Model’s compared

Y is the log of the UQ normalized read counts for a particular exonic region, zero values for all three samples in a line/mating status combination are then dropped for that line.

X1 is the effect of line

X2 is the effect of mating status

B signifies a fixed effect

Z signifies a random effect

Model 1

Y=+ B1X1+B2X2+B3X1X2+ ; ~ N(0,2)

Model 2

Y=+ B1X1+B2X2+B3X1X2+ ; ~ N(0,l2) where a separate variance for each line is fit

Model 3

Y=+ B1X1+B2X2+B3X1X2+ ; ~ N(0,m2) where a separate variance for each mating status is fit

Model 4

Y=+ **Z**1X1+B2X2+B3X1X2+ ; ~ N(0,2) Line as a random effect; hessian is not positive definite

Model 5

Y=+ **Z**1X1+B2X2+B3X1X2+ ; ~ N(0,l2) Line as a random effect ; where a separate variance for each line is fit; hessian is not positive definite

Model 6

Y=+ **Z**1X1+B2X2+B3X1X2+ ; ~ N(0,l2m2) Line as a random effect ; where a separate variance for each line is fit and a separate variance for each mating status is fit; hessian not positive definite

Model 7

Y=+ B1X1+B2X2+B3X1X2+ ; ~ N(0,i2) where a separate variance for each line/mating status combination is fit

Model 8

Y=+ **Z**1X1+B2X2+B3X1X2+ ; ~ N(0,l2i2) Line as a random effect ; where a separate variance for each line/mating status is fit; hessian is not positive definite

Model 9

Y=+ **Z**1X1+B2X2+**Z**3X1X2+ ; ~ N(0,l22) Line and line\*MS interaction as random effects

Model 10

Y=+ **Z**1X1+B2X2+**Z**3X1X2+ ; ~ N(0,l2i2) Line and line\*MS interaction as random effects ; where a separate variance for each line/mating status is fit; G matrix not positive definite