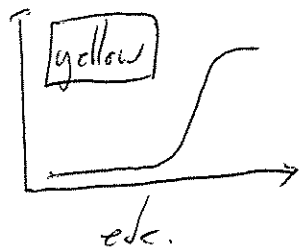
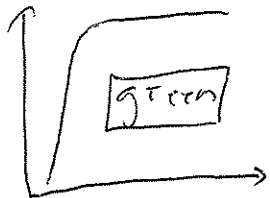
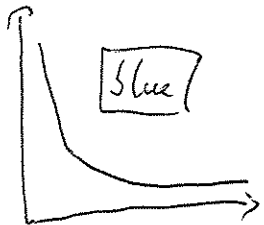
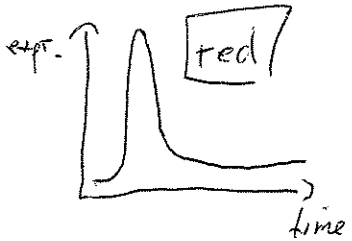


① Expression clustering for whole time-course

code = pattern (for example
from k-means clustering)

$$\left(\begin{matrix} \text{color} \\ \text{saturation} \end{matrix} = \text{strength of} \right. \\ \left. \text{selecting to pattern} \right) ?$$


time-course	I	II	III	IV	- - -
TC/promoter/ gene A	red	red	red	--	no color
B	red	red	red	--	
C	blue	blue	blue	--	
D	--	--	--	--	
:			no color	no color	--
:					
:					
:					
:					
:					
:					
:					

protein-coding
lncRNA
small RNA
rep/demand
orphan
novel

known ERG are
marked in gene name

Layout of the table can be done by clustering algorithm?

② Early response [0h-3h]

A. Gene expression ERG

		time-course	I	II	III	IV	...	
TC/promoter/ gene	A		red	red	..	..		predominating
	B		..	..	-	-		
	C		..	..	-	-		IncRNA
	D		..	..	-	-		

color = "red" consistent with ①

color saturation = "ER-relevance"

small RNA
affected
represents
novel

B. Enhancer expression

		time-course	I	II	III	IV	V	...	regulated gene
enhancer	eA		red?						A, B
	eB								A
	eC								A
	eD								C

color = "red"

color saturation = ER relevance