MMPC/MMHC Further Research

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Note to the reader

I apologize for having more than one slide, if I were there in person to deliver this presentation the presentation would be slimmed down. The slides are meant to be brief, with the reader spending no more than a dozen seconds on each slide.

Absolute Difference Correlation Algorithm

1. Start with a dataset, treating each feature as an “event”, and each row as an “experiment”. Our goal is to figure out if “events” are related by running successive “experiments”. This lets us see if changing one factor causes another to change

RAW DATA				
A	B	C	D	E
14	8	6	2	17
1	19	2	8	12
3	11	11	13	7
2	17	16	6	16
14	13	17	9	2

Absolute Difference Correlation Algorithm

2. From experiment to experiment, keep track of if each event increases, or decreases.

OBSERVE RELATIONS				
A	B	C	D	E
14	8	6	2	17
dec	inc	dec	inc	dec
1	19	2	8	12
inc	dec	inc	inc	dec
3	11	11	13	7
dec	inc	inc	dec	inc
2	17	16	6	16
inc	dec	inc	inc	dec
14	13	17	9	2

On a computer, you could improve this by selecting a single feature, looking at the change in that feature, and calculating the absolute difference between the change in that feature and other features. Select another feature, and repeat, like MMPC.

Absolute Difference Correlation Algorithm

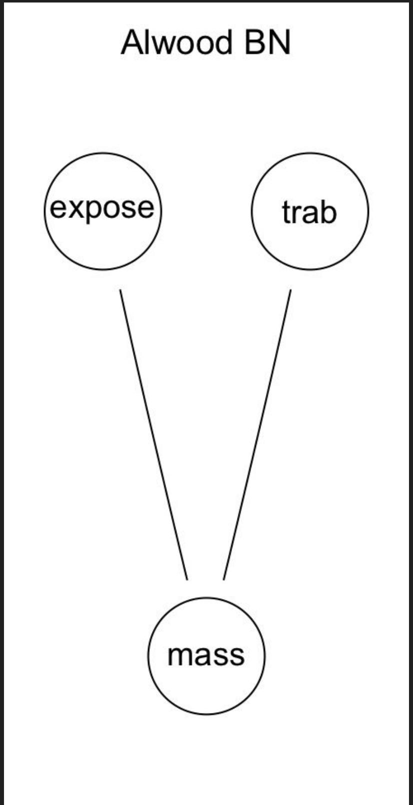
3. Set a criteria, and gather results. If events change together, they are likely correlated, and therefore there is likely a causal connection. Here a correlation matrix is used to visualize these relations

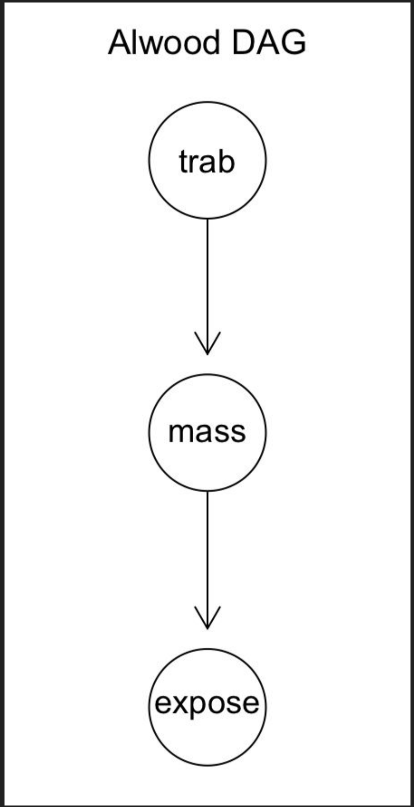
CORRELATION MATRIX					
	A	B	C	D	E
A	NA				
B	0/4	NA			
C	3/4	1/4	NA		
D	3/4	1/4	2/4	NA	
E	1/4	3/4	2/4	0/4	NA

CORRELATION RESULTS	
Criteria	+75% -> directly correlated, 0% –> inversely corelated
Direct	a change in A is directly correlated to a change in C and D, a change in B is directly correlated to a change in E
Indirect	a change in A is inversely correlated to a change in B, a change in D is inversely correlated to a change in E

MMPC/MMHC Findings

Alwood



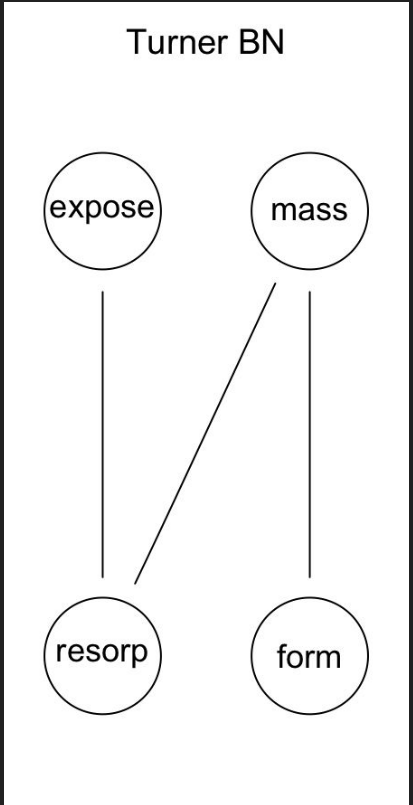


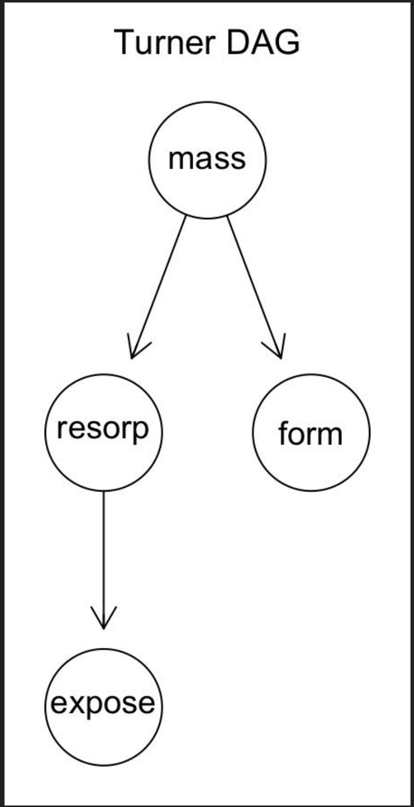

```
> cor(alwood, method="pearson")
           expose       trab       mass
expose  1.0000000  0.2597277 -0.4811904
trab    0.2597277  1.0000000 -0.7659131
mass   -0.4811904 -0.7659131  1.0000000
```

NOTE: In each dataset, all correlation tests by MMPC, MMHC, and cor() function are Pearson’s correlation test

QUESTION: when constructing a DAG or BN Skeleton using a correlation test, how is the directionality (inverse vs direct relation) used?

Turner

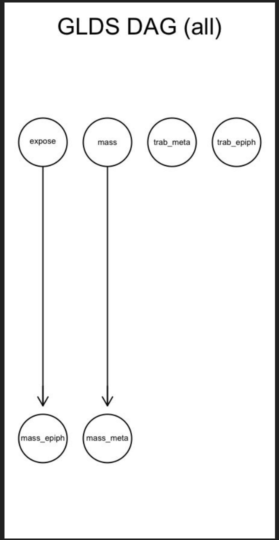


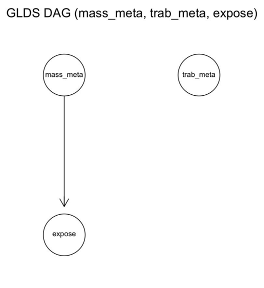


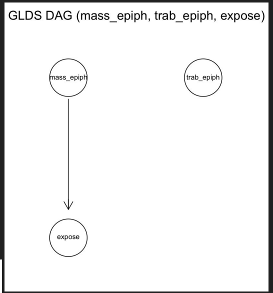
	expose	mass	resorp	form
expose	1.0000000	-0.6281854	-0.7246798	-0.4220525
mass	-0.6281854	1.0000000	0.7807571	0.5569316
resorp	-0.7246798	0.7807571	1.0000000	0.2949424
form	-0.4220525	0.5569316	0.2949424	1.0000000

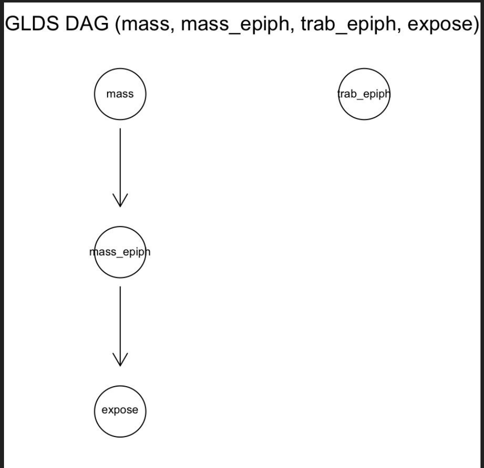
GLDS

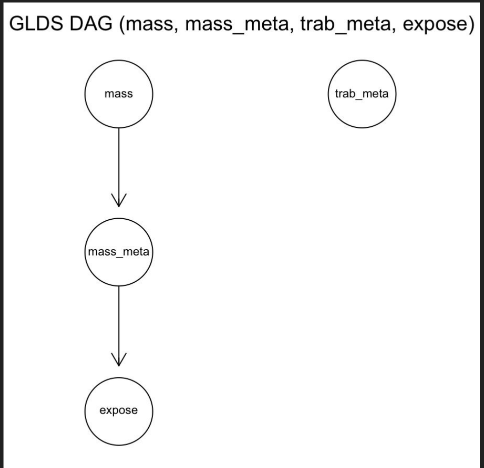
NOTE: All BN Skeletons were identical to DAGs, just missing directionality

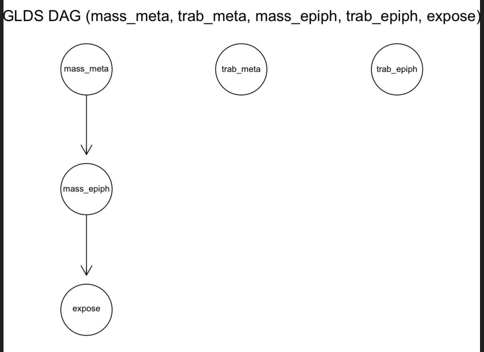






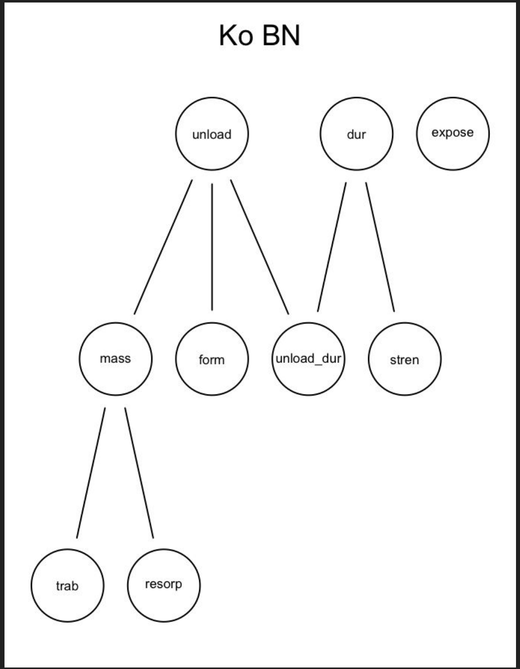


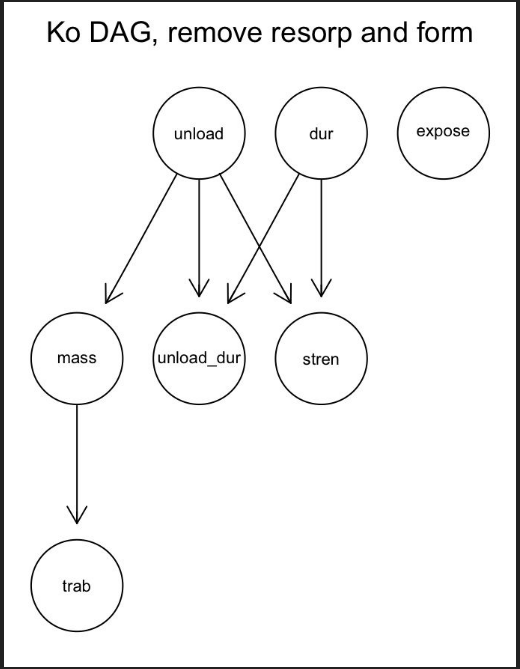




	expose	mass	mass_meta	mass_epiph	trab_meta	trab_epiph
expose	1.0000000	-0.5627702	-0.6748303	-0.9083700	-0.4849928	0.7994088
mass	-0.5627702	1.0000000	0.7504137	0.7333526	0.3055978	-0.5823740
mass_meta	-0.6748303	0.7504137	1.0000000	0.7517707	0.4375642	-0.5987569
mass_epiph	-0.9083700	0.7333526	0.7517707	1.0000000	0.4540335	-0.8119884
trab_meta	-0.4849928	0.3055978	0.4375642	0.4540335	1.0000000	-0.4988618
trab_epiph	0.7994088	-0.5823740	-0.5987569	-0.8119884	-0.4988618	1.0000000

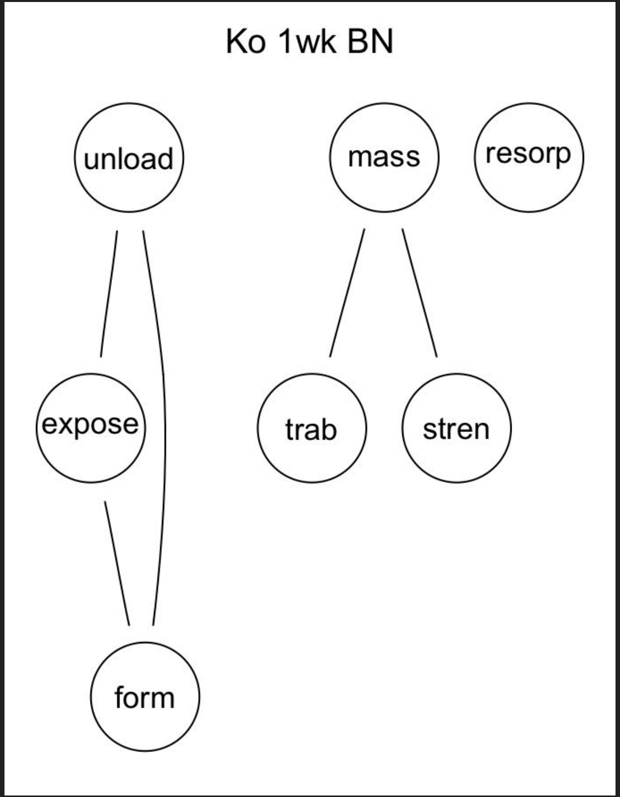
Ko (all)

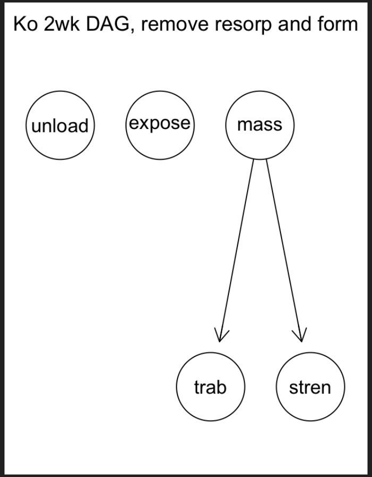


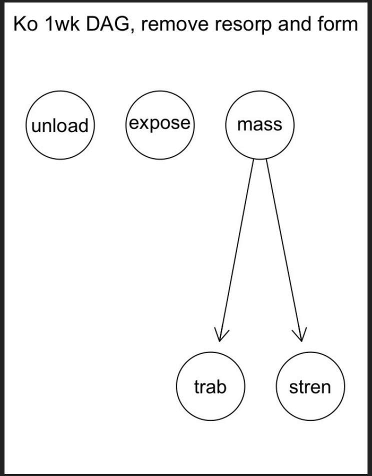


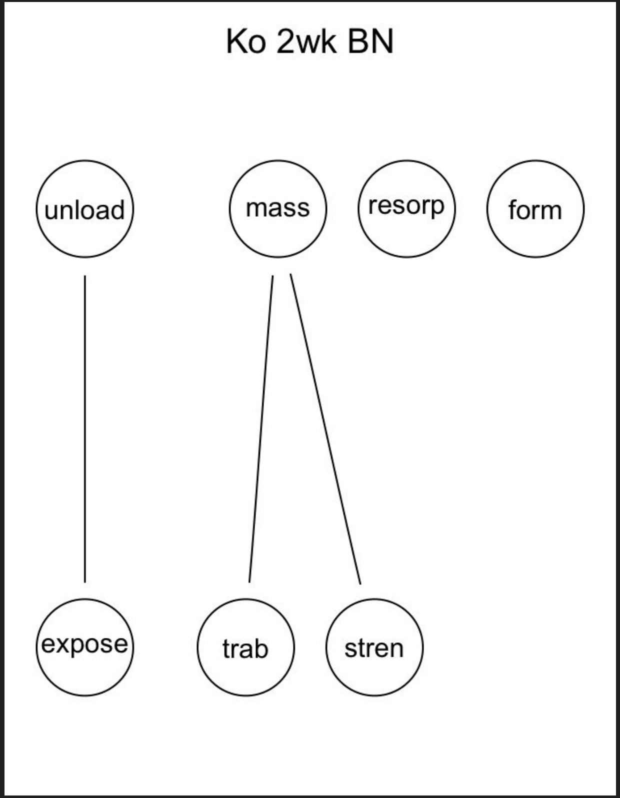
	unload	dur	expose	mass	trab	stren	resorp	form	unload_dur
unload	1.00000000	-0.01665351	0.73002360	-0.40703663	-0.2648031	-0.26416620	NA	NA	0.73002360
dur	-0.01665351	1.00000000	0.53252615	-0.05869164	-0.1022392	0.19173187	NA	NA	0.53252615
expose	0.73002360	0.53252615	1.00000000	-0.33973707	-0.2458744	-0.06668496	NA	NA	1.00000000
mass	-0.40703663	-0.05869164	-0.33973707	1.00000000	0.7963975	0.26241598	NA	NA	-0.33973707
trab	-0.26480309	-0.10223923	-0.24587441	0.79639752	1.0000000	0.18725064	NA	NA	-0.24587441
stren	-0.26416620	0.19173187	-0.06668496	0.26241598	0.1872506	1.00000000	NA	NA	-0.06668496
resorp	NA	NA	NA	NA	NA	NA	1	NA	NA
form	NA	NA	NA	NA	NA	NA	NA	1	NA
unload_dur	0.73002360	0.53252615	1.00000000	-0.33973707	-0.2458744	-0.06668496	NA	NA	1.00000000

Ko (1wk and 2wk)



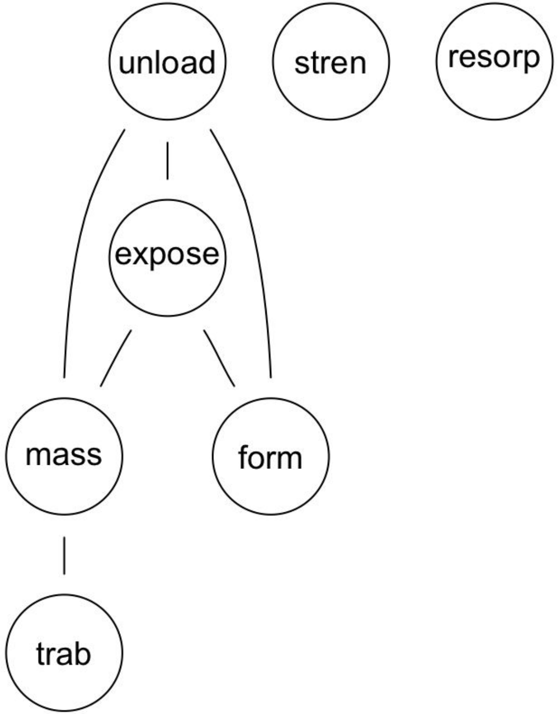




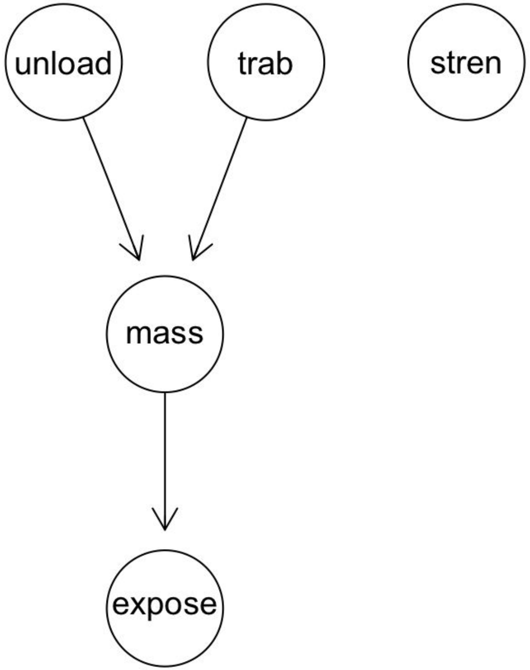


Ko (4wk)

Ko 4wk BN



Ko 4wk DAG, remove resorp and form



Ko 4wk DAG, remove NA rows