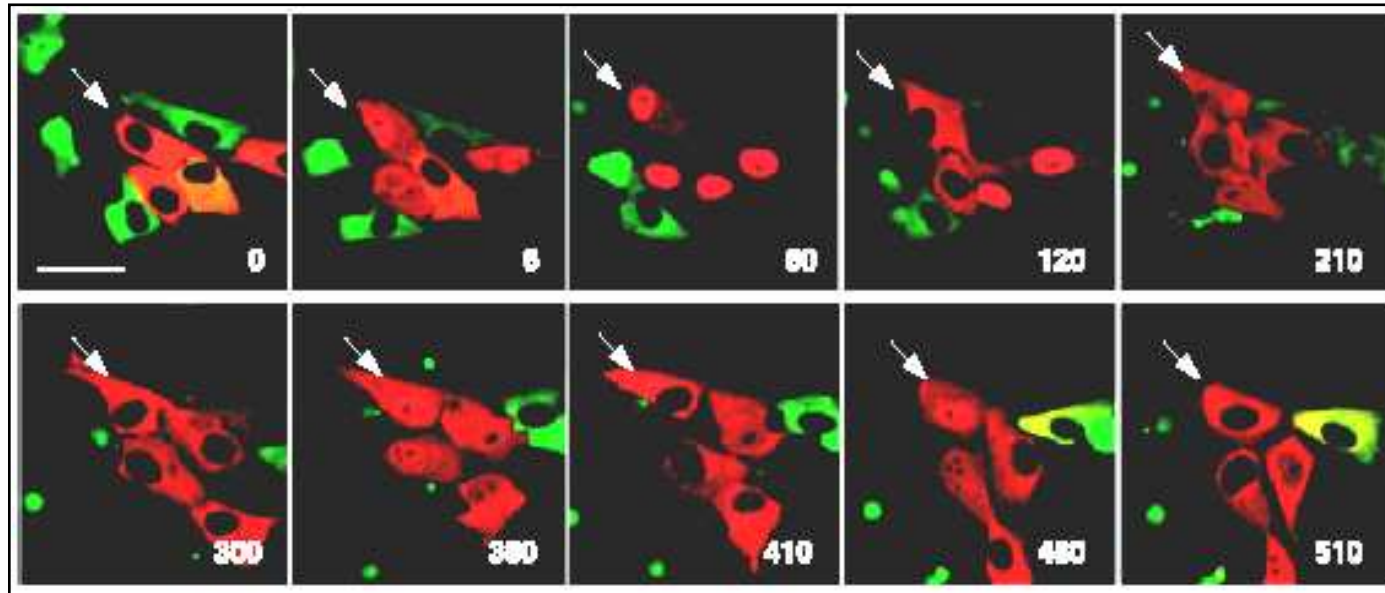


How the number of alleles influences gene expression

Beata Hat
Pawel Paszek
Marek Kimmel
Kazimierz Piechor
Tomasz Lipniacki

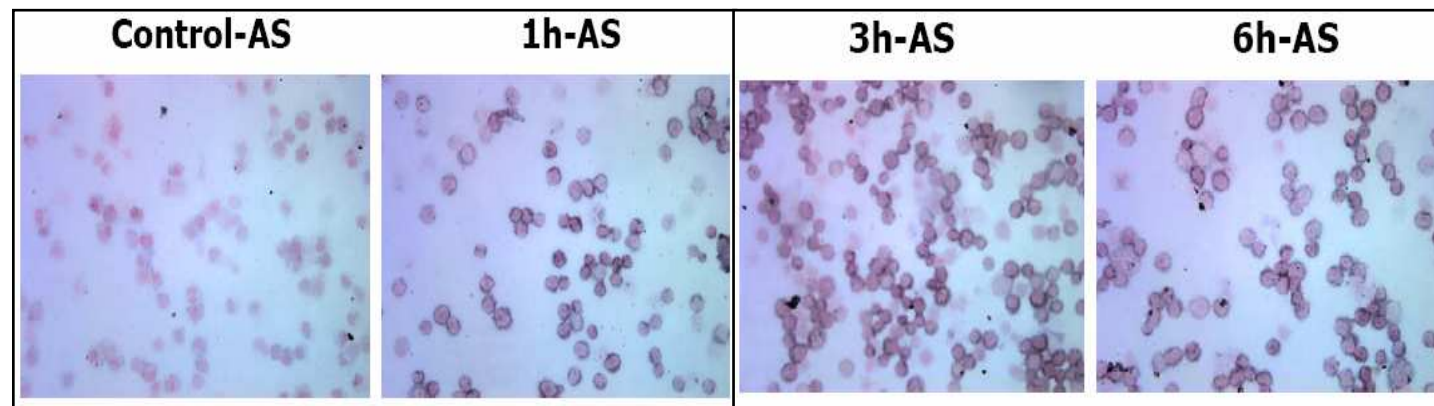
Single cell experiments

Cytoplasm - nucleus oscillations in NF- κ B (red) and I κ B α (green) system after TNF treatment



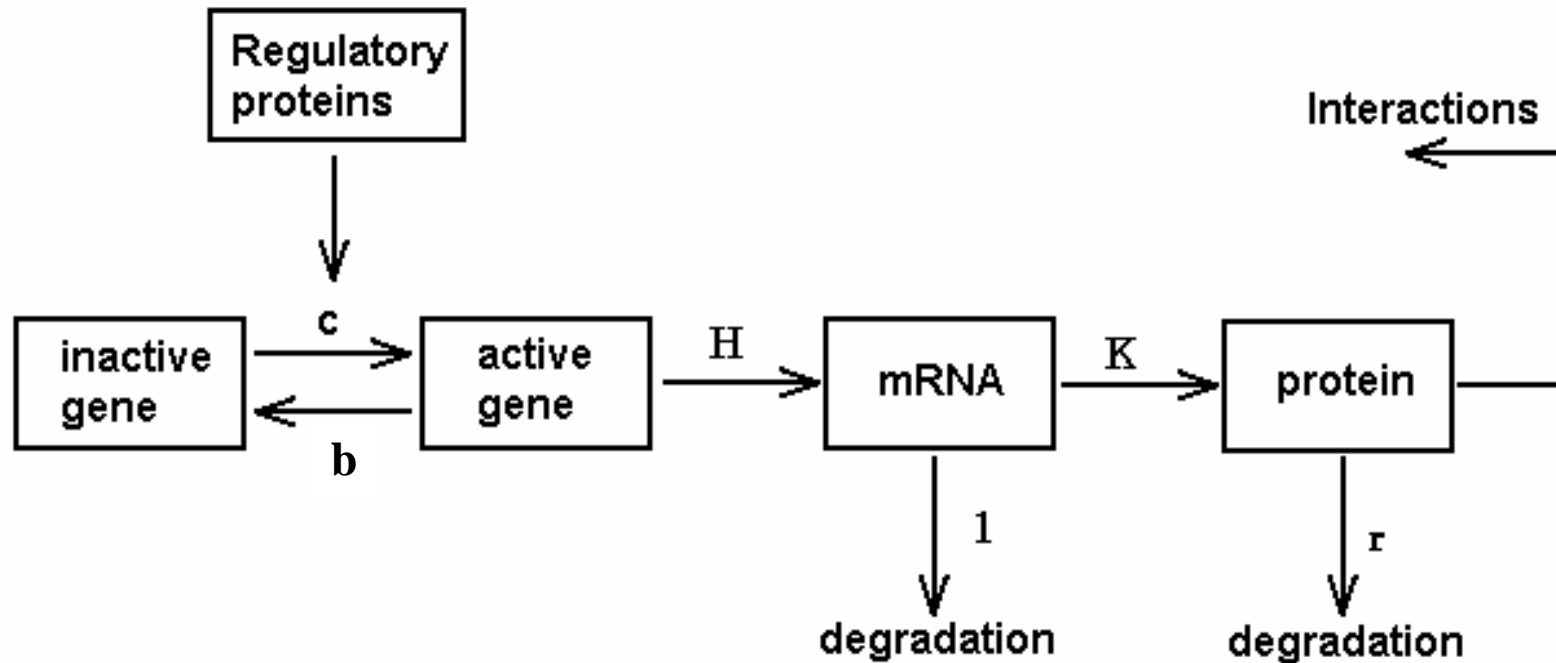
Immortal cancer cell line (SK-N-AS cells), M.R.H. White group

IL8 mRNA level after TNF treatment



Immortal cancer cell line (HeLa cells), A. Brasier group

The main steps in gene expression



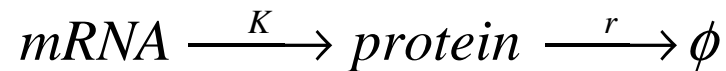
The number of molecules involved:

$$1 \leq DNA \leq mRNA \leq protein \leq 10^6$$

The aim of this work

- How increase in number of gene alleles due to the cancer development or genome duplication in a cell cycle influences its regulation
- How the loss of one allele or its transcriptional inactivity can result in haploinsufficiency disease for autoregulated genes
- To deduce the behavior of „normal” cells from experiments on the transfected cells

A single haploidal gene without feedback regulation



G - gene state

H - transcription rate

K - translation rate

r - protein degradation rate

$$G(\mathbf{I}) = 0, \quad G(\mathbf{A}) = 1$$

Continuous approximation

$$\frac{dx(t)}{dt} = HG(t) - x(t)$$

$$\frac{dy(t)}{dt} = Kx(t) - ry(t)$$

$x(t) :=$ # of mRNA molecules

$y(t) :=$ # of protein molecules

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Probability density functions

$$f = f(x, y, t) = P(\# \text{ of mRNA} = x, \# \text{ of protein} = y, G(t) = 0)$$

$$g = g(x, y, t) = P(\# \text{ of mRNA} = x, \# \text{ of protein} = y, G(t) = 1)$$

The continuity equations for $f(x, y, t)$ and $g(x, y, t)$

$$\frac{\partial f}{\partial t} + \text{div}\left[f\left(\frac{dx}{dt}, \frac{dy}{dt}\right)\Big|_{G=0}\right] = byg - cf$$

$$\frac{\partial g}{\partial t} + \text{div}\left[f\left(\frac{dx}{dt}, \frac{dy}{dt}\right)\Big|_{G=1}\right] = -byg + cf$$

$$\frac{\partial f}{\partial t} - \frac{\partial}{\partial x}(xf) + r \frac{\partial}{\partial y}((Kx - ry)f) = byg - cf$$

$$\frac{\partial g}{\partial t} + \frac{\partial}{\partial x}((H - x)g) + r \frac{\partial}{\partial y}((Kx - ry)g) = -byg + cf$$

Haploidal gene with feedback

- The protein degradation time is much larger than mRNA one (the protein is synthesized directly from the gene and regulates its own expression)



$$\frac{dy(t)}{dt} = G - y(t)$$

$y(t)$ - protein level

$$\frac{dx(t)}{dt} = HG(t) - x(t)$$

$$\frac{dy(t)}{dt} = Kx(t) - ry(t)$$

We have the following continuity equations for $f(y,t)$ and $g(y,t)$

$$\frac{\partial f}{\partial t} + \frac{\partial}{\partial y}(-y \cdot f) = b(y)g - c(y)f$$

$$f(y,t) := \Pr(\text{prot. level} = y, G = 0)$$

$$\frac{\partial g}{\partial t} + \frac{\partial}{\partial y}((1-y) \cdot g) = -b(y)g + c(y)f$$

$$g(y,t) := \Pr(\text{prot. level} = y, G = 1)$$

For $\frac{\partial f}{\partial t} = \frac{\partial g}{\partial t} = 0$ we obtain $f(y) = \exp\left[\int_0^y \left(\frac{b(z)}{1-z} + \frac{c(z)-1}{z}\right) dz\right]$

$$g(y) = \frac{yf(y)}{1-y}$$

Diploidal gene with feedback

$$\frac{d}{dy}(-y \cdot f_0) = b \cdot f_1 - 2c \cdot f_0$$

$$\frac{d}{dy}((1-y) \cdot f_1) = 2c \cdot f_0 - (b+c) \cdot f_1 + 2b \cdot f_2$$

$$\frac{d}{dy}((2-y) \cdot f_2) = c \cdot f_1 - 2b \cdot f_2$$

$$f_0(y) := \Pr(\text{prot. level} = y, G=0)$$

$$f_1(y) := \Pr(\text{prot. level} = y, G=1)$$

$$f_2(y) := \Pr(\text{prot. level} = y, G=2)$$

In the case without feedback

$$(c(y) = c_0 \text{ and } b(y) = b_0)$$

the functions $f_0(y)$, $f_1(y)$, $f_2(y)$

are given by the convolution formulas

$$f_0(y) = \int_{s_1}^{s_2} f(z)f(y-z)dz$$

$$f_1(y) = 2 \int_{s_1}^{s_2} g(z)f(y-z)dz$$

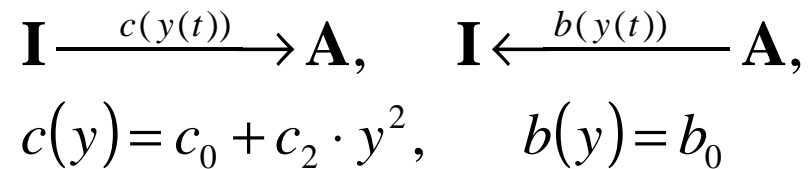
$$f_2(y) = \int_{s_1}^{s_2} g(z)g(y-z)dz$$

where $s_1 = 0$ and $s_2 = y$ for $0 \leq y \leq 1$

$s_1 = y-1$ and $s_2 = 1$ for $1 < y \leq 2$

Positive Feedback

We consider the external induction of self-activating gene

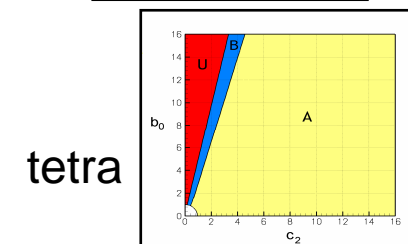
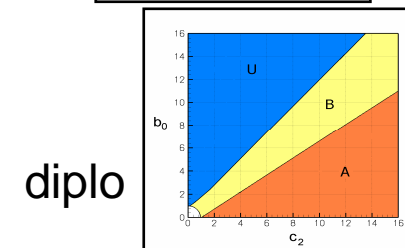
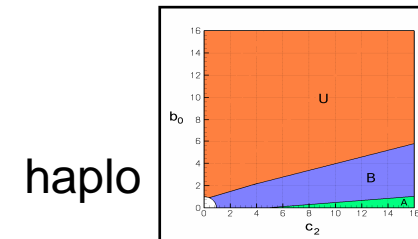


There are three patterns of N - allelic ($N = 1, 2, 4$) gene activation corresponding to different pairs of c_2 and b_0 in (c_2, b_0) - plane

{A} - mode in which gene remains Active
(i.e. $E_0(y) > \frac{1}{2}$) for all c_0

{B} - mode in which gene activates for some c_0
and distribution $\rho(y)$ is transiently Bimodal

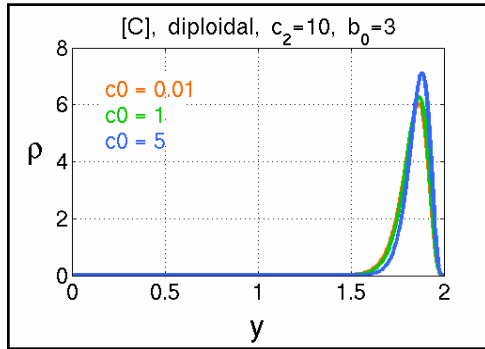
{U} - mode in which gene activates for some c_0
and its distribution $\rho(y)$ remains Unimodal



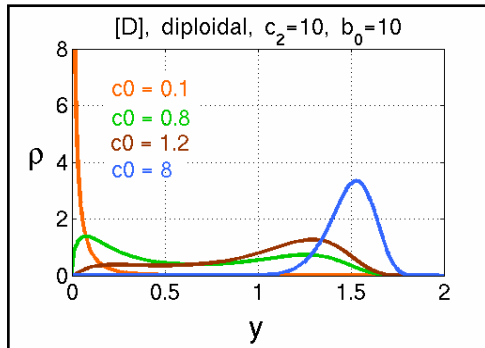
Protein distributions

3 modes of diploidal gene activation

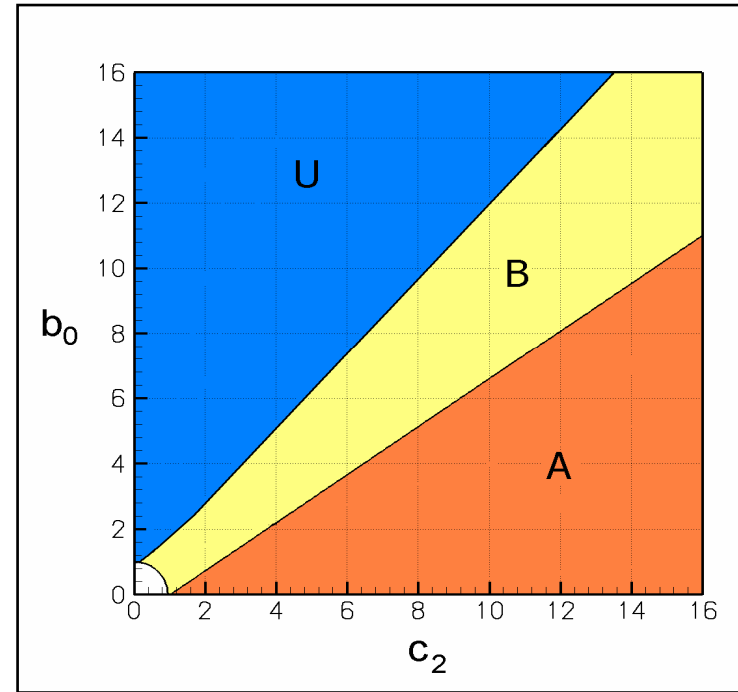
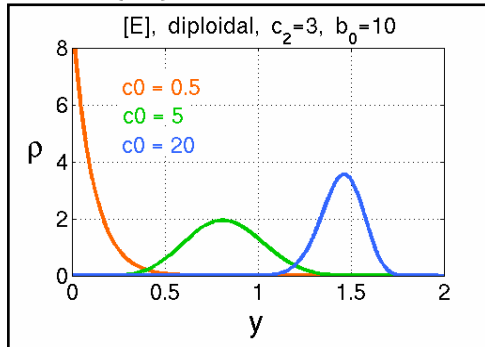
{A} - mode



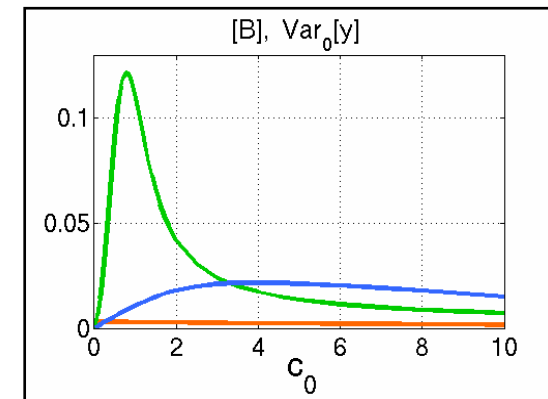
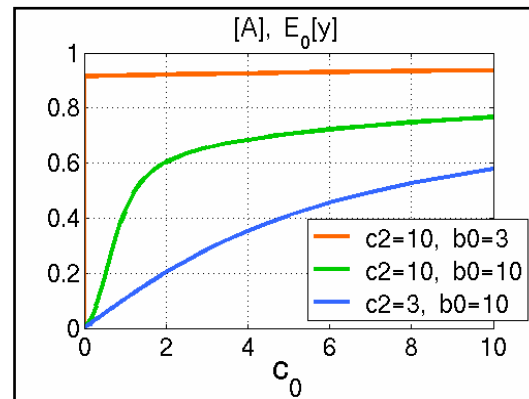
{B} - mode



{U} - mode

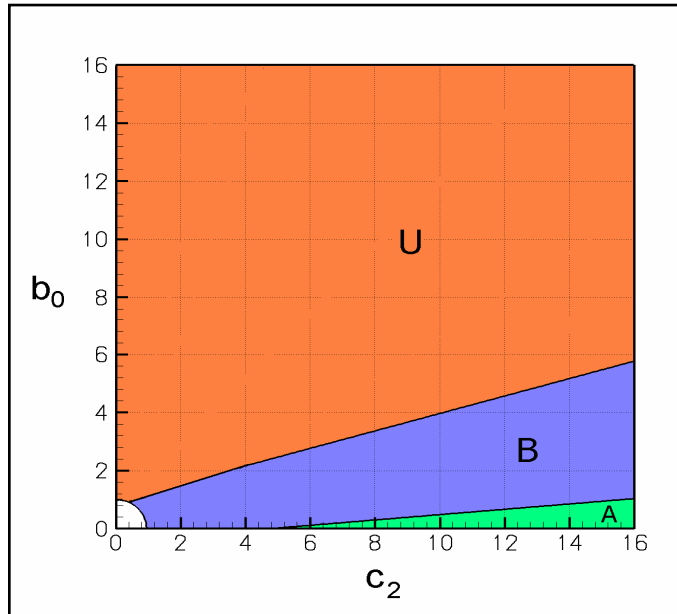


Mean and variance (per gene copy)



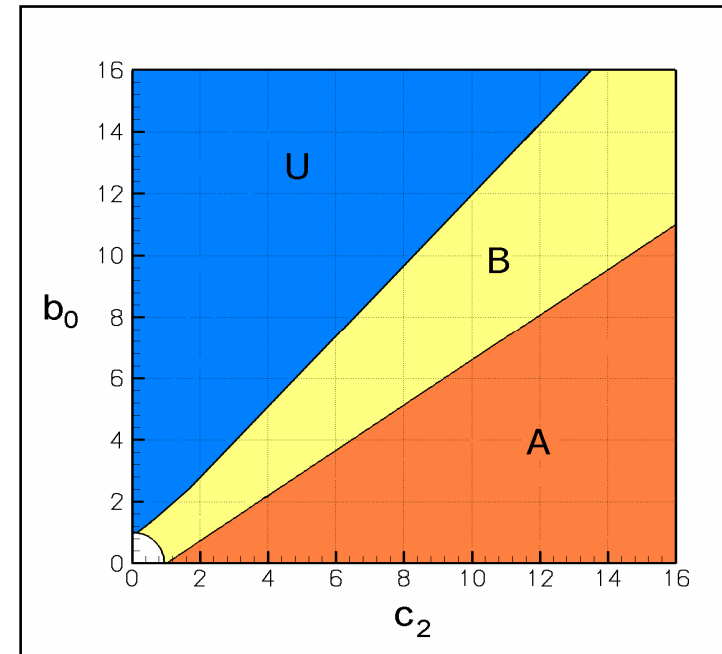
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haploidal gene

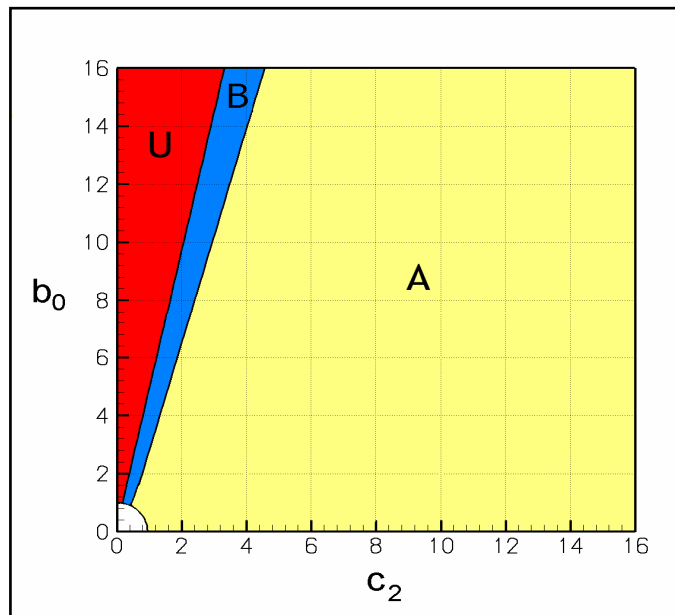


3 regions in (c_2, b_0) - plane corresponding to 3 modes of activation

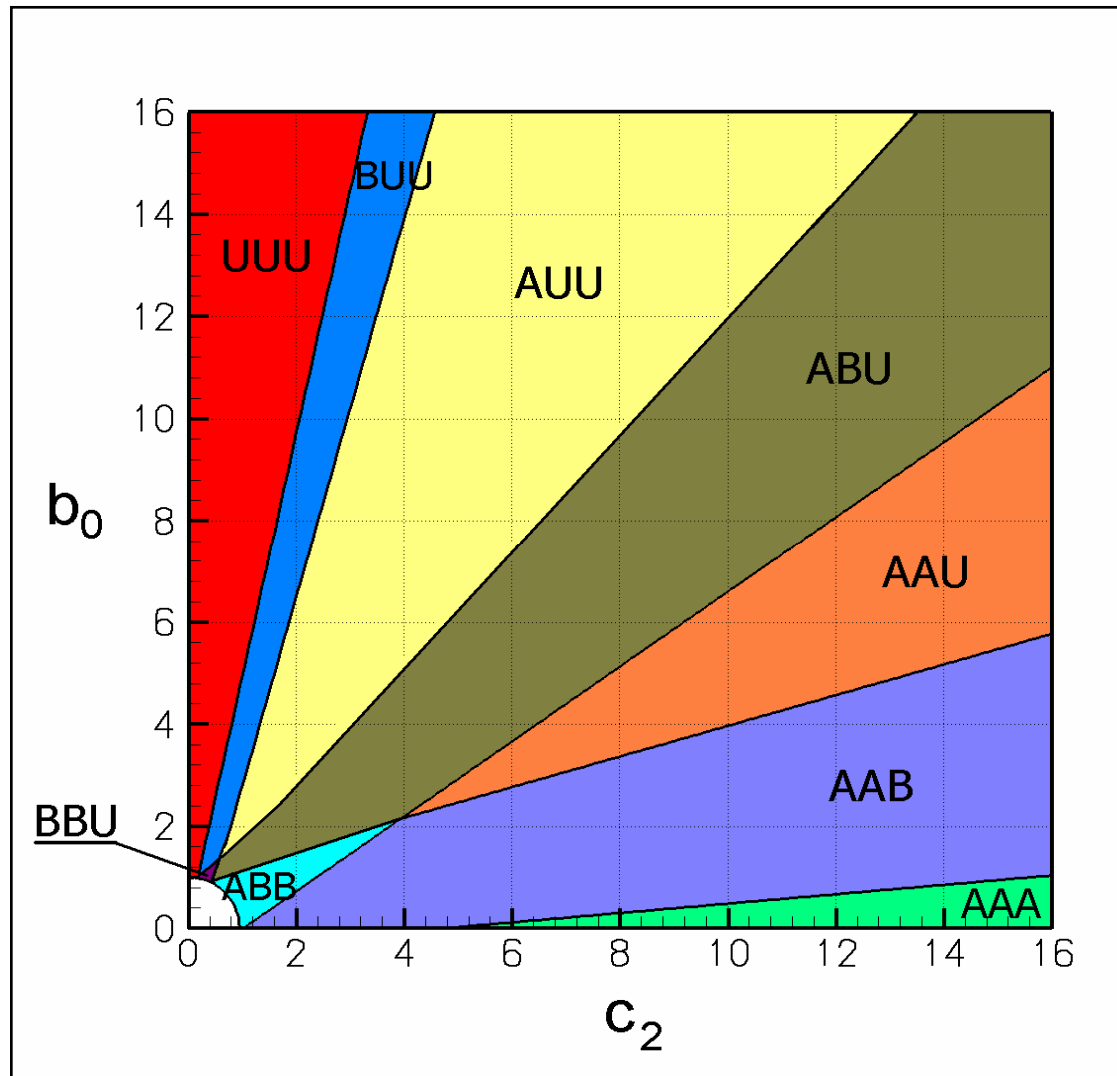
diploidal



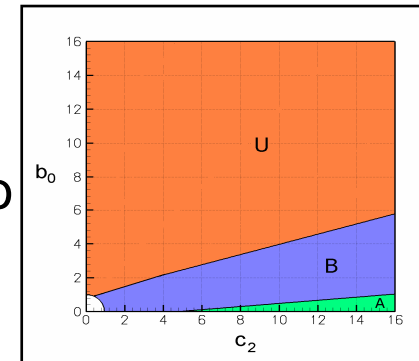
tetraploidal



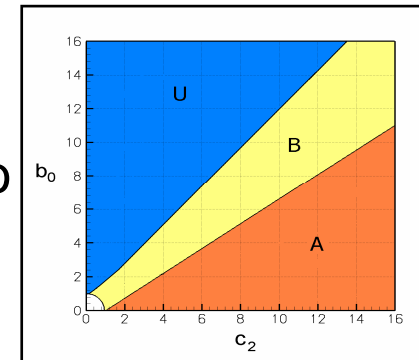
9 possible patterns of 1-,2- and 4-copy-gene-system activation



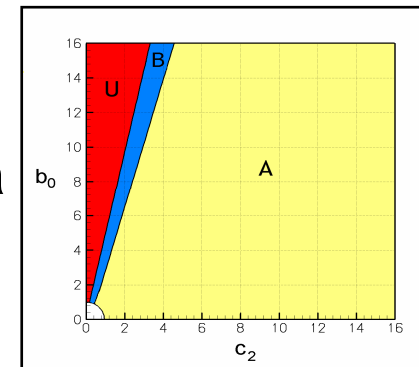
haplo



diplo

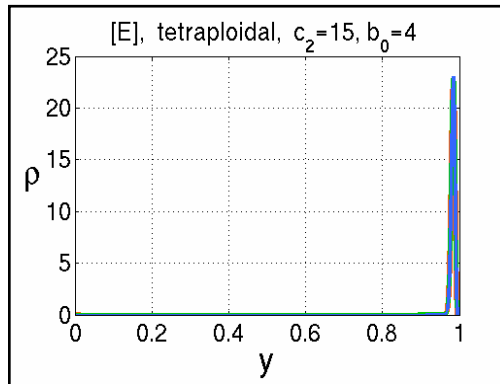
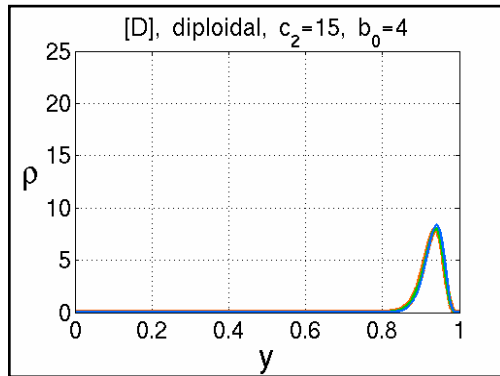
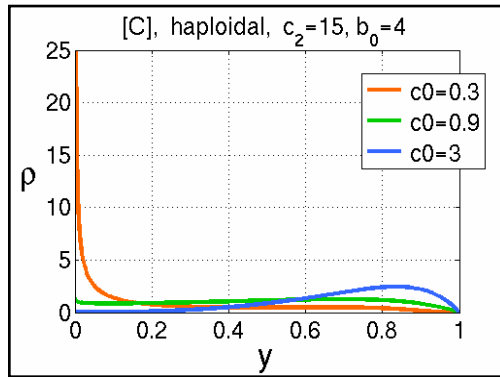
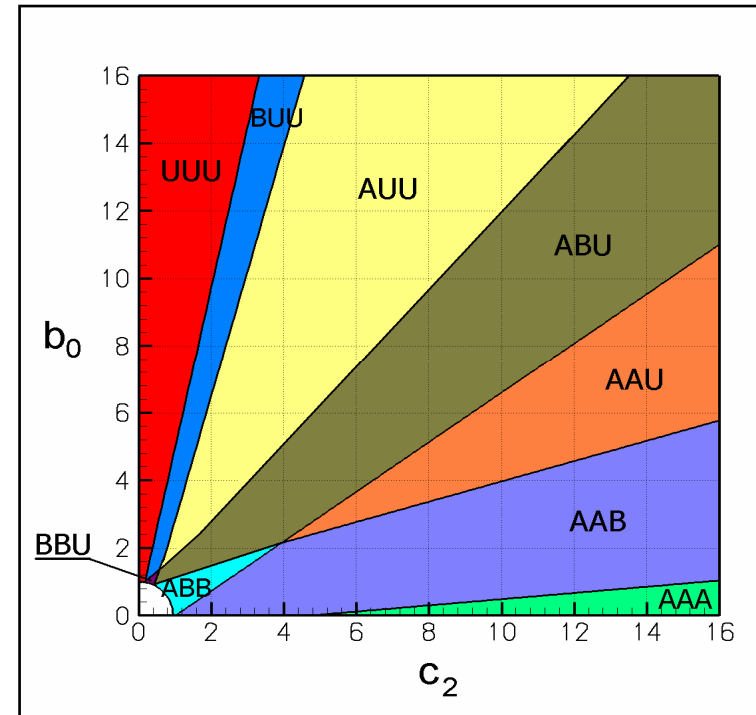


tetra

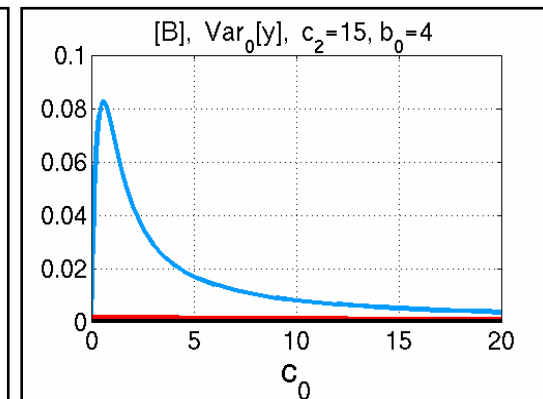
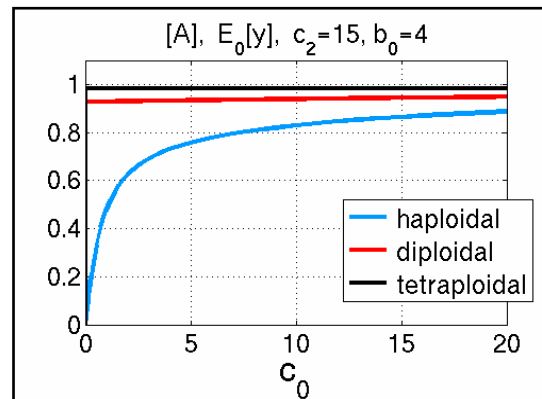


{ABU} sector denotes that tetraploidal gene is in the {A}-mode, diploidal - in the {B}-mode, haploidal - in the {U}-mode

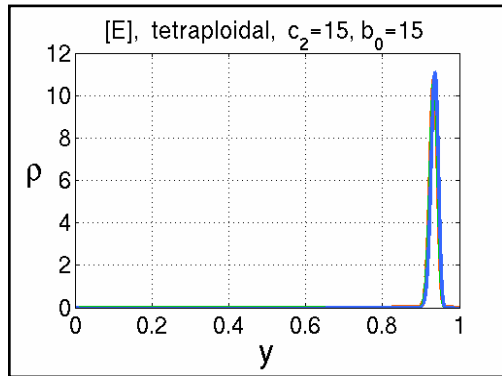
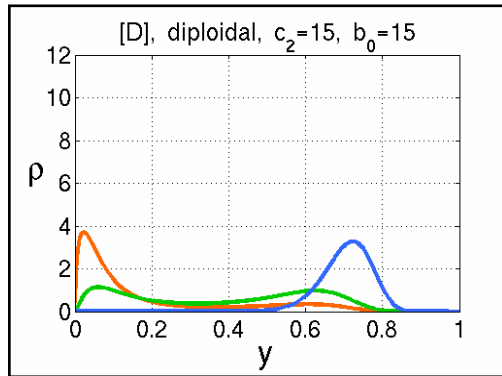
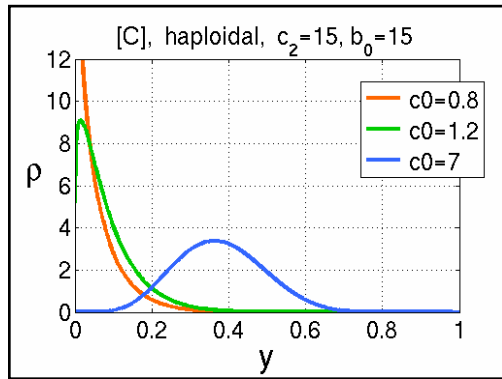
Protein distributions

Mode {AAB}, $c_2 = 15, b_0 = 4$ 

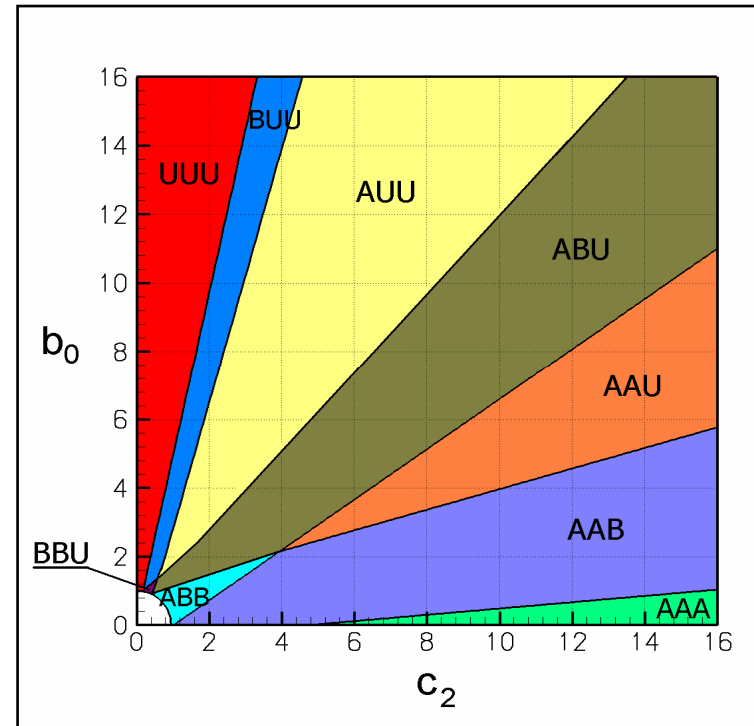
Mean and variance of the protein (per gene copy)



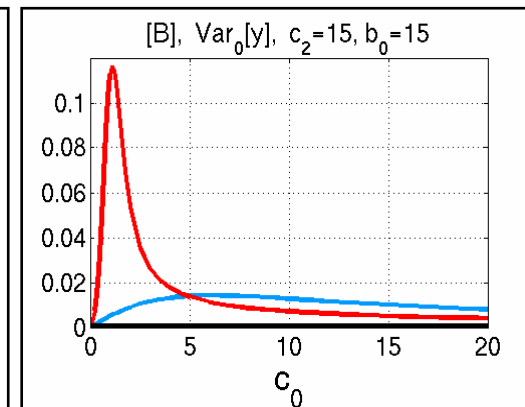
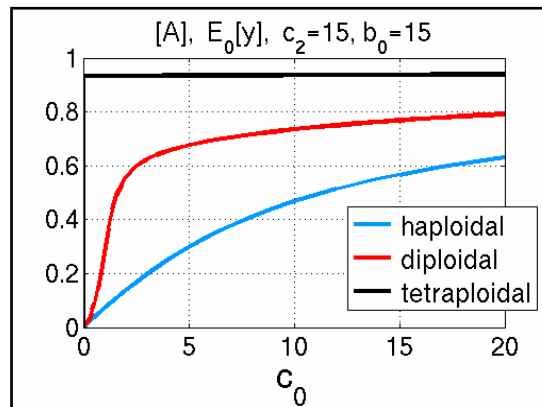
Protein distributions



Mode {ABU}, $c_2 = 15, b_0 = 15$



Mean and variance of the protein (per gene copy)



Take Home Conclusions

Considering the simultaneous activation of a haploid, diploid and tetraploid gene there exist nine modes of gene activation

- allele loss may stop the persistent gene activity and lead to disease if the constant level of gene product is required
- gene duplication may result in a persistent activity and lead to disease when haploid or diploid gene is „designed” to act as a switch