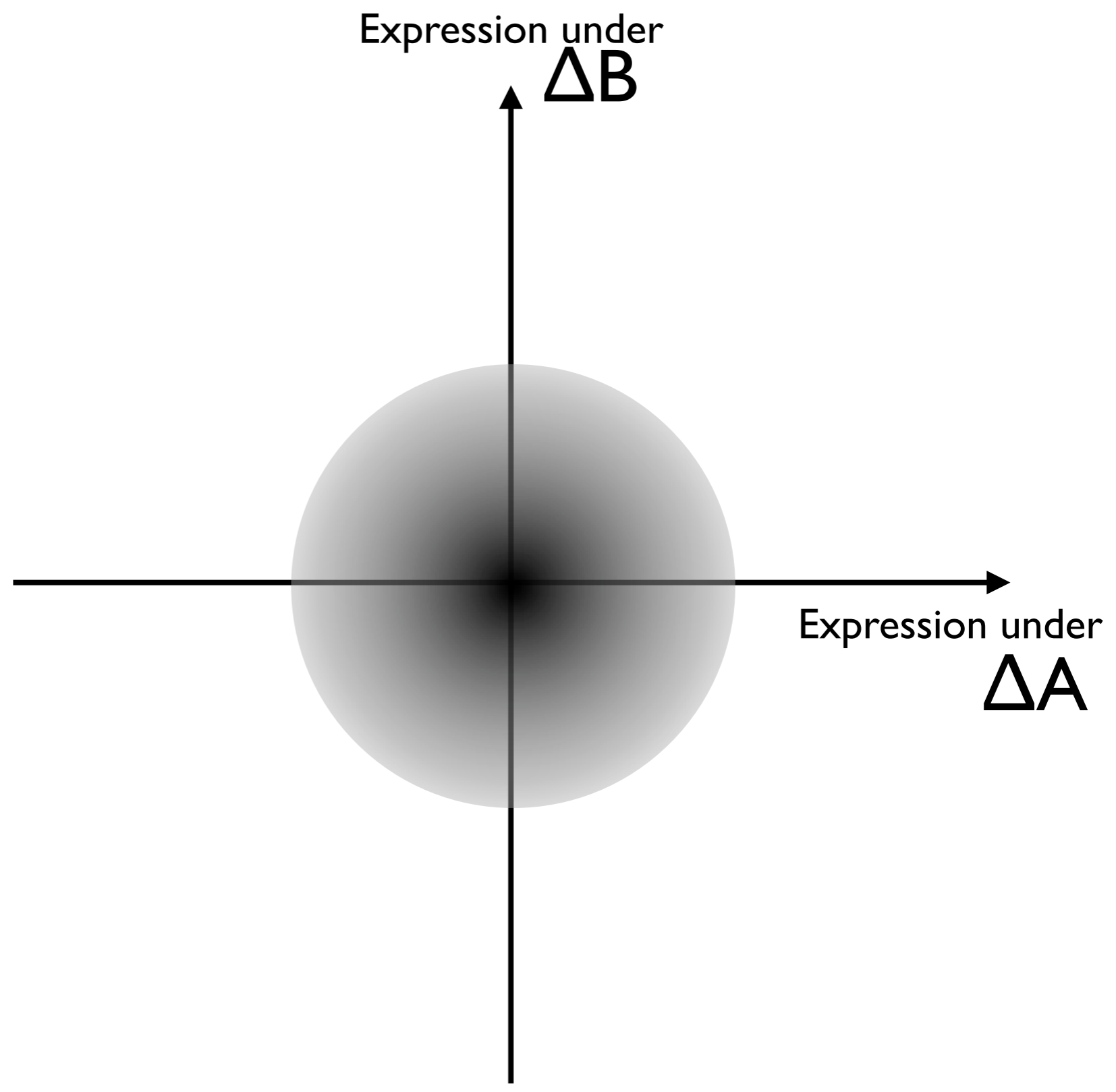
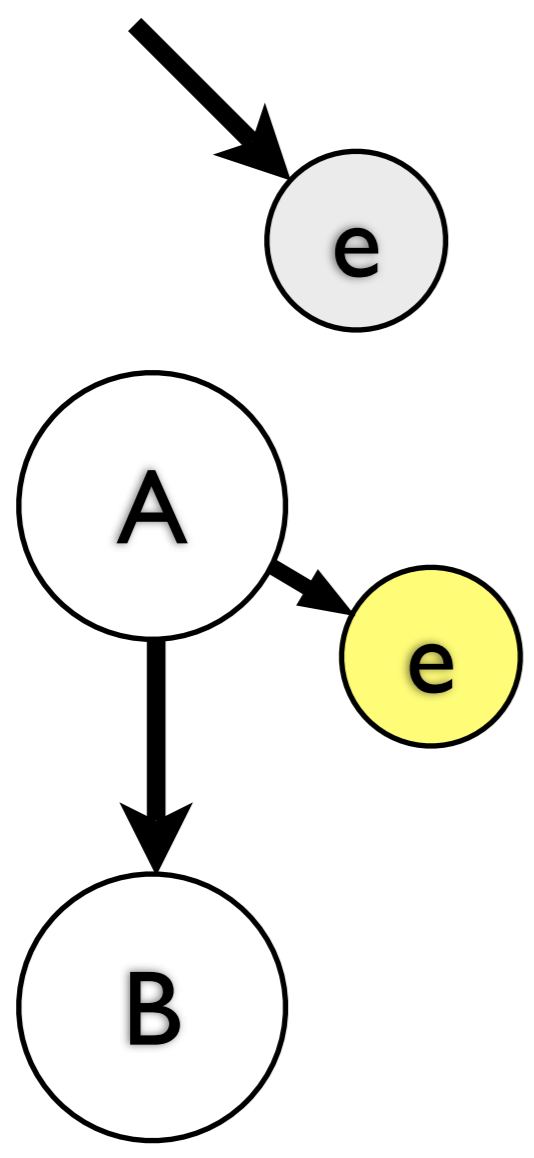
Charlie Vaske  
Stuart Lab Meeting  
November 20, 2007

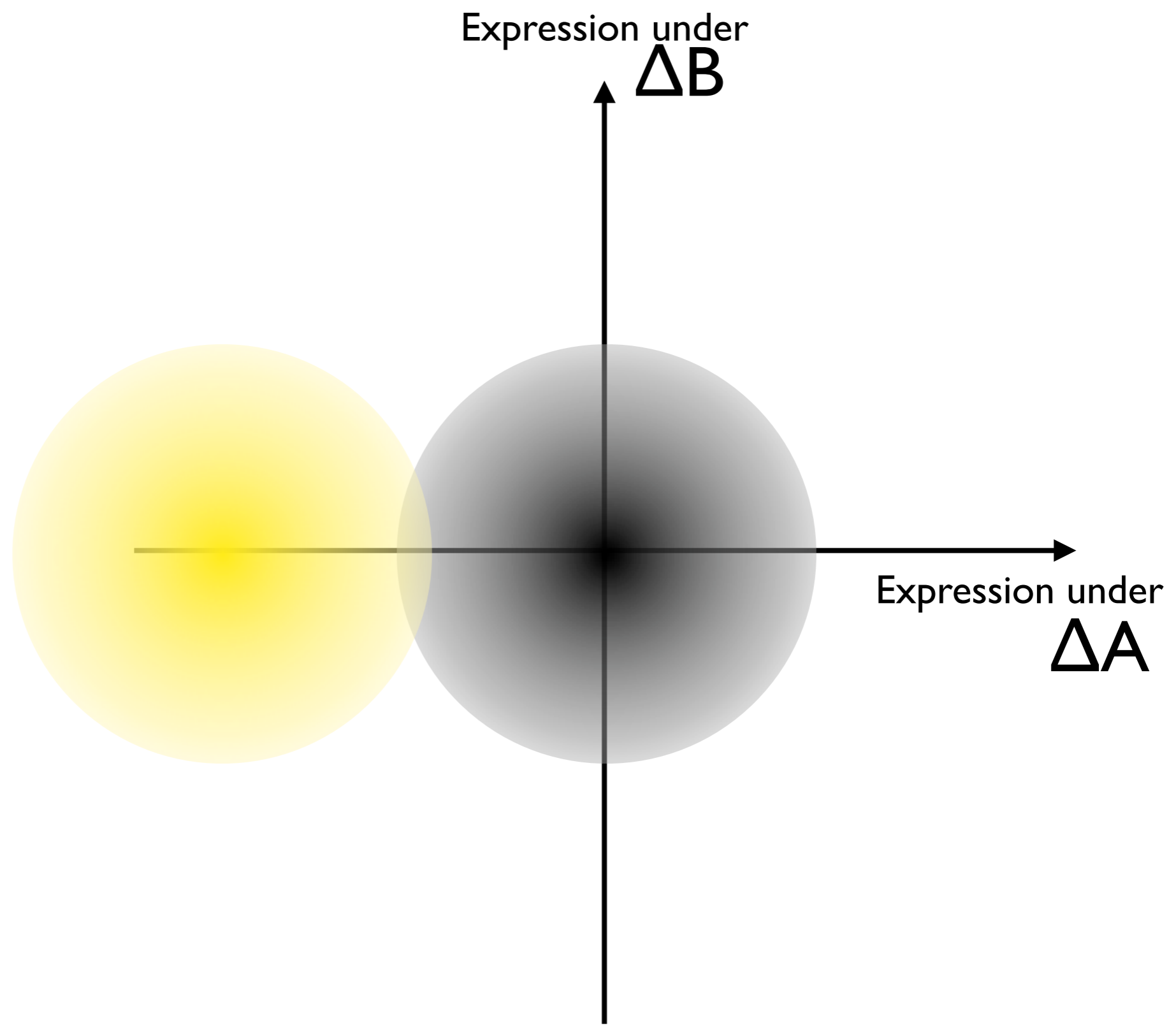
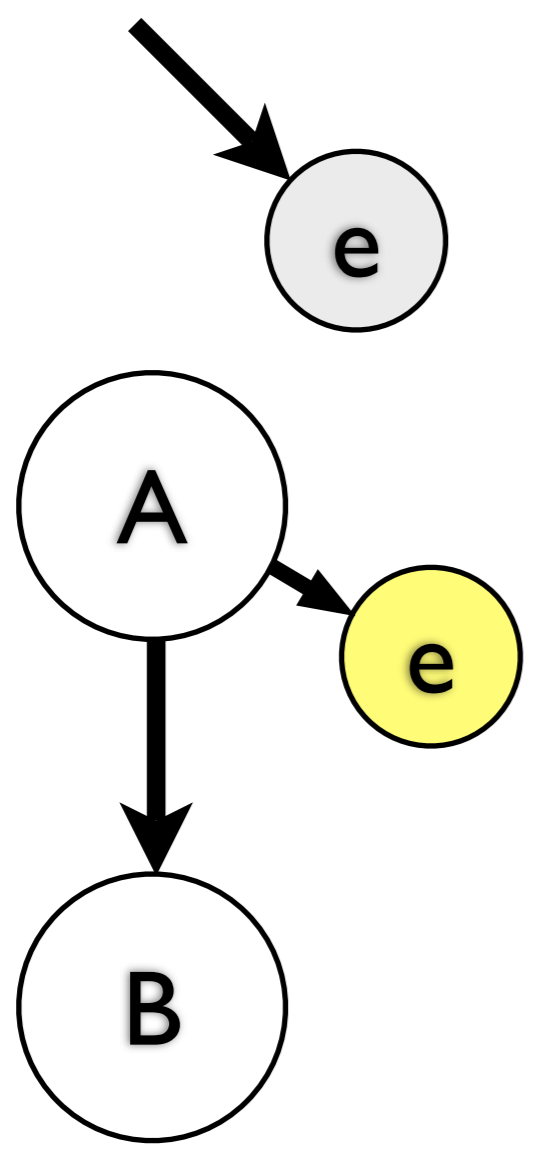


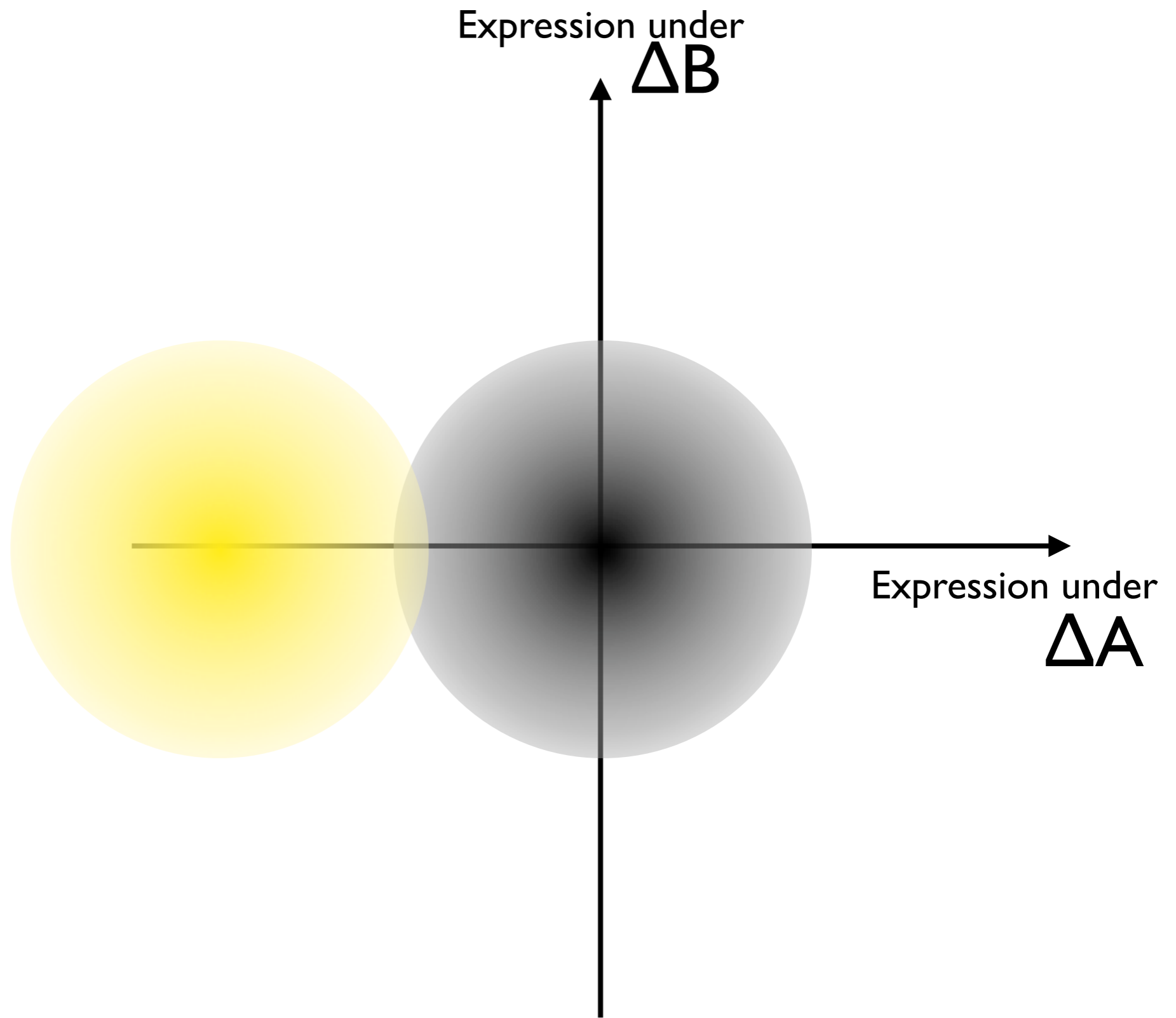
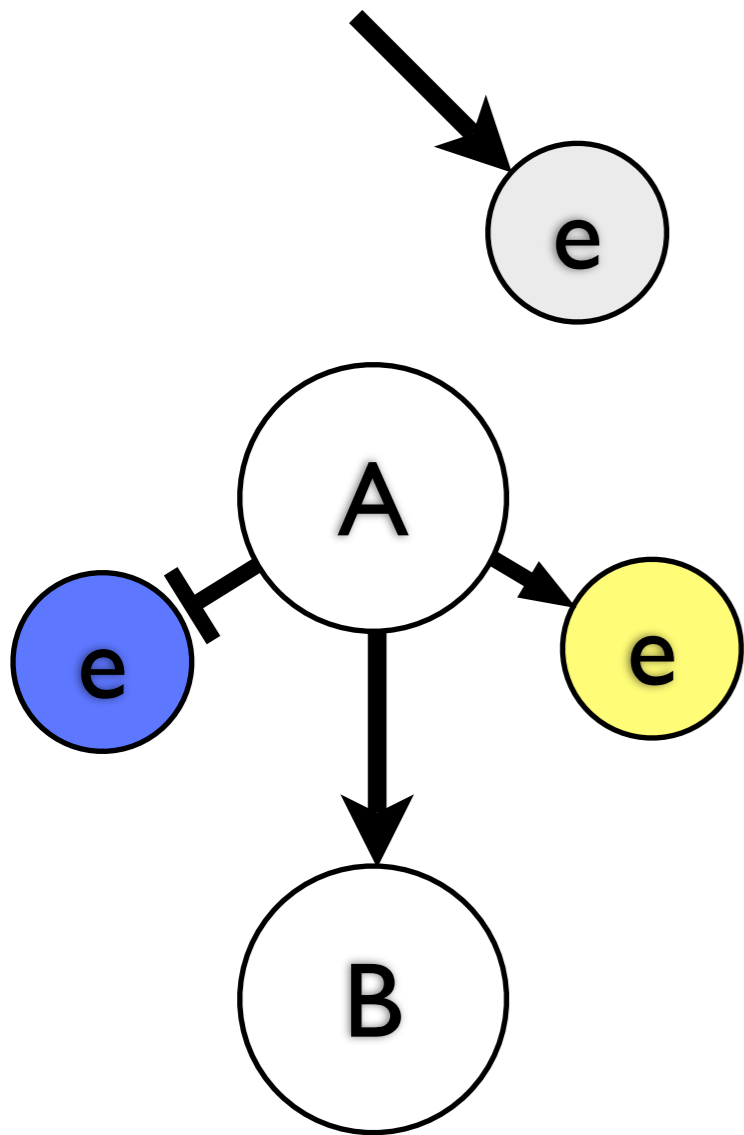




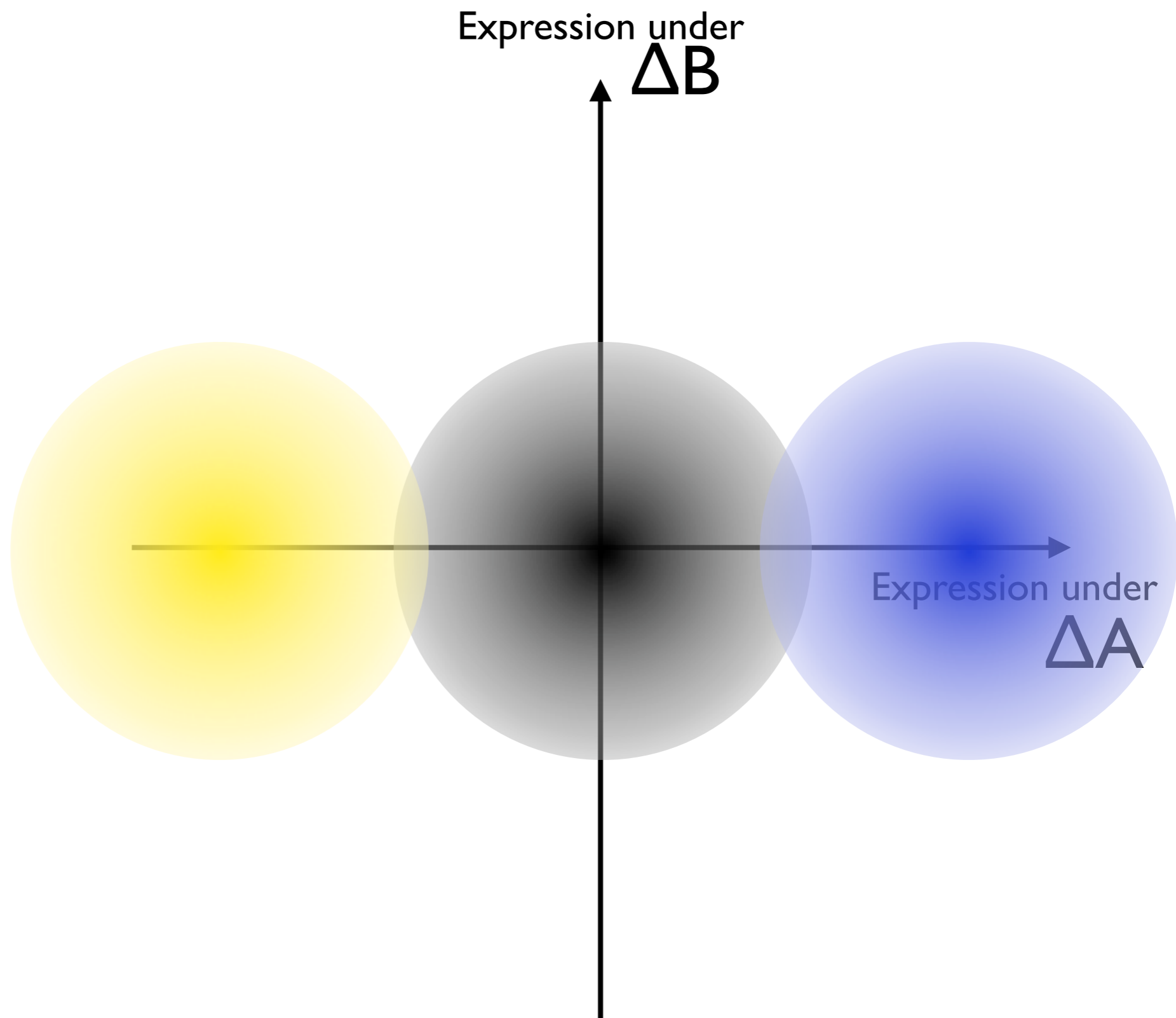
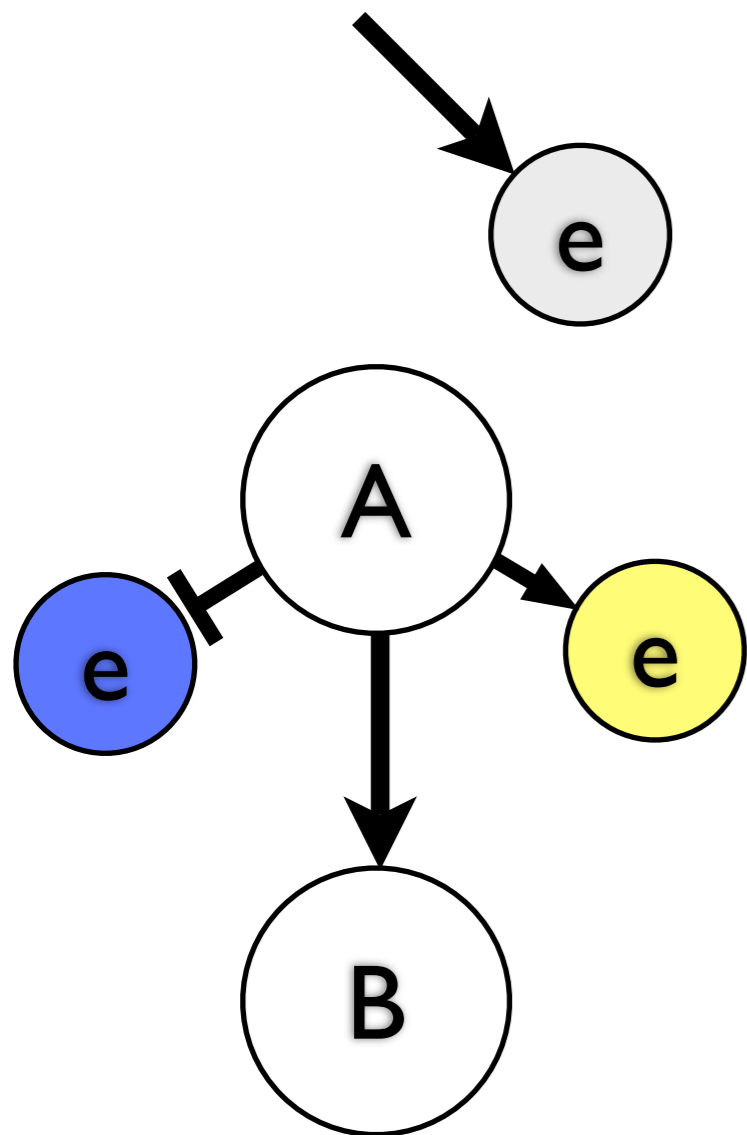


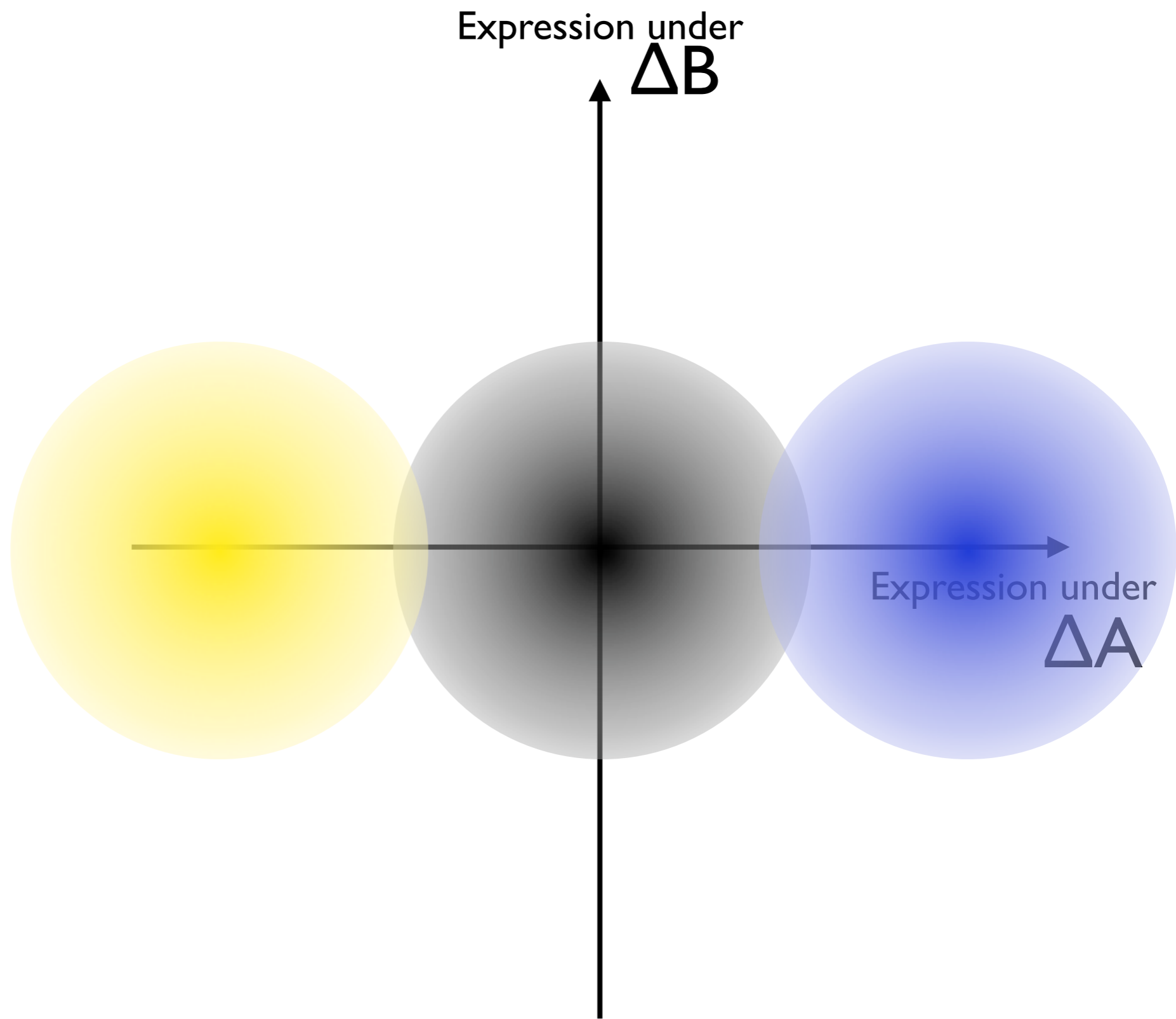
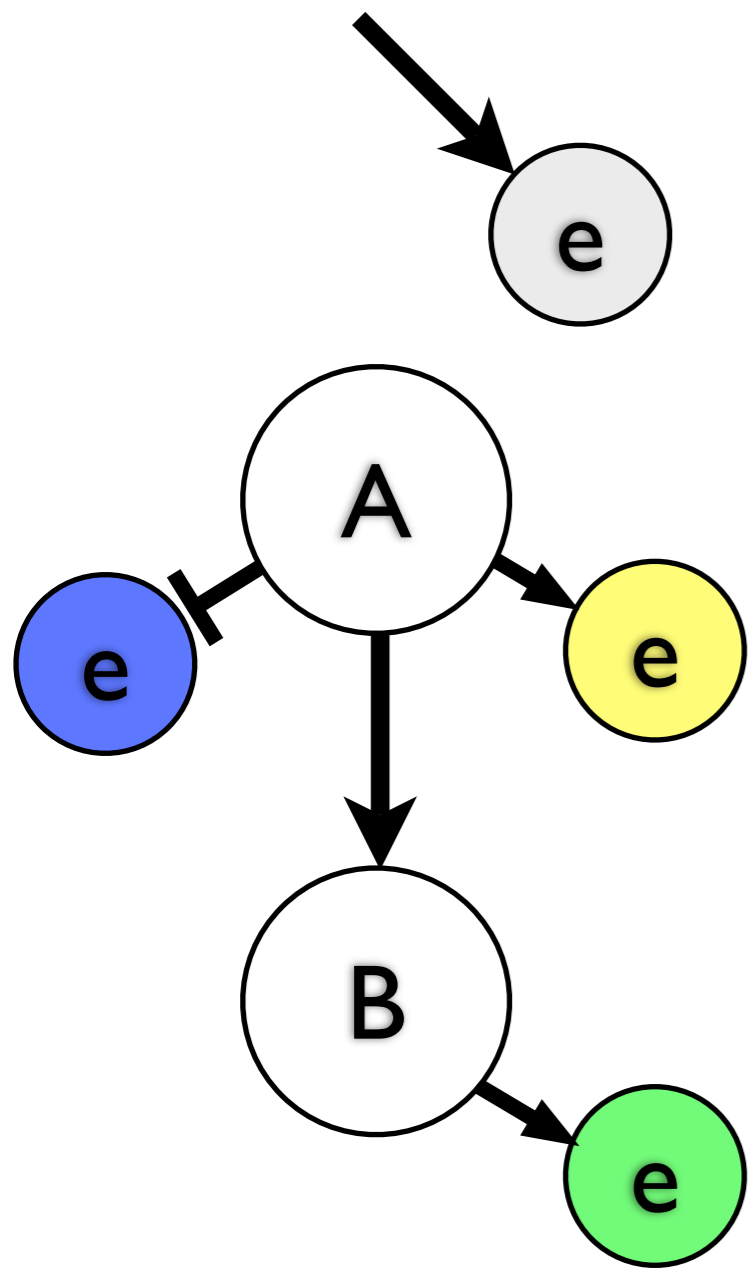


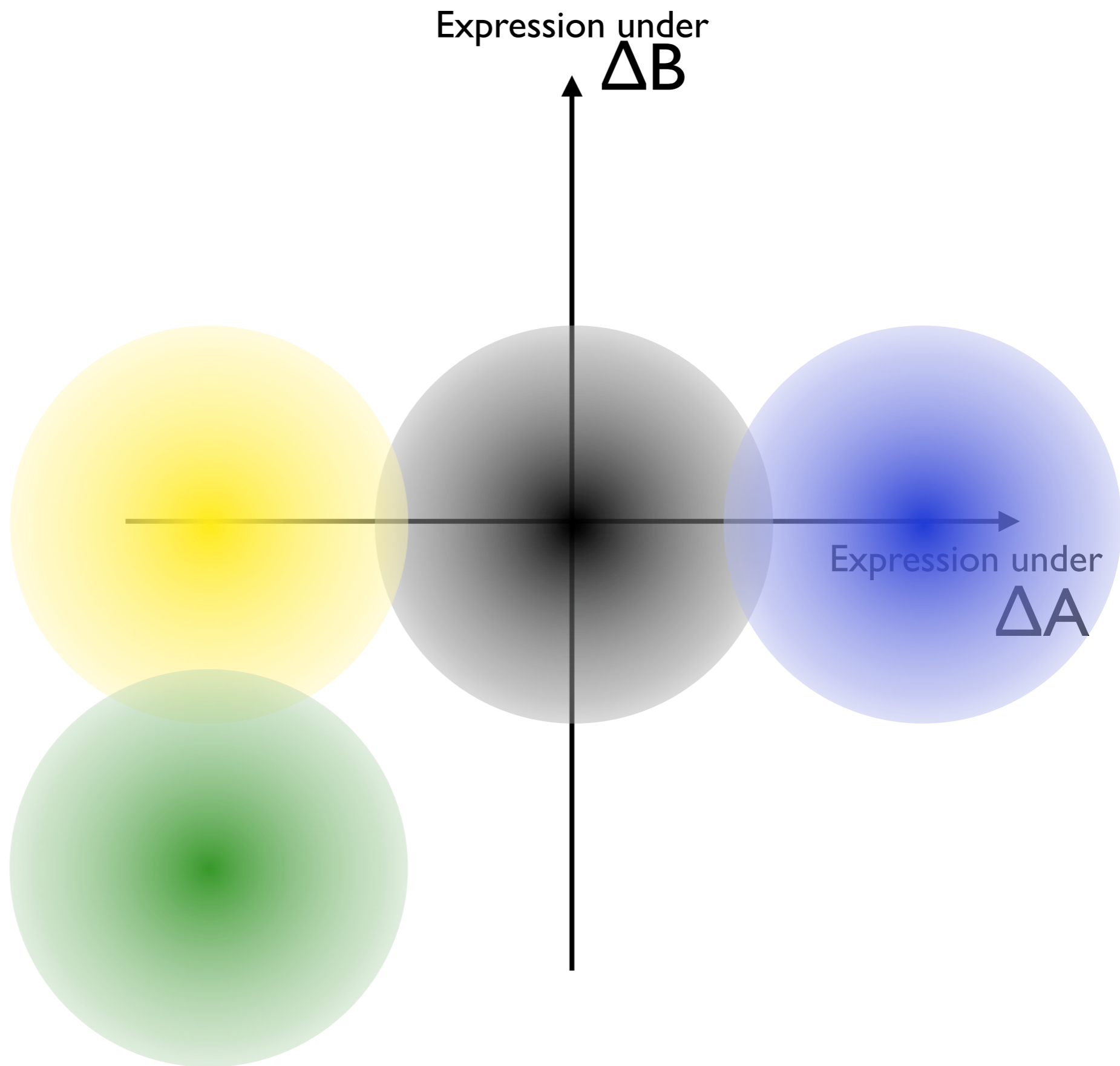
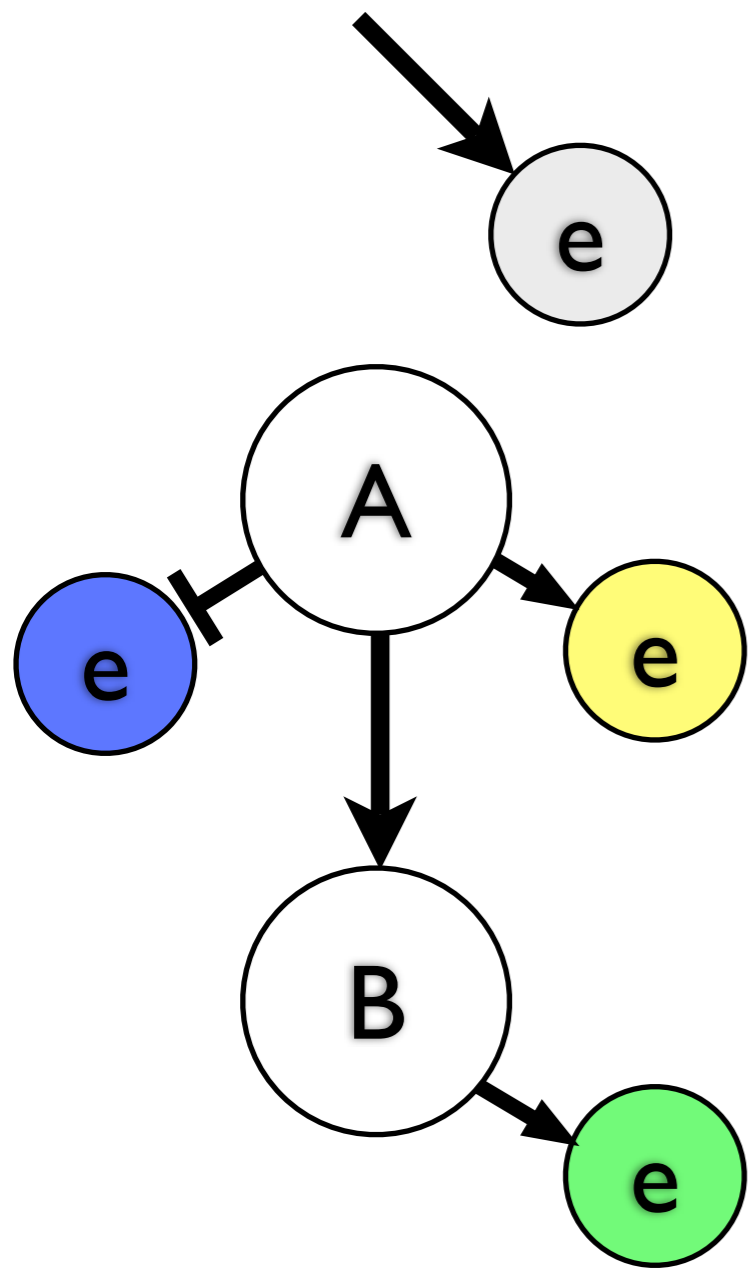


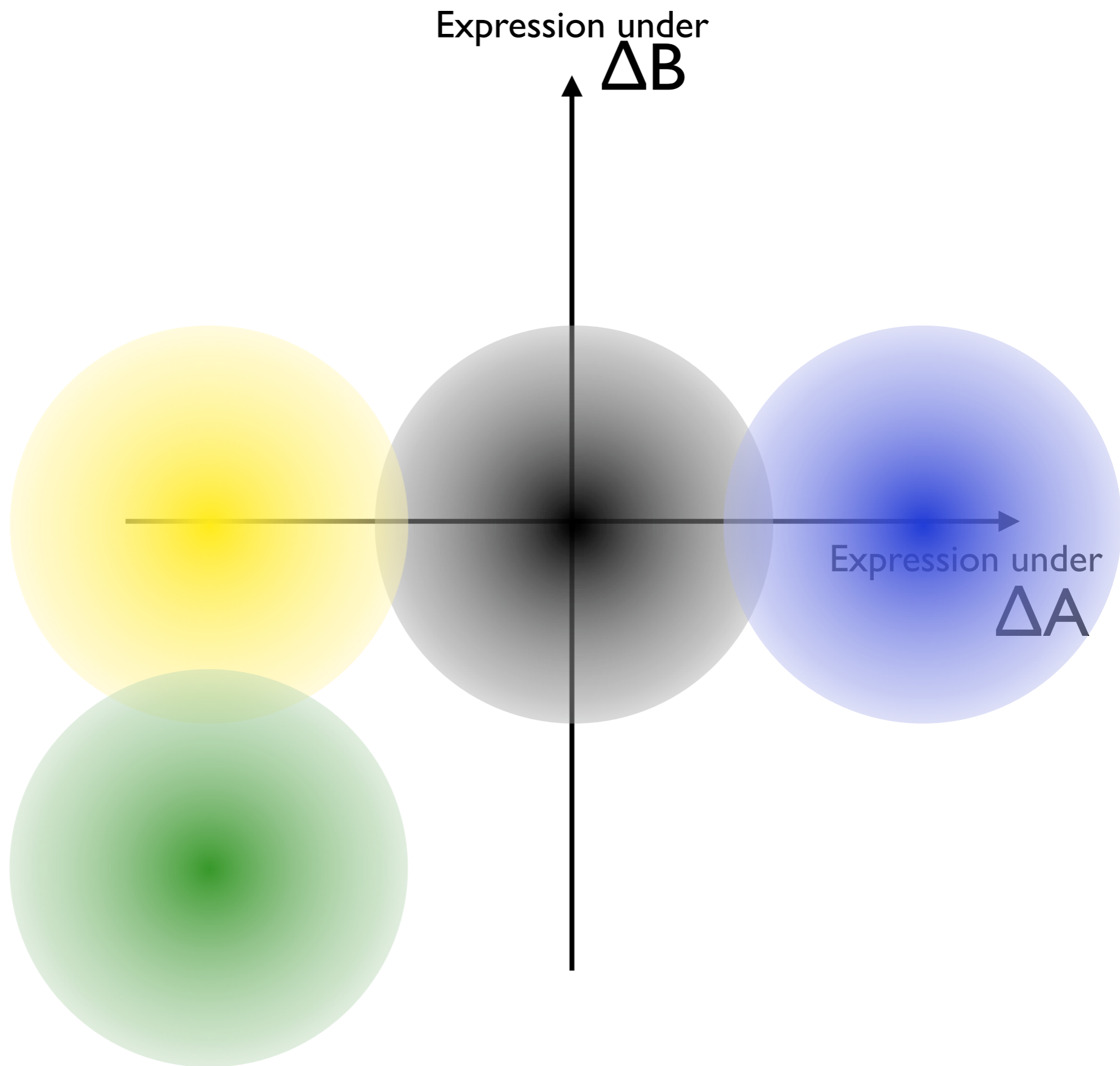
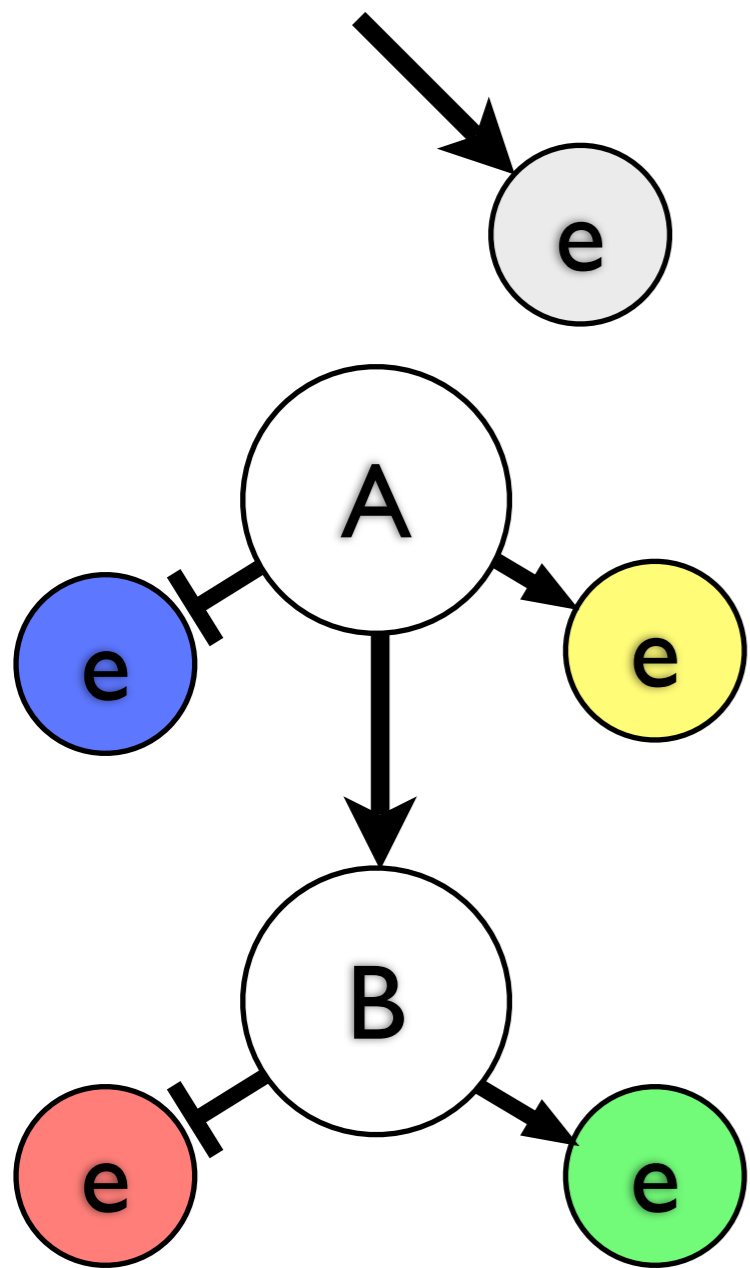


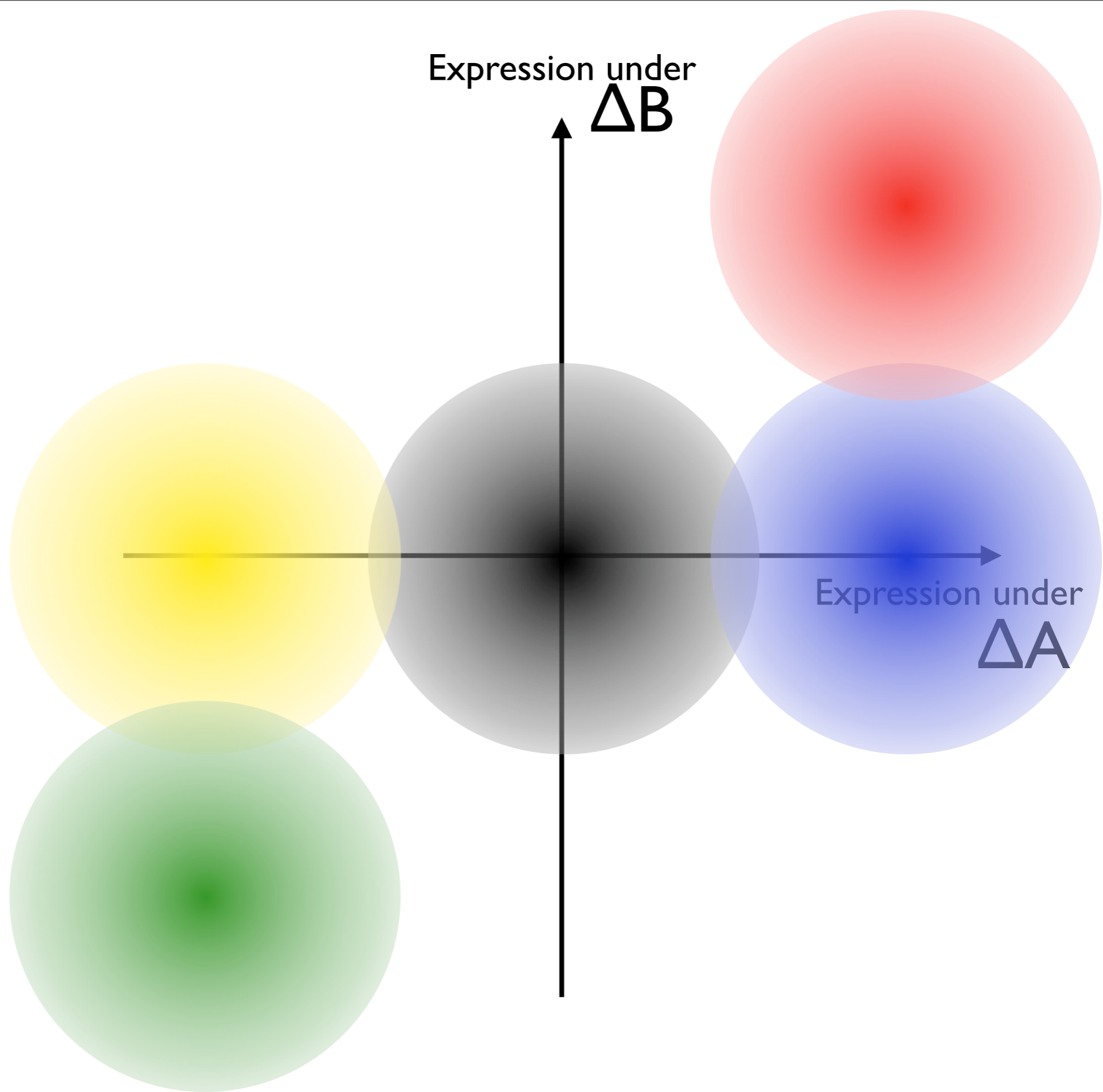
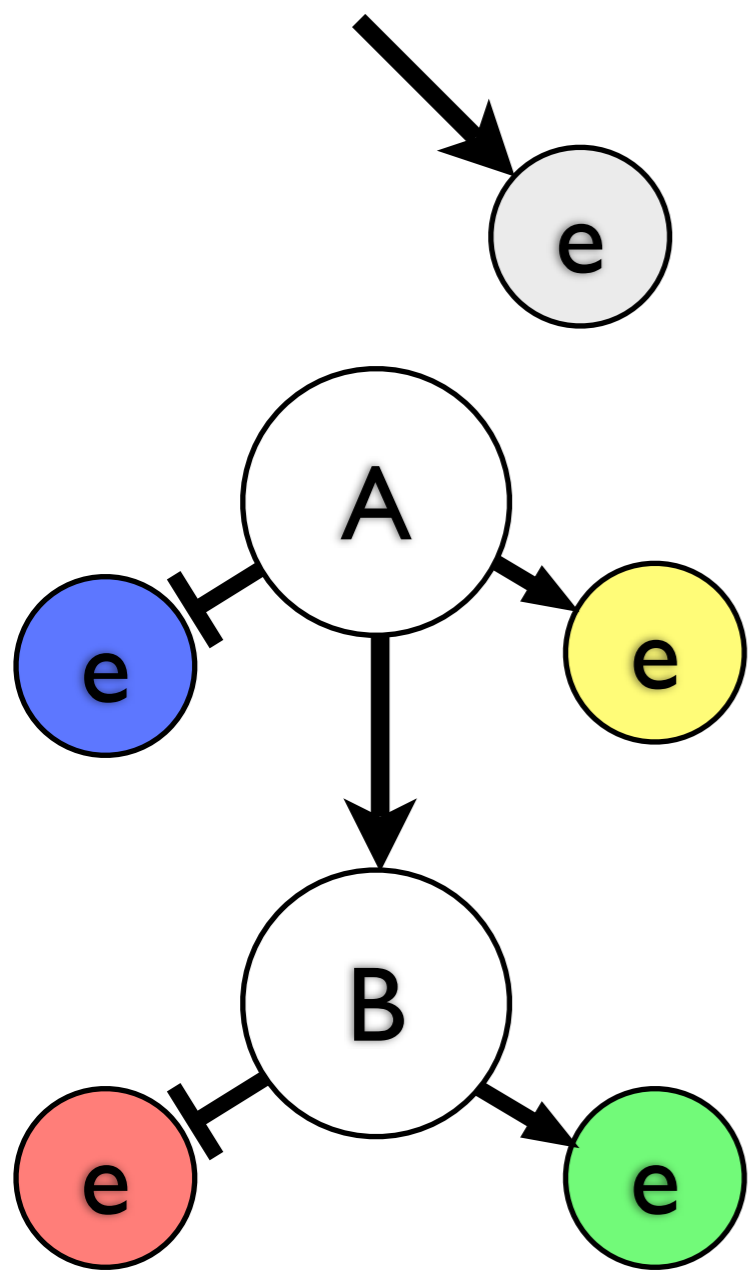




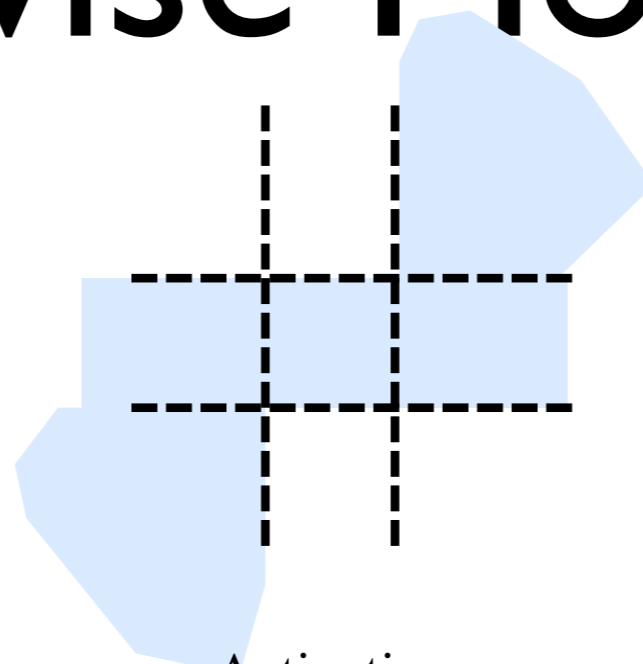
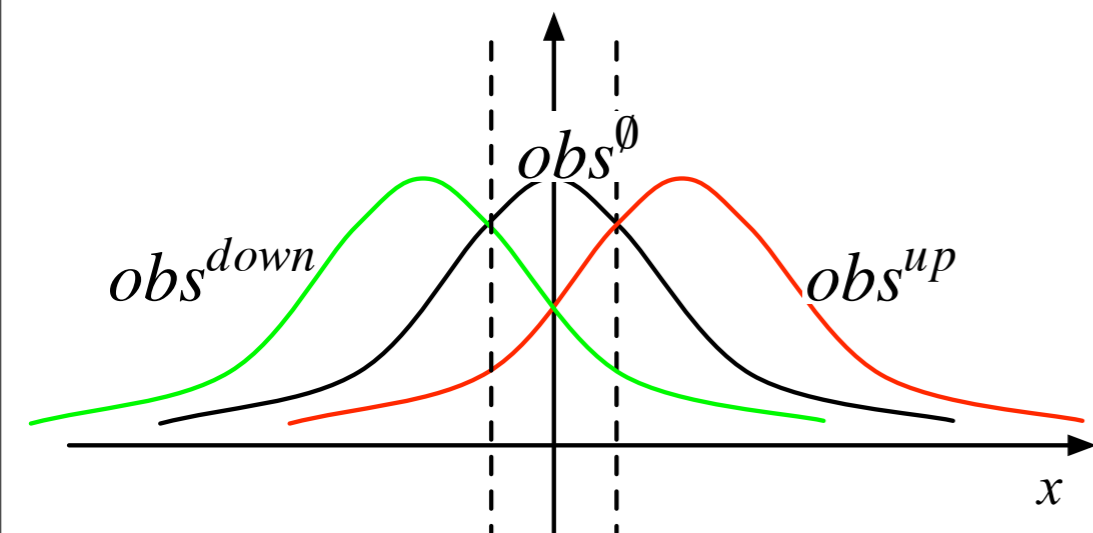




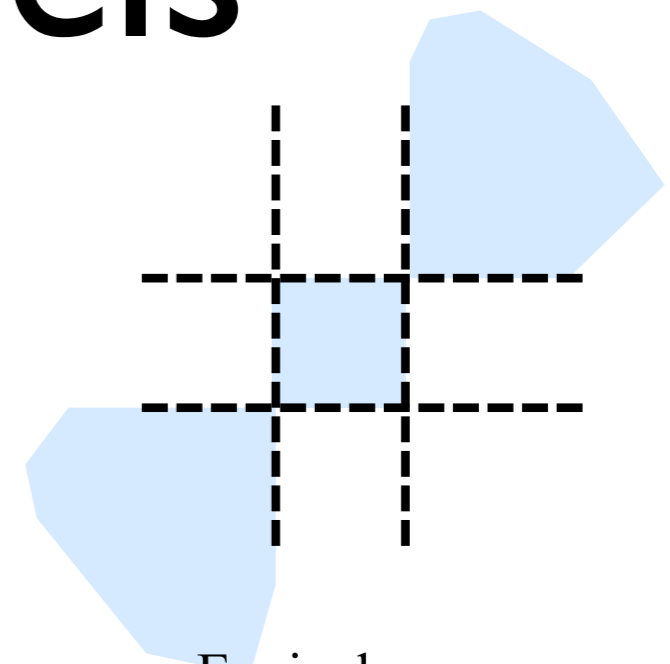




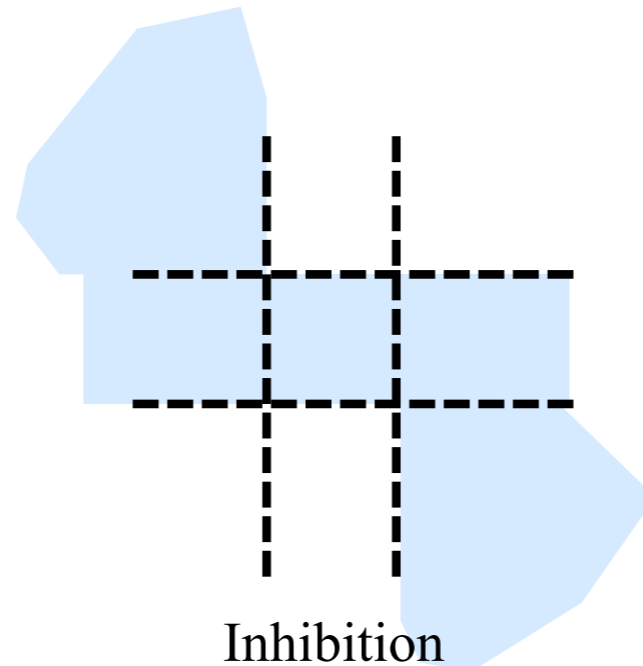
# Pairwise Models



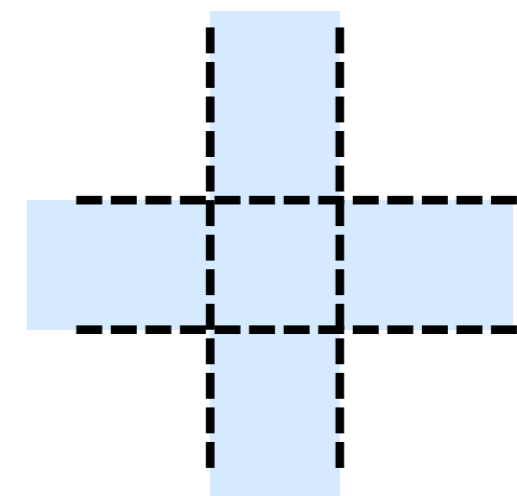
Activation  
 $A \rightarrow B$



Equivalence  
 $A \leftrightarrow B$



Inhibition  
 $A \dashv B$



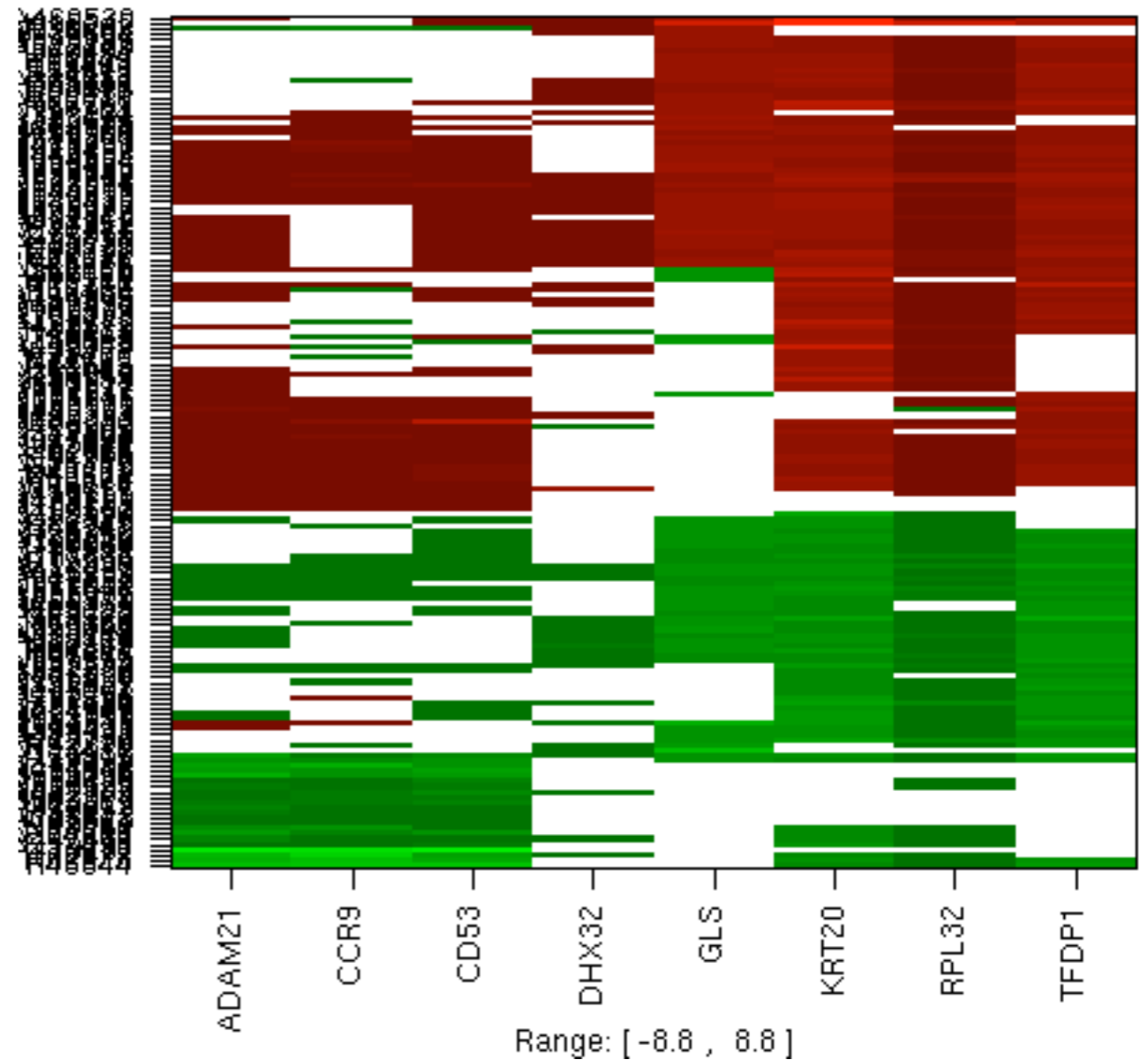
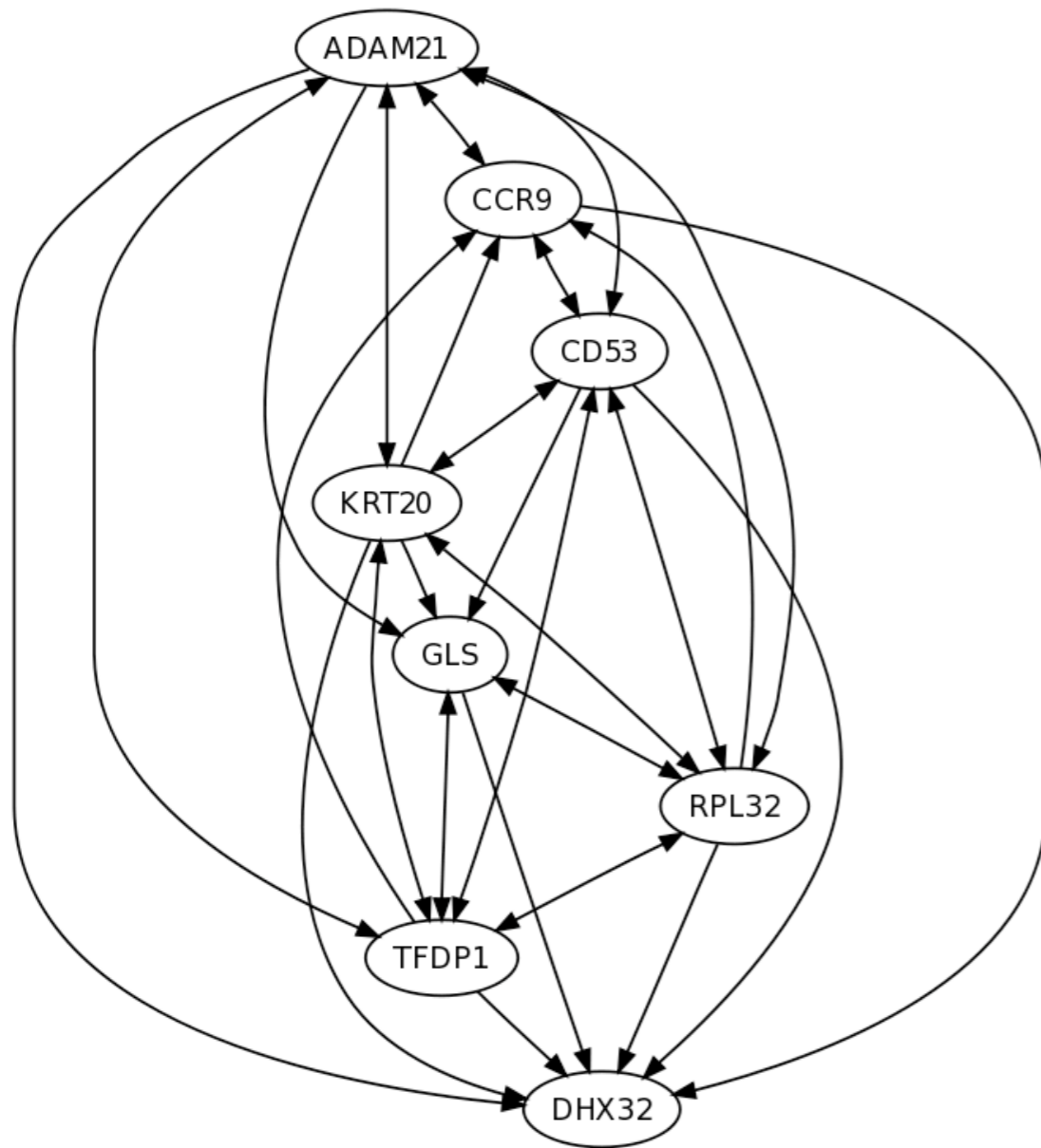
Non-interaction  
 $A \neq B$

1. Predict

2. Expand

3. Visualize

# Example network prediction



# Leave one out

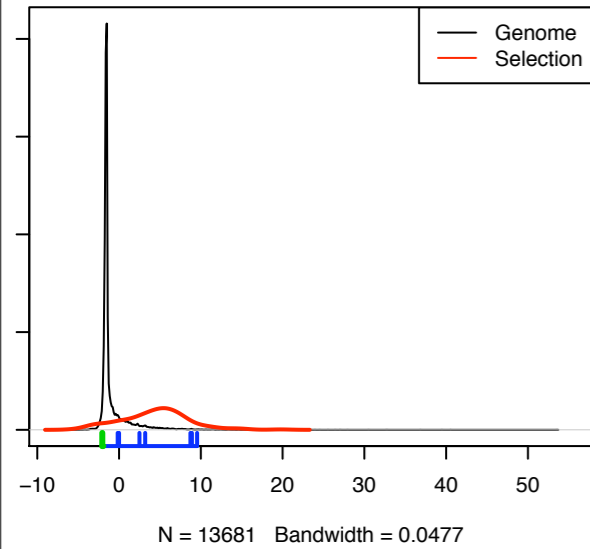
- Hold out data for one knockdown
- Predict network
- Score likelihood of each gene to be regulated by that network
- Current rank highly in list, even with missing data

	<b>ADAM21</b>	<b>CCR9</b>	<b>CD53</b>	<b>DHX32</b>	<b>GLS</b>	<b>KRT20</b>	<b>RPL32</b>	<b>TFDP1</b>
<b>ADAM21</b>	13238	13101	13231	13154	13375	13308	13203	13231
<b>CCR9</b>								
<b>CD53</b>	822	802	801	754	615	967	744	939
<b>DHX32</b>	106	112	101	53	29	20	31	38.5
<b>GLS</b>	2131	1264	1877	494	437	182	252	128.5
<b>KRT20</b>	132	156	132	114	64	102	48	46
<b>RPL32</b>	122	117	120	44	30	31	37	20.5
<b>TFDP1</b>	652	521	712	323	266	146	182	173

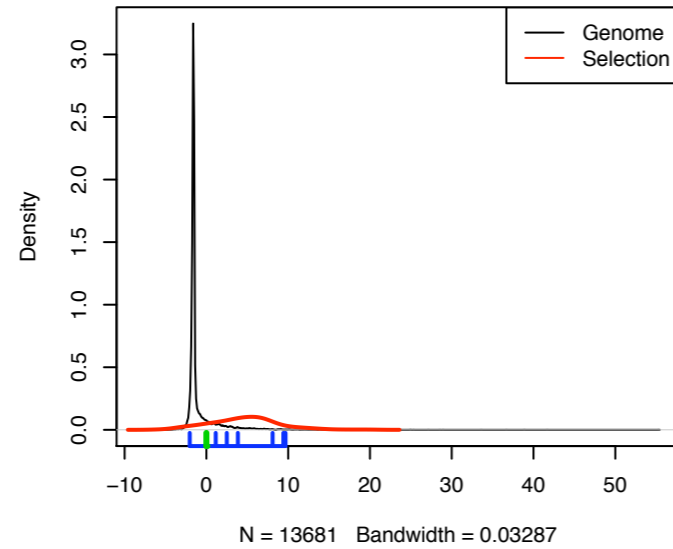


# Leave one out

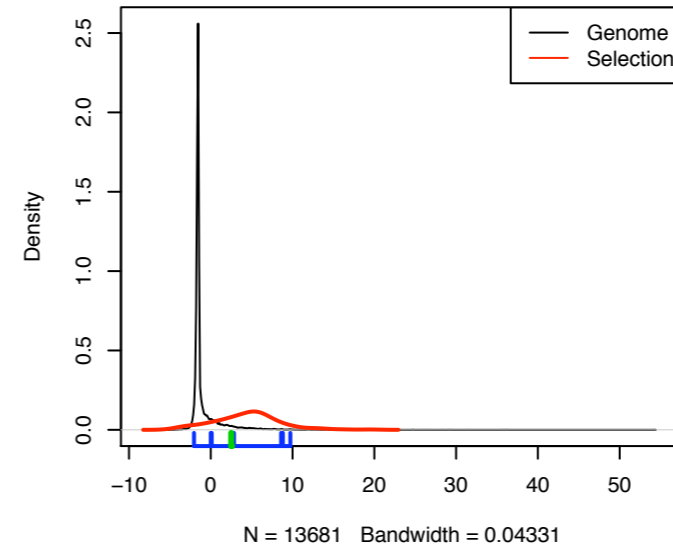
**ADAM21**



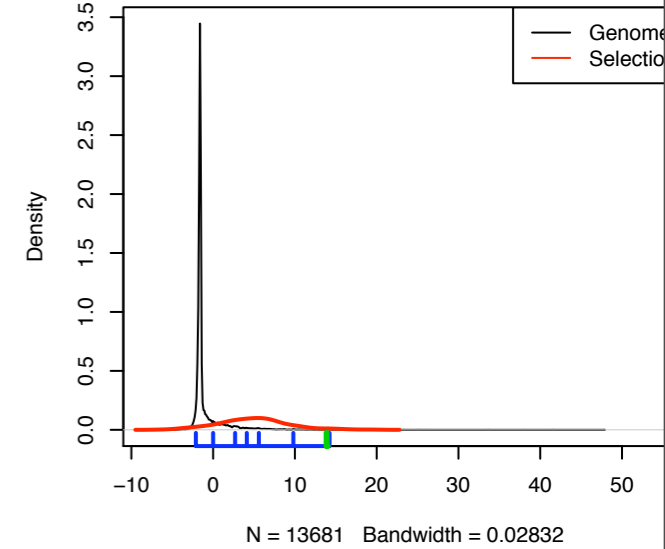
**CCR9**



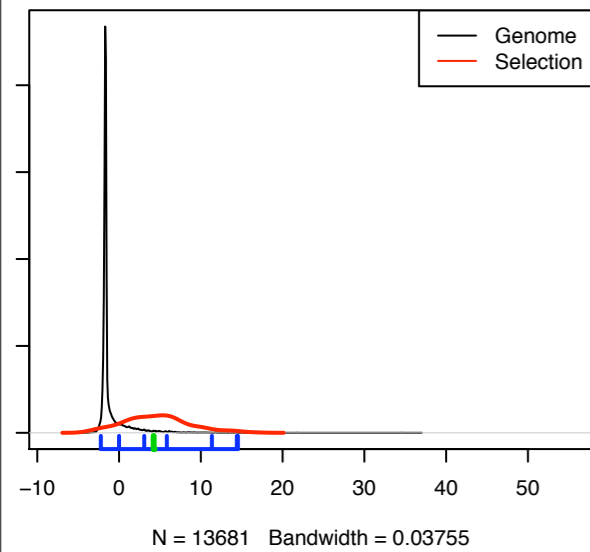
**CD53**



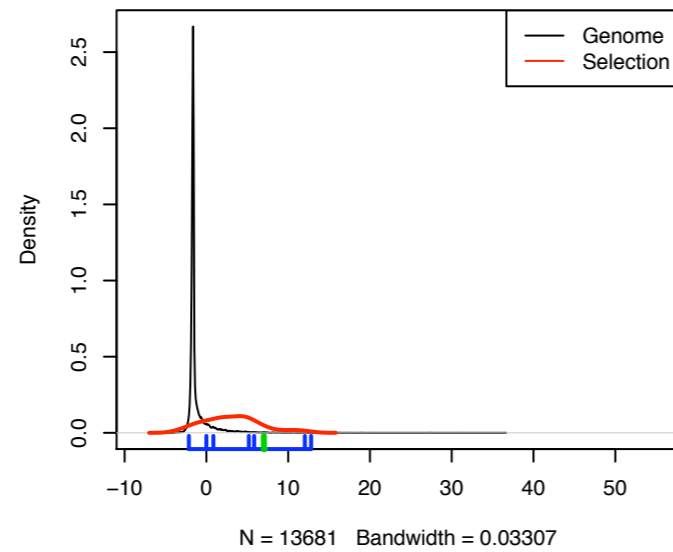
**DHX32**



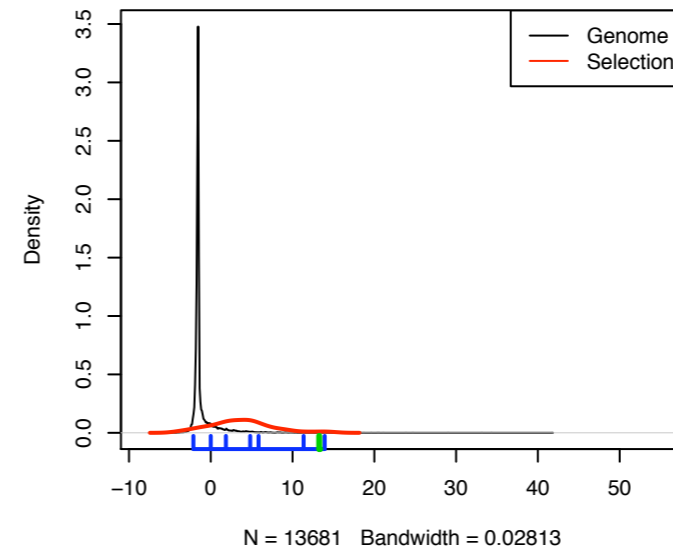
**GLS**



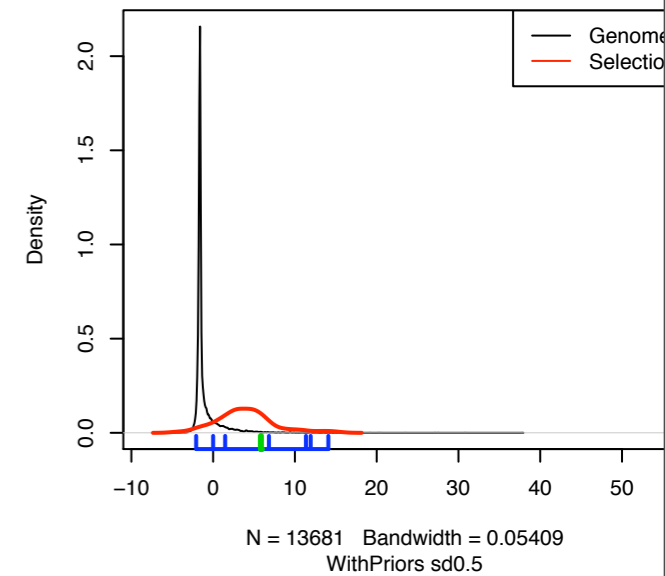
**KRT20**



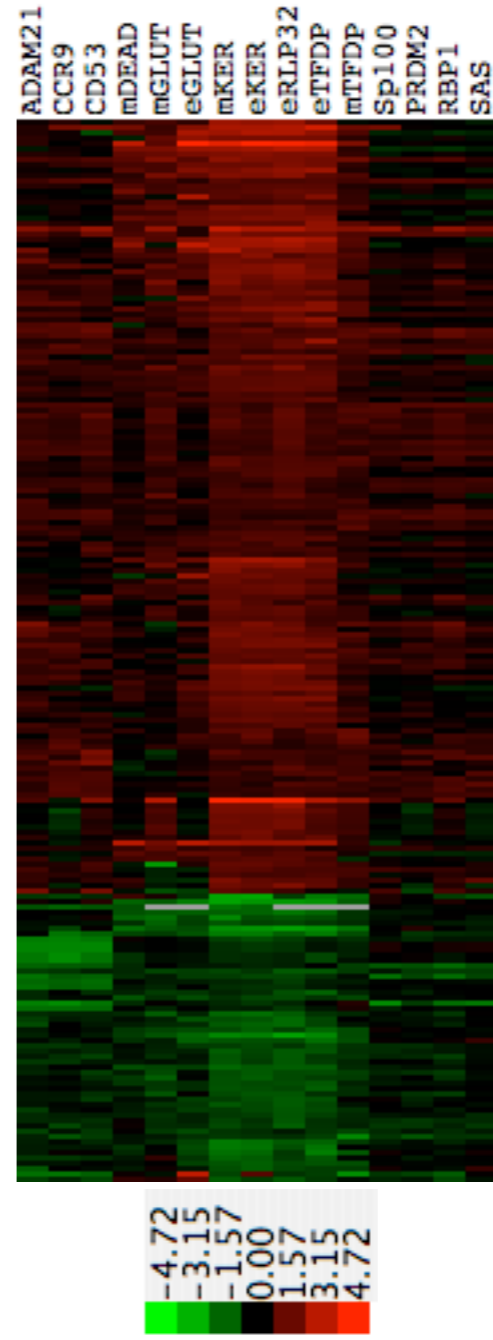
**RPL32**



**TFDP1**

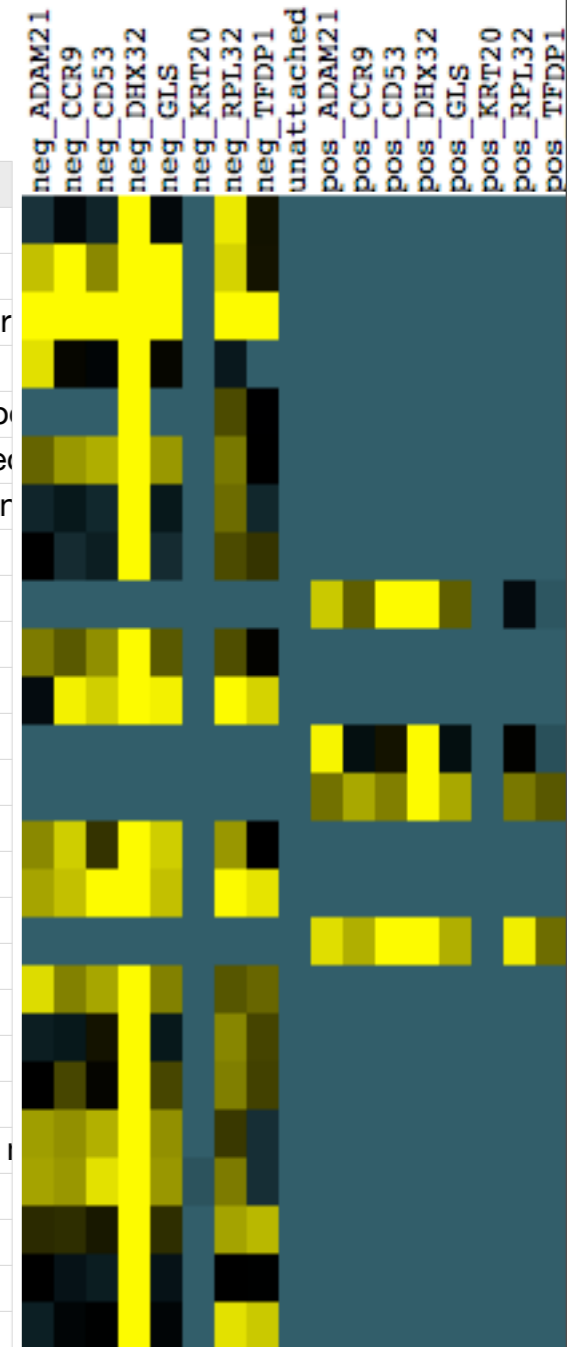


# Top 200



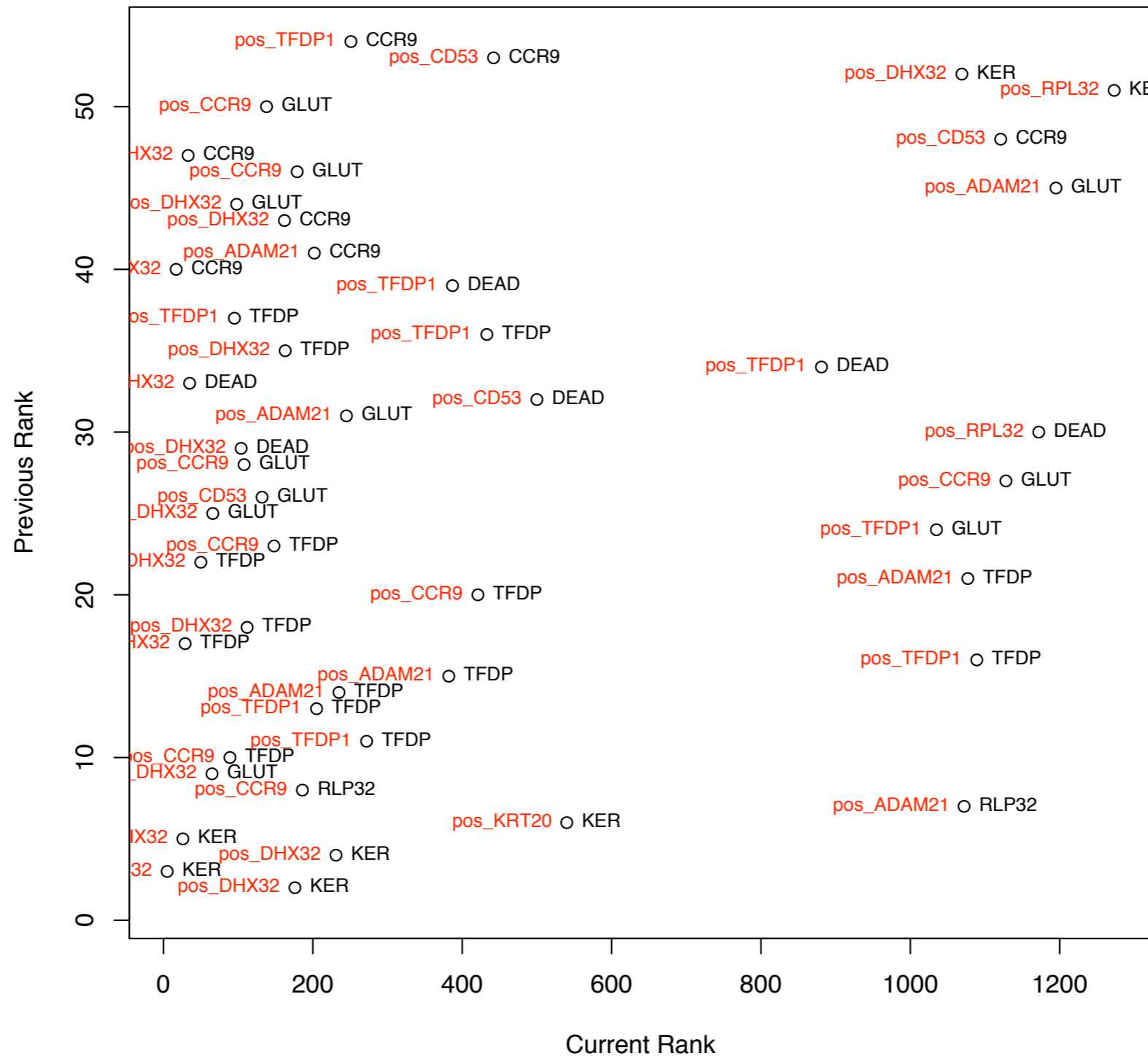
# Top Predictions

Spot	II	rank	Annotation
AA857098	54.1999	1	Hs.445827 - COL5A2 MGC105115 collagen, type V, alpha 2
N56888	41.9941	2	Hs.567242 - C3AR1 AZ3B C3AR HNFAG09 complement component 3a receptor 1
N69453	41.515	3	Hs.33756 - LOC442096 - similar to Kruppel-like factor 7 (ubiquitous); ubiquitous Kruppel-like transcription factor
AA173755	40.8286	4	Hs.13640 - ROBO1 DUTT1 FLJ21882 SAX3 roundabout, axon guidance receptor, homolog 1 (Drosophila)
AI139498	31.3696	5	Hs.387207 - SGCD 35DAG CMD1L DAGD MGC22567 SG-delta SGD sarcoglycan, delta (35kDa dystrophin-asso
AA634379	28.8688	6	Hs.510697 - LOC441708 - similar to CDC42-binding protein kinase alpha isoform A; ser-thr protein kinase relate
R28649	28.5032	7	Hs.532363 - HIPK1 KIAA0630 MGC26642 MGC33446 MGC33548 Myak Nbak2 homeodomain interacting proteir
AI022231	28.3755	8	Hs.292925 - KIAA1212 APE DKFZp686D0630 GIV GRDN HkRP1 KIAA1212
AA609282	26.8037	9	Hs.531575 - FLJ40172 - hypothetical protein FLJ40172
AA115300	24.5383	10	Hs.133421 - LIFR SJS2 STWS SWS leukemia inhibitory factor receptor
R56916	24.4632	11	Hs.22907 - LOC283824 - hypothetical protein LOC283824
AA459401	23.6942	12	Hs.275464 - KLK10 NES1 PRSSL1 kallikrein 10
H79241	23.1131	13	Hs.16230 - TTC22 FLJ20619 tetratricopeptide repeat domain 22
AA999990	22.3184	14	Hs.478553 - ACA4 ACA4 snoRNA ACA4 small nucleolar RNA
AA775447	22.2445	15	Hs.212838 - LOC144571 - hypothetical protein LOC144571
W95595	21.9444	16	Hs.556031 - PSORS1C1 C6orf16 SEEK1 psoriasis susceptibility 1 candidate 1
AA598794	21.697	17	Hs.410037 - CTGF CCN2 IGFBP8 MGC102839 NOV2 connective tissue growth factor
AA682293	20.7239	18	Hs.325404 - PAH PKU PKU1 phenylalanine hydroxylase
R06601	20.3125	19	Hs.188518 - MT1M MGC118949 MGC40498 MT1 MT1K metallothionein 1M
AA025380	20.1632	20	Hs.524134 - GATA3 HDR MGC2346 MGC5199 MGC5445 GATA binding protein 3
H20809	20.1018	21	Hs.21213 - MYO5A GS1 MYH12 MYO5 MYOXIN MYR12 myosin V myosin Va myosin VA (heavy polypeptide 12, 1
AI018242	19.7189	22	Hs.278815 - OTUB2 C14orf137 FLJ21916 MGC3102 OTB2 OTU2 OTU domain, ubiquitin aldehyde binding 2
AA778089	19.443	23	Hs.163244 - LRRN1 KIAA1497 NLRR-1 leucine rich repeat neuronal 1
AA233079	18.8072	24	Hs.401316 - IGFBP1 AFBP IBP1 IGF-BP25 PP12 hIGFBP-1 insulin-like growth factor binding protein 1
AA927187	18.6785	25	Hs.493512 - RAB27A GS2 HsT18676 MGC117246 RAB27 RAM RAB27A, member RAS oncogene family



# Pairwise vs. Linear rank

Previous and current rank.



# Previous Predictions

- Scored the likelihood of each linear model of genes
- Averaged all models to assign a probability to each link
- Sent predictions off to collaborator

GB#	Attachment	Annotation
AA449107	0.8657	SEC24D KIAA0755 SEC24 related gene family, member D ( <i>S. cerevisiae</i> )
AI016190	0.8657	EIF2AK2 EIF2AK1 MGC126524 PKR PRKR eukaryotic translation initiation factor 2-alpha kinase 2
H02328	0.8495	none
W92257	0.8495	FAM43A FLJ90022 family with sequence similarity 43, member A
H94236	0.8495	EST (may contain Alu)
AA292074	0.8495	UBE2L6 MGC40331 RIG-B UBCH8 ubiquitin-conjugating enzyme E2L 6
AA461108	0.7244	none
AA776810	0.7244	ZNF610 DKFZp547A1010 FLJ36040 MGC102679 zinc finger protein 610
AA055968	0.7121	SNCG BCSG1 SR synuclein, gamma (breast cancer-specific protein 1)
H77826	0.7048	none
AA707217	0.7048	NARG1 Ga19 NAT1 NATH TBDN100 NMDA receptor regulated 1
AA676636	0.7048	TRIM33 PTC7 RFG7 TF1G TIF1G TIF1GAMMA TIFGAMMA tripartite motif-containing 33
H87940	0.7048	C6orf168 MGC2817 dJ273F20 chromosome 6 open reading frame 168
AA707084	0.7048	LOC123688 - similar to RIKEN cDNA C630028N24 gene
AA625789	0.7048	KIAA0652 - KIAA0652
AA256507	0.7048	ATXN1 ATX1 D6S504E SCA1 ataxin 1
T71648	0.6947	none
AA776749	0.6947	C1orf114 FLJ25846 RP1-206D15.2 chromosome 1 open reading frame 114
AA449832	0.6947	AP1S2 DC22 MGC:1902 SIGMA1B adaptor-related protein complex 1, sigma 2 subunit
AA702768	0.6947	CAPN12 MGC20576 calpain 12
AI005114	0.6947	TBC1D22A C22orf4 HSC79E021 TBC1 domain family, member 22A
AA707686	0.6947	none
AA425401	0.6947	STK24 MST-3 MST3 MST3B STK3 serine/threonine kinase 24 (STE20 homolog, yeast)
R20648	0.6844	none
AA719156	0.6844	TSP50 - testes-specific protease 50
AA069414	0.6844	GFAP FLJ45472 glial fibrillary acidic protein
R08816	0.6844	ACP5 MGC117378 TRAP acid phosphatase 5, tartrate resistant
W23757	0.6844	KRT13 CK13 K13 MGC3781 keratin 13
AI005275	0.6631	ADAM9 KIAA0021 MCMP MDC9 Mitng ADAM metalloproteinase domain 9 (meltrin gamma)
AA490256	0.6612	GNAI3 87U6 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
AA404276	0.6226	none
AA872296	0.6067	EFTUD2 KIAA0031 Snrp116 U5-116KD elongation factor Tu GTP binding domain containing 2
AA099748	0.5739	EST
W44340	0.5739	ACO2 MGC20605 MGC33908 aconitase aconitase 2, mitochondrial
AA968436	0.564	none
H92235	0.564	SCRN3 FLJ23142 SES3 secernin 3
AA427528	0.564	ZNF350 ZBRK1 ZFQR zinc finger protein 350
AA456007	0.5597	RBM5 G15 H37 LUCA15 RMB5 RNA binding motif protein 5
T97992	0.5558	none
N63366	0.4409	CHORDC1 CHP1 cysteine and histidine-rich domain (CHORD)-containing 1
R06862	0.4399	none
H19227	0.4399	ST3GAL6 SIAT10 ST3GALVI ST3 beta-galactoside alpha-2,3-sialyltransferase 6
AI016360	0.4373	TCTEX1D1 FLJ40873 MGC125768 RP11-266I14.2 Tctex1 domain containing 1
H75599	0.437	SGK SGK1 serum/glucocorticoid regulated kinase
W96273	0.437	RAB3IP ELI14660 ELI122548 MGC71495 RABIN3 RAB3A interacting protein (rabin3)

# ctions

Essential for invasiveness

Non-essential for invasiveness

# Problem: flipped sign

Previous and current rank

