Mendelian dominant model

a=180 bx=0.05 by=0.5 k=2 f=2

— x (L genotype)
— y2 (non−L, hom "slow sex")
— y1 (non−L, het)
— y0 (non−L, hom wildtype)

(65, 0%)

% (y-axis)

T (years) (x-axis)