Graphic explanation of response prediction in long-term selection program

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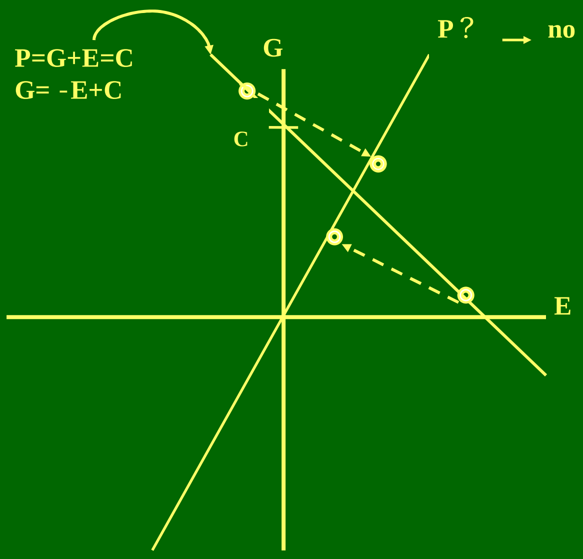
slide No.1



P=G+E=C
G= -E+C

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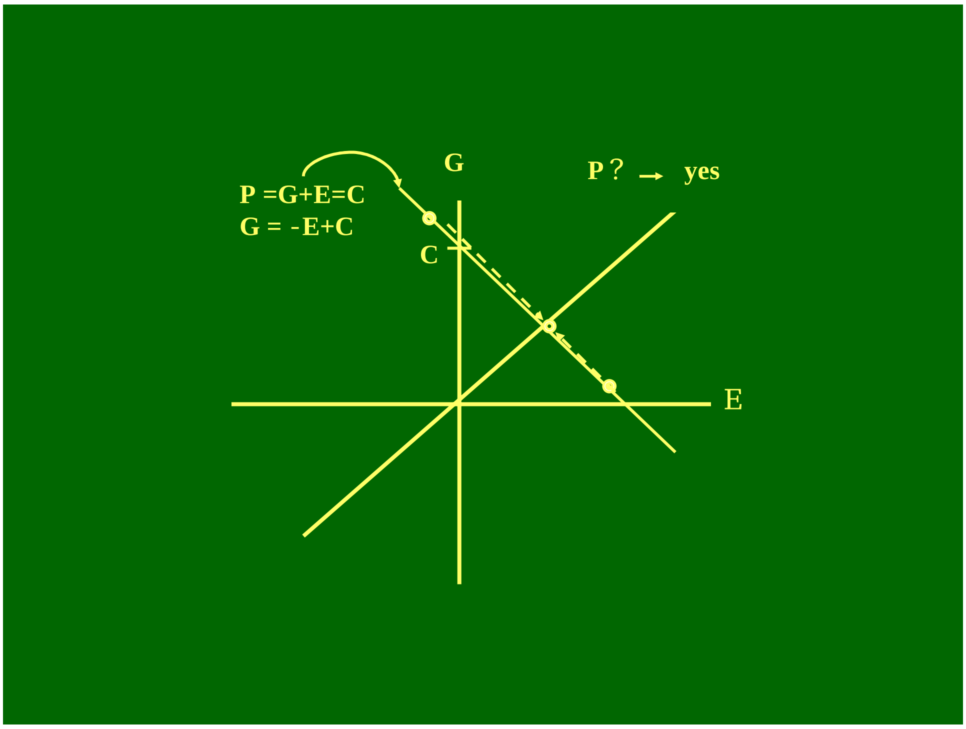

P =G+E=C

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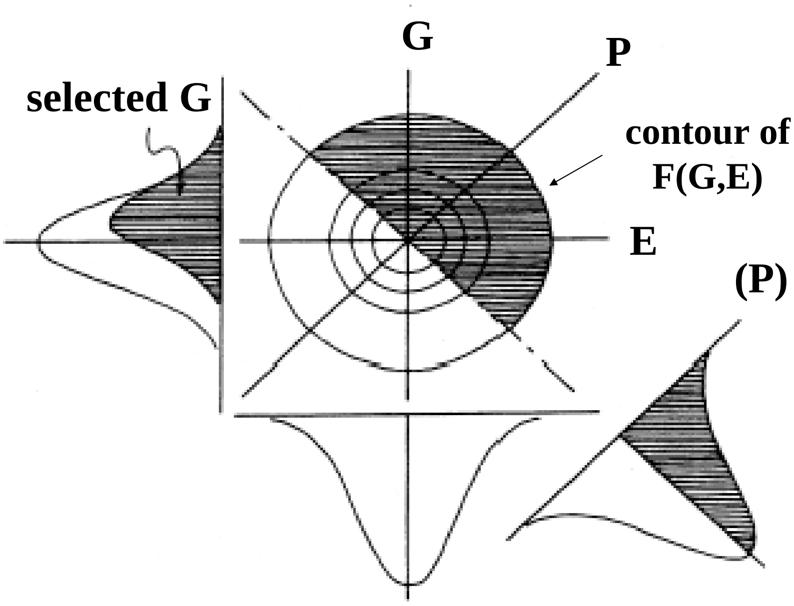
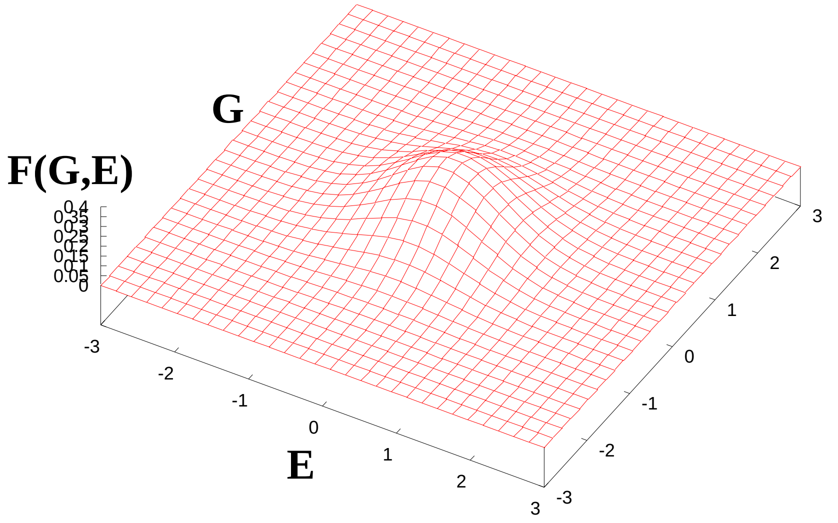
slide No.3



slide No.4

Bivariate normal distribution
Change of view point (Linear h^2=0.5)



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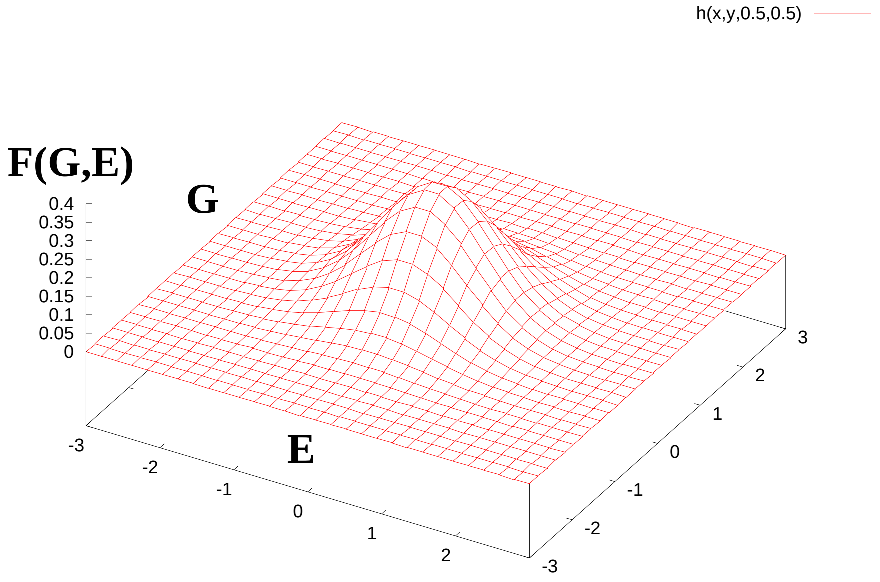

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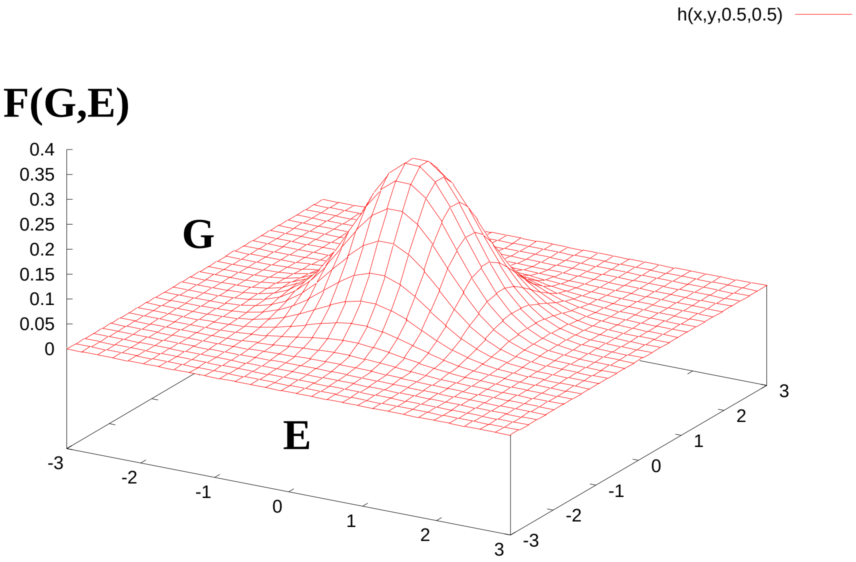

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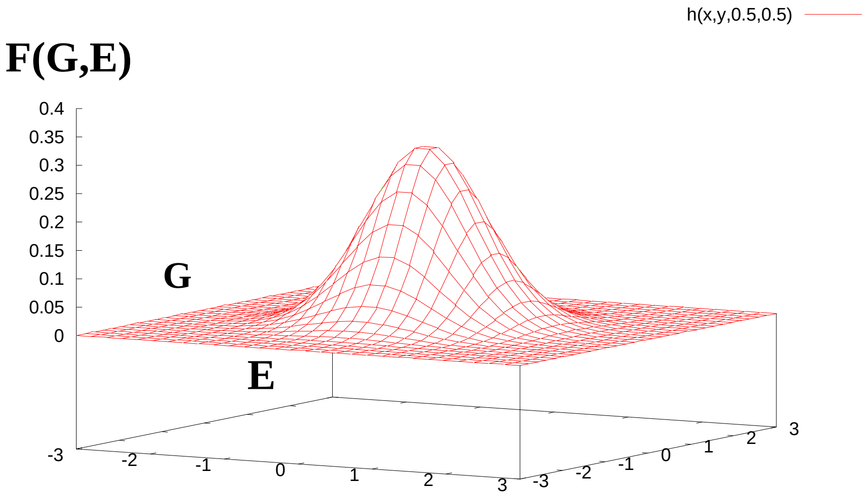

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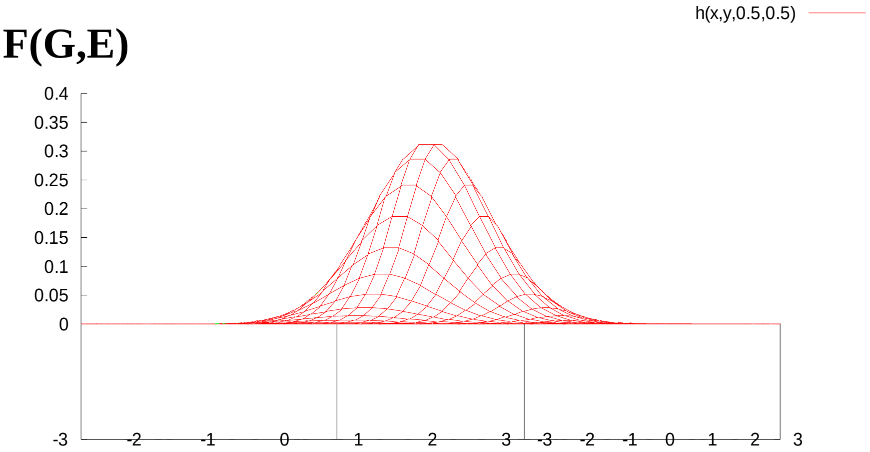
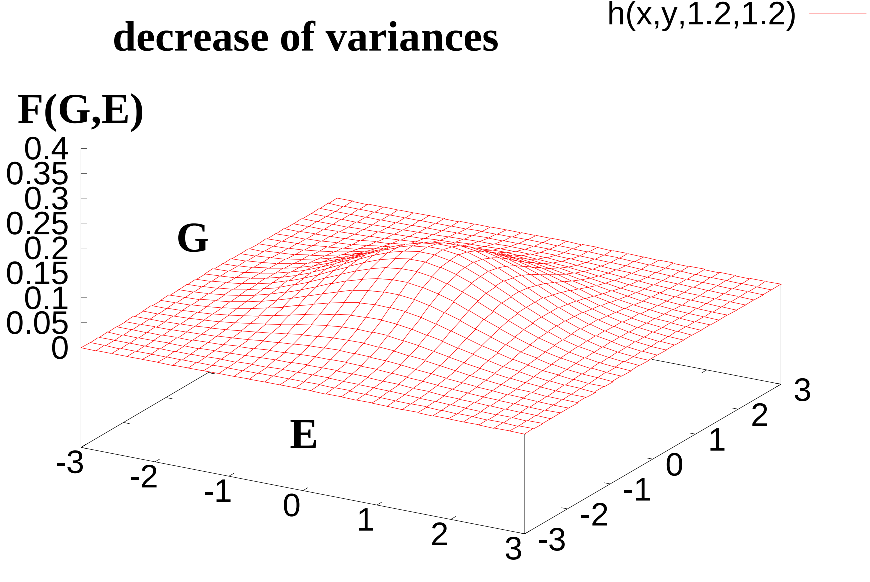


slide No.9

Bivariate normal distribution decrease of variances



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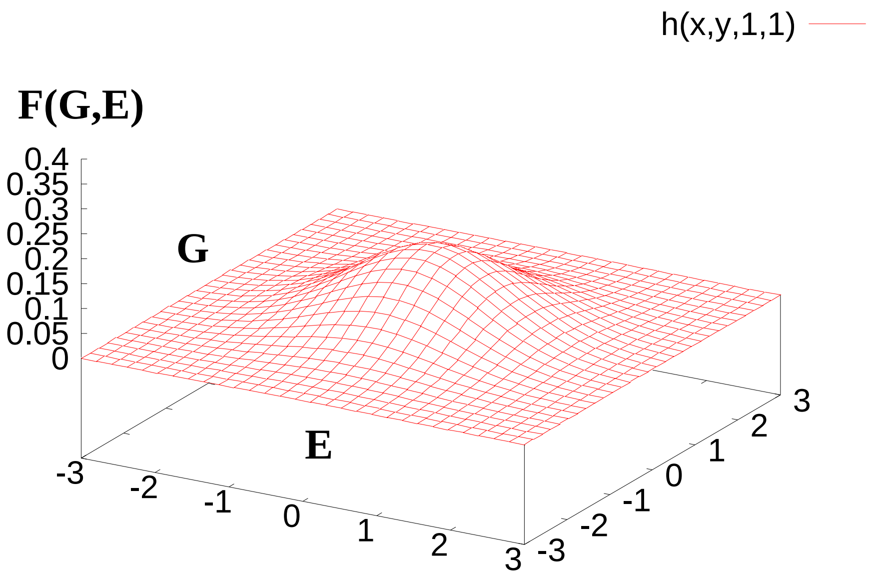

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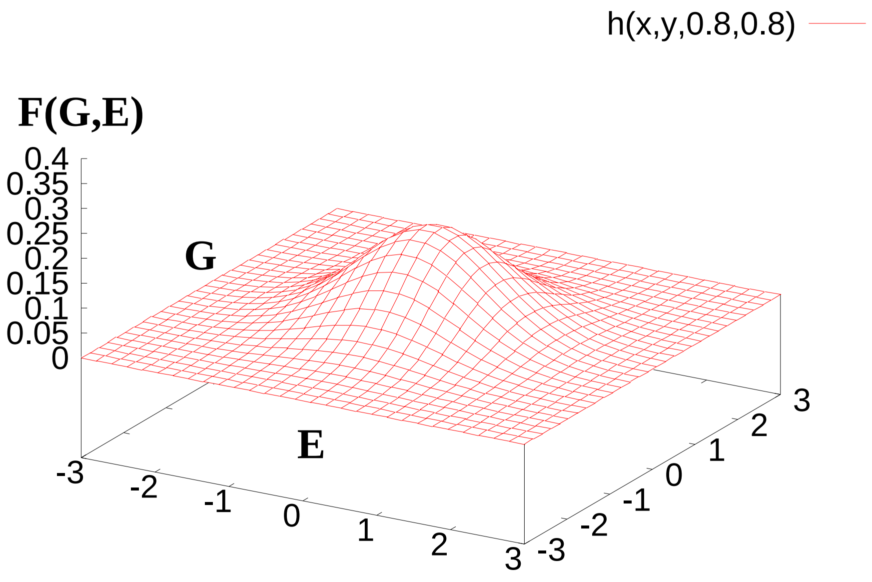

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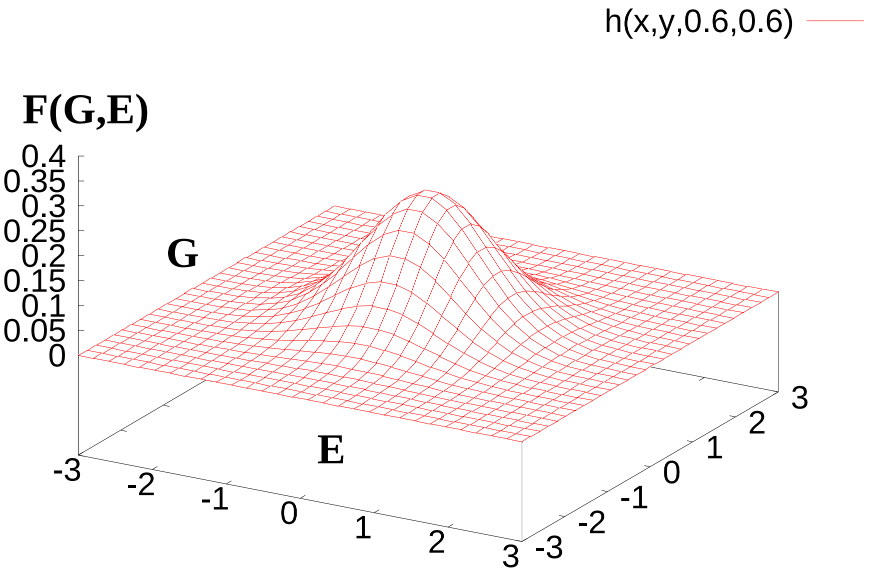

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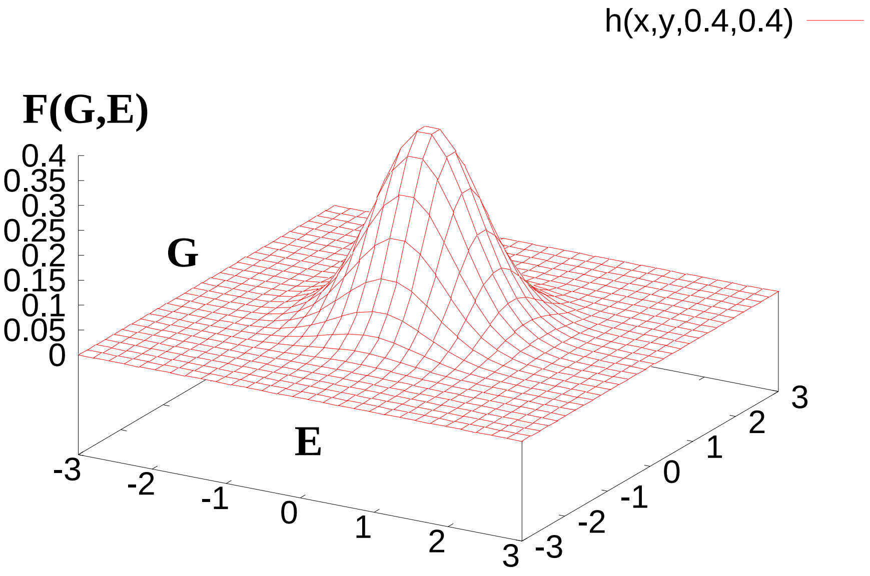

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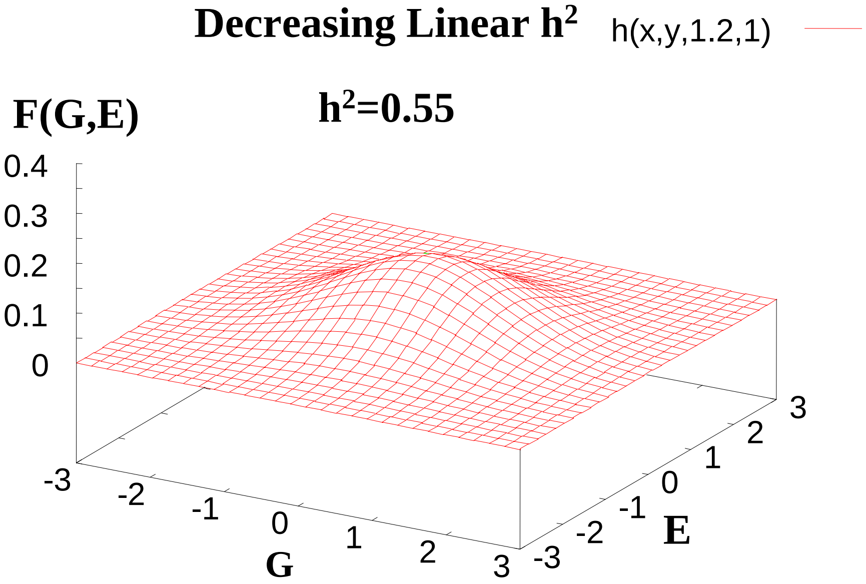
Decreasing Linear h^2



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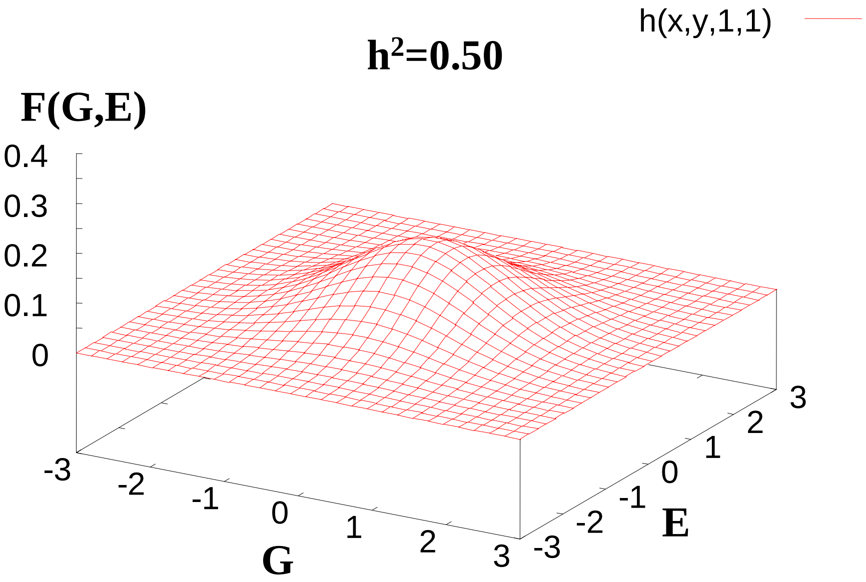

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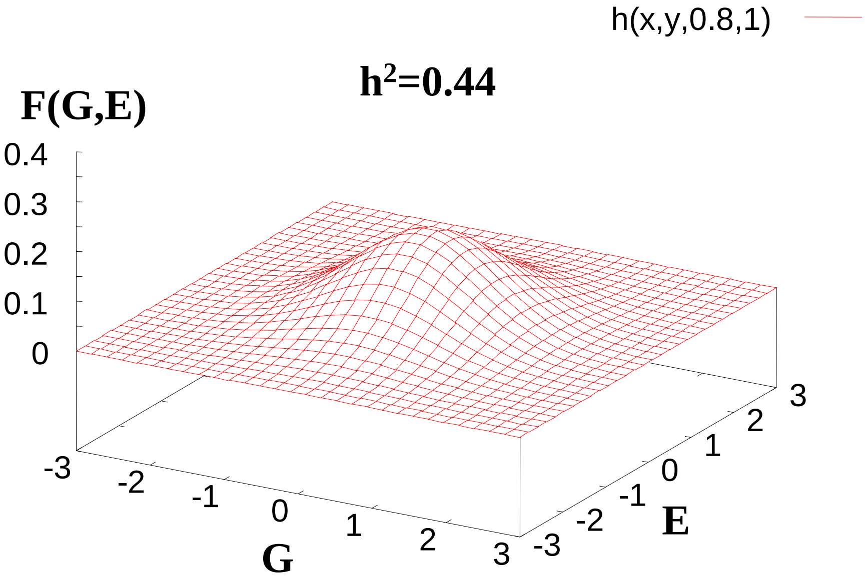

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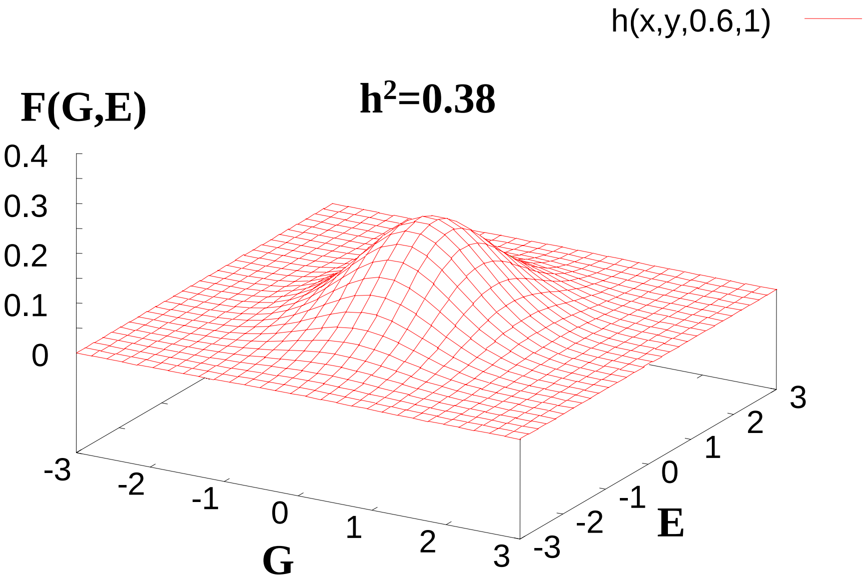

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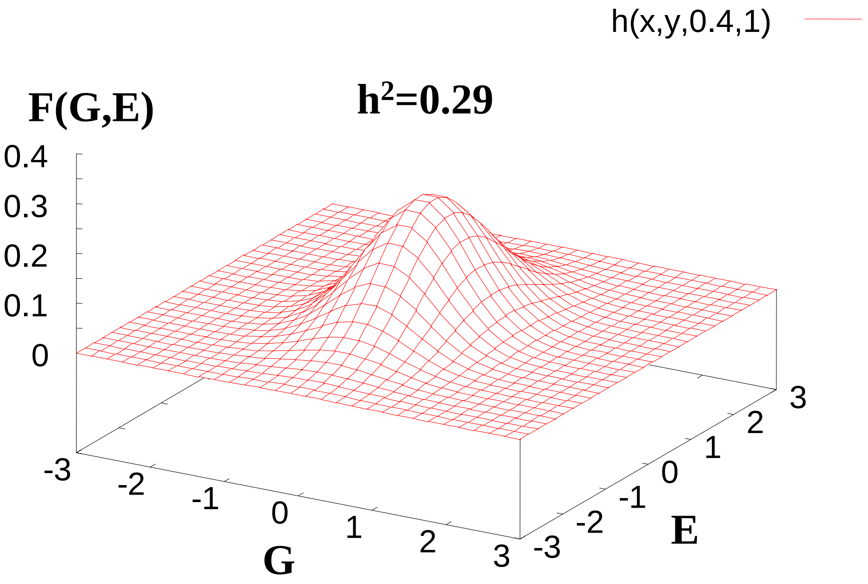

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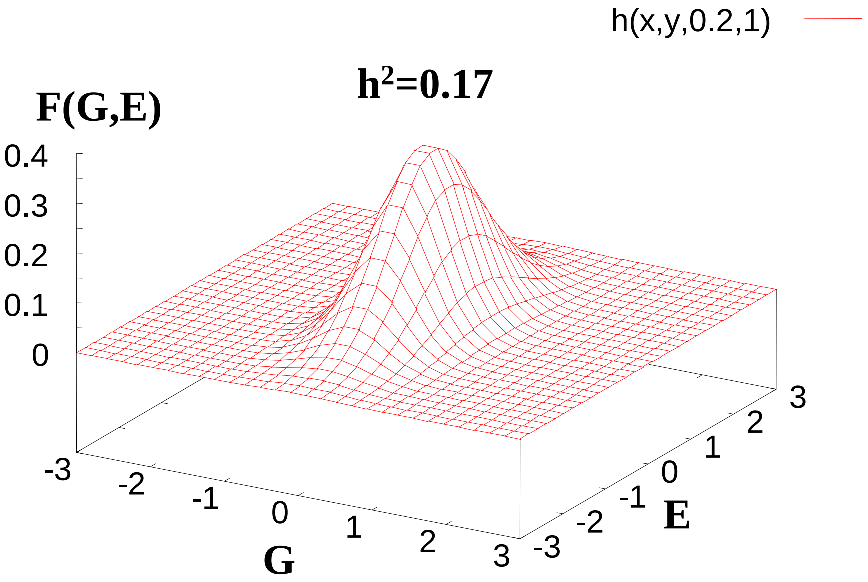
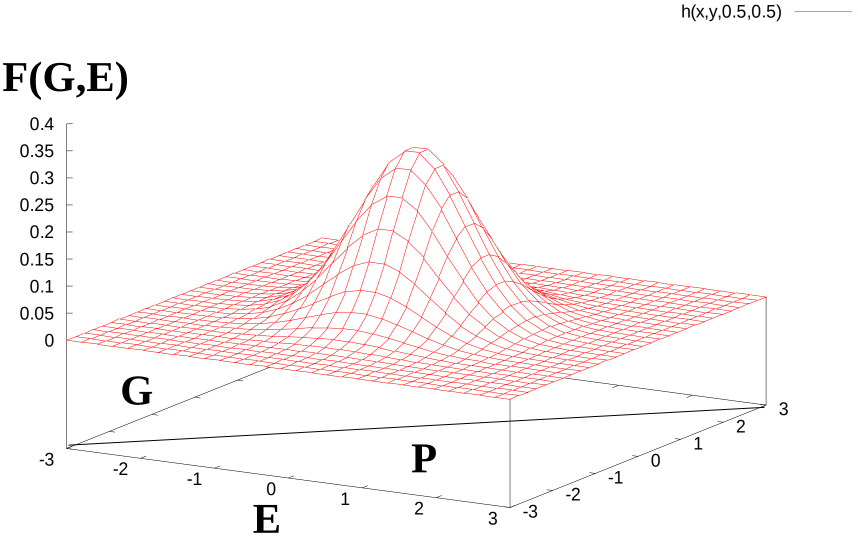


slide No.20

Truncation selection based on P



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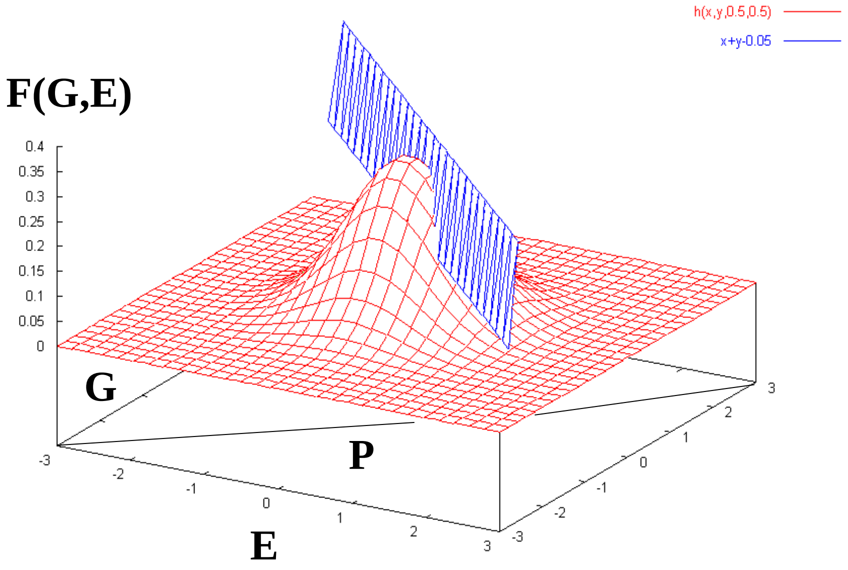

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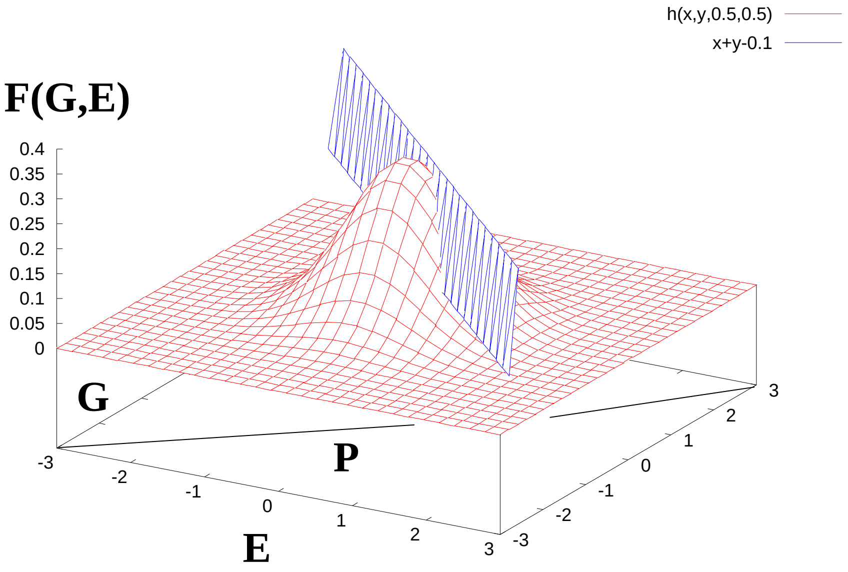

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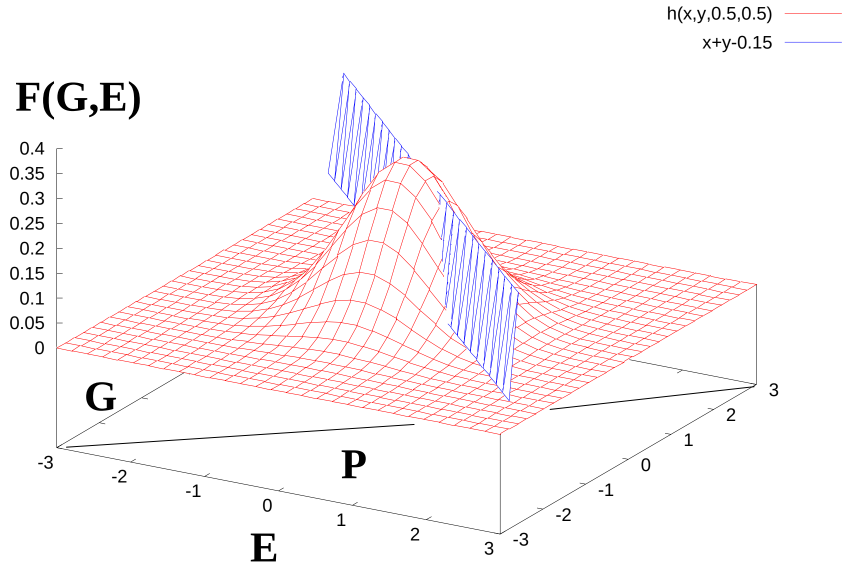

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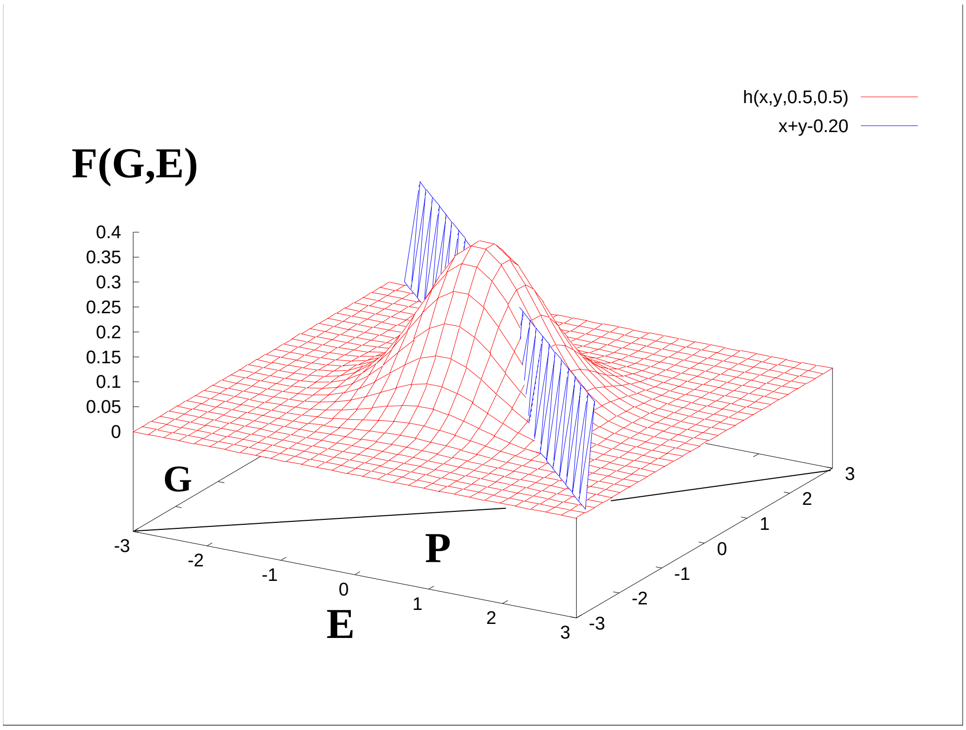

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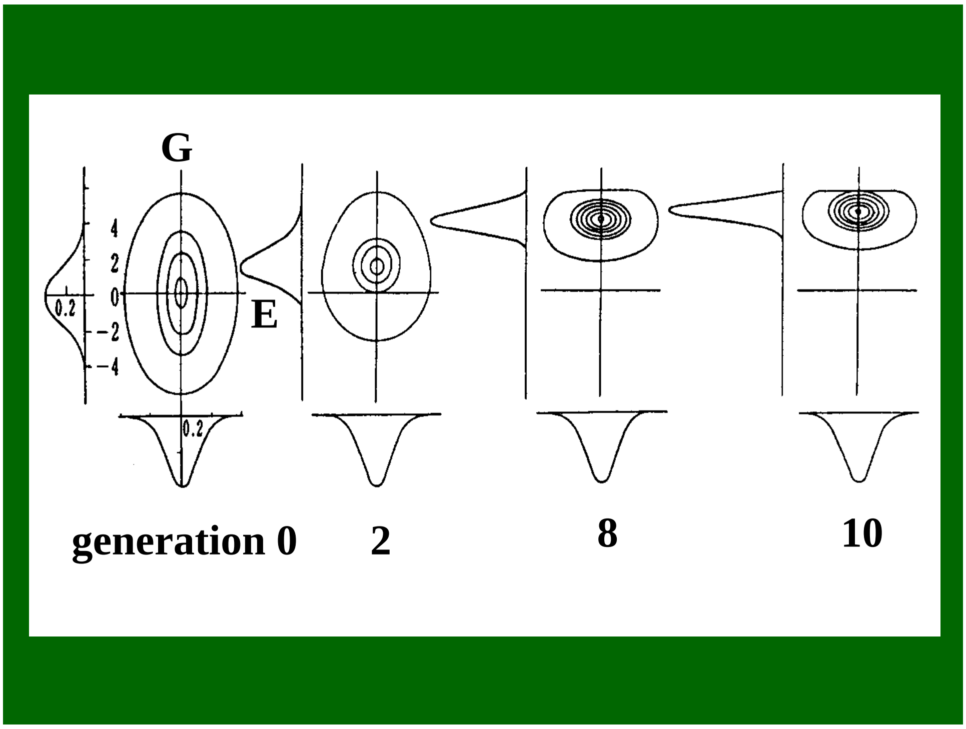

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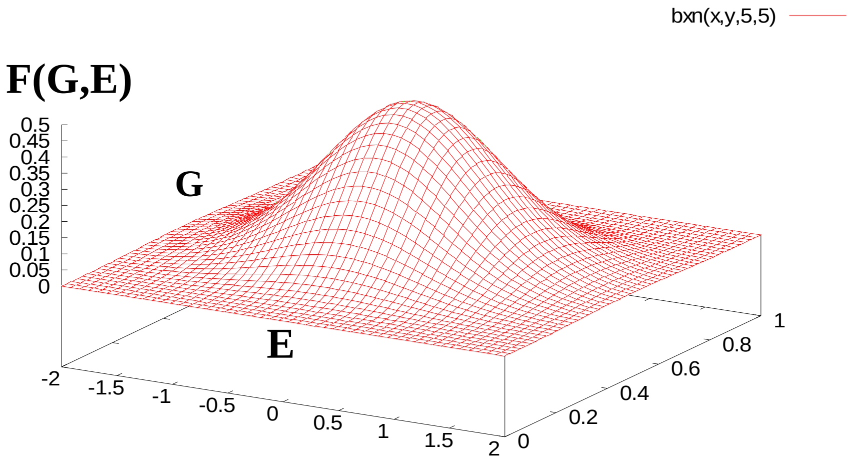
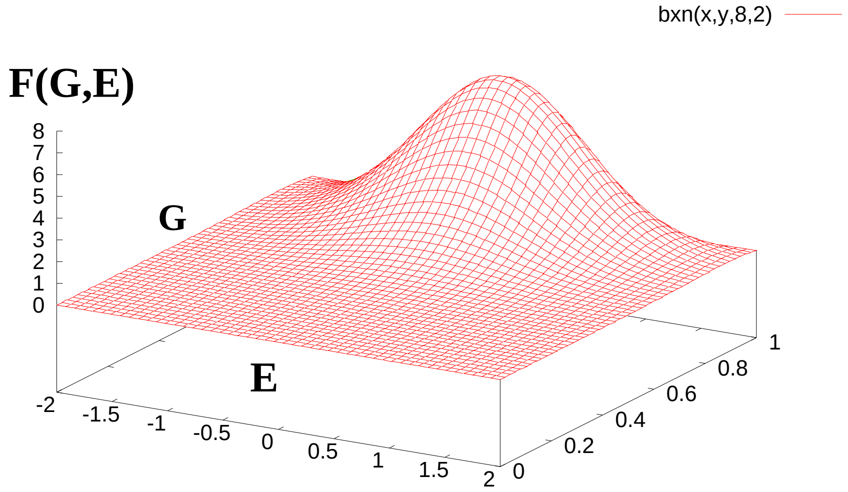


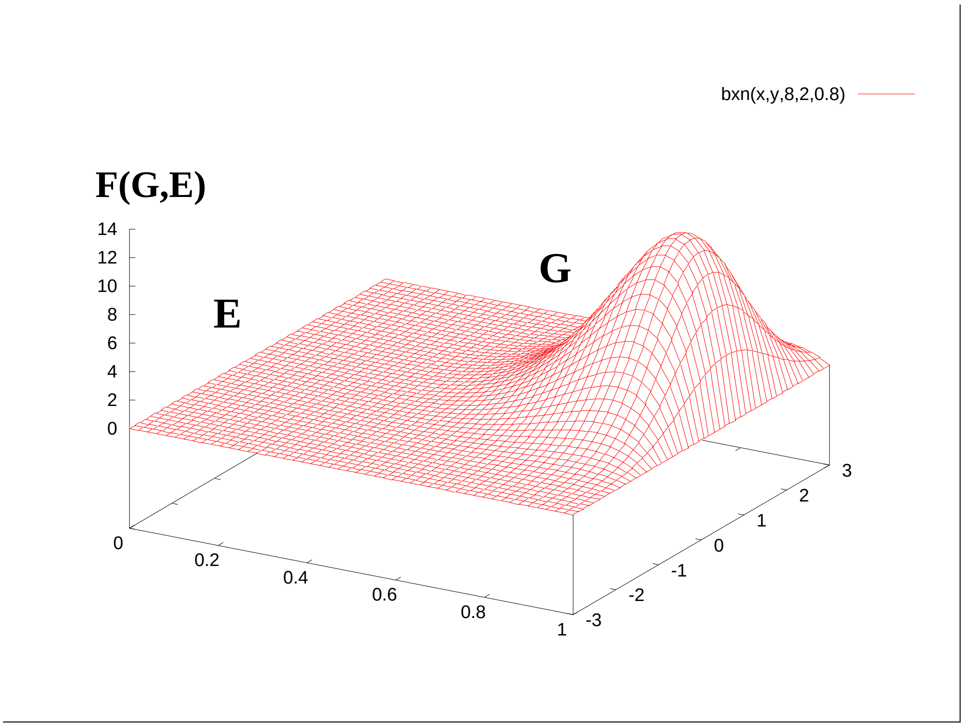
BASE POPULATION

slide No.27



GENERATION 10

slide No.28



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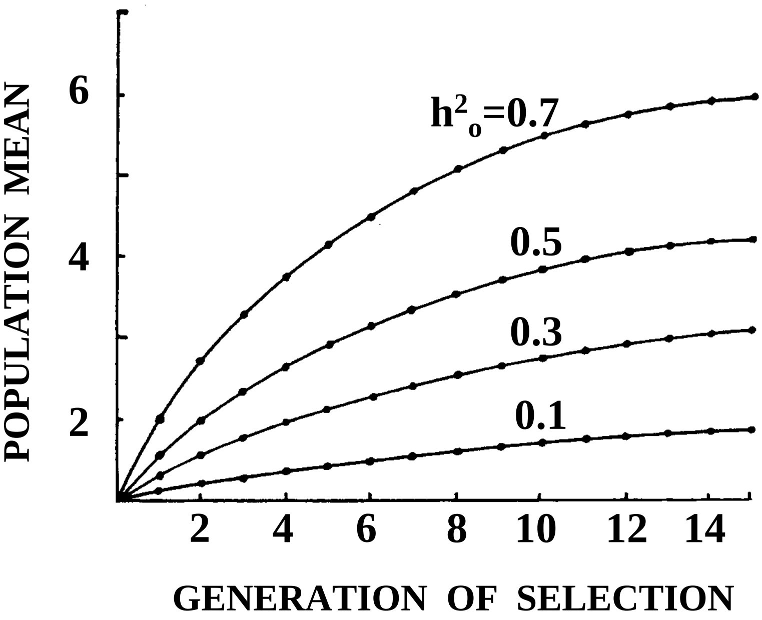

slide No.30

SLIDE No.1 Title

SLIDE No.2

On a rectangular coordinate system defined by the axis of breeding value G and environmental effect E, we draw a graph of phenotypic value P=G+E=a constant value C to find where the axis of P is. Since G+E=C means G = -E+C, the graph of P=C is like this. The intersection with G axis is C and this angle is 45 degrees. If we draw a line which intersects with the graph of P=C not at right angles, the projections of all the points on the P=C on this line are on different points with each other. If this is the P axis, all the points on P=C should be projected at one point. So this is not the P axis.

SLIDE No.3

If we draw a line that intersects with P=C at right angles, all the points on P=C are projected at one point on this line. As a result, this line only is the P axis. It is clear that the P axis passes through the origin because when G and E are both zero, P also is zero.

SLIDE No.4

On the coordinate system, these are the contour lines of the bivariate distribution of G and E, and here is the peak. Truncation selection based on P means to take a part of bivariate distribution of G and E cut by the plane which stands perpendicularly on the GE surface. And the projection of the selected part to the G axis gives us the marginal distribution of G for the selected part.

SLIDE No.5 to No.9

In the previous slide, I presented the graph in three dimensional space on a two dimensional plane using contours of the bivariate distribution. Now let us take a bird’s eye view of the graph. This is a bivariate normal distribution of G and E. The following slides are the view of this graph from points getting lower.

SLIDE No.10 to No.14

This is also bivariate distribution of G and E.

The following slides show the decrease of genetic and environmental variance with the same rate.

SLIDE No.15 to 20

Decrease of linear heritability is illustrated in the following slides. In this graph, G axis is here and E axis is here.

Heritability is 0.55 in this graph, and 0.50, 0.44, 0.38, 0.29 and 0.17. The genetic variance is relatively smaller than the environmental variance.

SLIDE No.21 to 25

Truncation selection based on P is illustrated in the following slides. This is the P axis.

SLIDE No.26

Now we return once to the two dimensional graph to see the change in bivariate distribution of G and E with increasing generation of selection. These are the

contour lines of the bivariate distribution. At generation two, the distribution of G is predicted to show weak positive skewness, in other words a longer tail to the higher value, which is caused by the truncation of the lower values. And at generation 10 the skewness is inversely negative, with a longer tail to the lower value. Because as the population mean approaches the selection limit, the tail to the higher value is crashed by the selection pressure and relatively longer tail remains to the lower direction.

Once the distribution of G is skewed, the relationships between G and E, and G and P are not linear anymore.

Strictly speaking, it is impossible to describe the genetic characteristics of the population by using linear regression and simple correlation. We have to use curvilinear relationships instead.

SLIDE No.27

Returning to a bird's eye view again, this is the

bivariate distribution of G and E at generation zero,

SLIDE No.28

and this is generation 10. If we rotate this graph 90 degrees clockwise around this axis,

SLIDE No.29

we can get this graph and see the negative skewness of the distribution of G.

SLIDE No.30

Using this method we can predict curvilinear response to repeated selection. Further this method can be extended to multiple trait selection with selection index or predicted aggregate genotype.