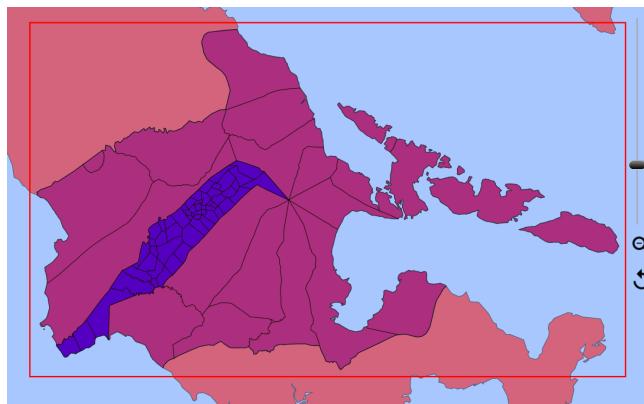
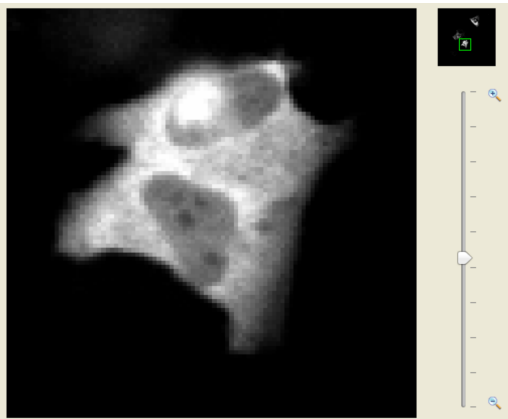
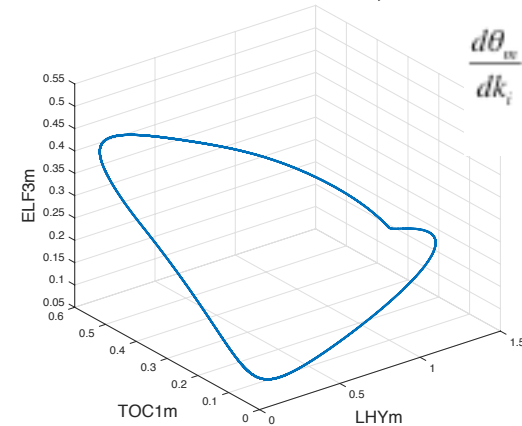


Paul Brown, University of Warwick

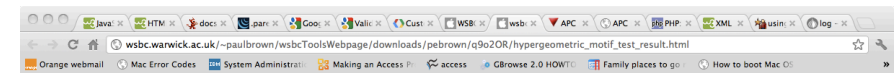
- Background in experimental biology
- ODE models of gene networks
- Image analysis
- Bioinformatics tools
- Infectious disease modeling



ELF3m v TOC1m v LHYm from PlantClock, DiurnalEx



$$\frac{d\theta_{w_i}}{dk_i} = \frac{\sum_{j=1}^{mN} \frac{\partial y_{w_i}}{\partial k_i} \frac{dy_{w_i}}{dt_i} T}{\sum_{j=1}^{mN} \frac{dy_{w_i}}{dt_i} T \frac{dy_{w_i}}{dt_i} T}$$



Hypergeometric Motif Test results

This analysis was run with the following input parameters

Species	Arabidopsis	Promoter maximum length	
Gene list	sample_input_some_clusters.txt	Motif clustering threshold	0.05
Maximum number of binding sites	5	Single promoter threshold	
Use all genes	TRUE	Universe file	
Test for large overlaps	TRUE		

Showing 31/349 weight matrices and 3/3 clusters

		1 52 genes	3 97 genes	2 247 genes
P\$GAMYB_Q1	M00345		0.006526627	
P\$CG1_Q6	M00440			0.000742472
P\$CPHF1_Q1	M00942			0.001551263
P\$P_Q1	M00226			0.004083588
P\$PBF_Q1	M00355		0.001891883	0.001243380
P\$ARF_Q2	M00438			0.00778848
P\$ALF1_Q2	M00479	0.000909495	0.003780809	
P\$ATMYB15_Q1	M00969			0.002046663
P\$ID1_Q1	M01021			0.001476370
P\$BPC1_Q2	M01126			
P\$PBF_Q2	M01130			
P\$DOF_Q2	M01136			
P\$PYRIMIDINEBOXSRMY1A	S-000259			
P\$BOXINTPATPB	S-000296			
P\$EFANTRNR	S-000368			
P\$MARBOX1	S-000083			
P\$MARARS	S-000064			

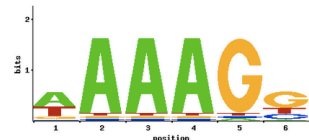
Filter values

Filter and colour-code p-values and visualise the most important by setting the colours and thresholds below

- Set the first p-threshold to the most stringent (lowest) value. Any p-values <= to this will be shown in the selected colour
- Set the other thresholds to increasingly less stringent (higher) values
- The left column displays the logos represented by the corresponding weight matrix, and the top row displays the cluster names plus the number of genes each contains
- Any p-values greater than the highest threshold will not be displayed
- Any weight matrix with no p-value displayed for any cluster will be hidden, eliminating that row
- Likewise, any cluster with no p-value displayed for any weight matrix will be hidden, eliminating that column
- Note that the p-values have not been corrected for multiple testing
- Hover the mouse pointer over a cell to display its contents below the table, or click on row or column headings for more information

p <= 0.0001
p <= 0.001
p <= 0.01

Clear Apply



- Multi dimensional models
- Multiple levels of uncertainty
- Database of outputs
- New set of inputs -> interpolate outputs
- Model too complex to be done analytically
- Can we train a neural network to determine relationship between inputs and outputs?